



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 157319

TO: Nita M Minnifield
Location: REM-3C01/3C18
Art Unit: 1645
Thursday, June 30, 2005

Case Serial Number: 08/170344

From: Paul Schulwitz
Location: Biotech-Chem Library
REM-1A65
Phone: 571-272-2527

Paul.schulwitz@uspto.gov

Search Notes

1 of 2

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157319

From: Pak, Michael
Sent: Thursday, June 23, 2005 9:18 AM
To: STIC-Biotech/ChemLib
Cc: Minnifield, Nita
Subject: FW: sequence search approval--08/170344

Dear STIC,

Please search the multiple sequence search set forth below.

Thanks,

Mike Pak

-----Original Message-----

From: Minnifield, Nita
Sent: Wednesday, June 22, 2005 11:17 AM
To: Pak, Michael
Subject: sequence search approval--08/170344

Michael,

08/170344

This case has been ABN since 01/97; however Applicants petitioned to have it revived and of course it was revived. There are 74 short peptide sequences in the claims that it appears I have examined in the past. However, I don't see any sequence search results in the eDAN file. I need a commercial and interference search done. Please approve so I can get this case moved.

STIC

Please do commercial and interference sequence search on SEQ ID NO: 1-75 (all aa sequences) of this application.

Please provide a paper copy of all results.

Thanks,
Minnifield,
71976
Art Unit 1645
Office REM-3C01
Mailbox REM-3C18
571-272-0860

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2-_____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2005, 18:23:48 ; Search time 11.2 Seconds
(without alignments)
77.317 Million cell updates/sec

Title: US-08-170-344-9
Perfect score: 52
Sequence: 1 CVYCKQQLL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	158	1 W6WLS	protein E6 - human
2	45	86.5	149	1 W6WL35	E6 protein - human
3	41	78.8	149	1 W6WL31	E6 protein - human
4	41	78.8	151	1 W6WL51	E6 protein - human
5	41	78.8	153	2 S36503	E6 protein - human
6	41	78.8	155	1 W6WL56	E6 protein - human
7	41	78.8	155	2 A44890	E6 protein - human
8	41	78.8	158	1 W6WLPR	E6 protein - human
9	40	76.9	148	2 S36515	E6 protein - human
10	40	76.9	954	2 S57108	hypothetical prote
11	39	75.0	150	2 S36544	E6 protein - human
12	39	75.0	329	2 T28412	ORF MSV251 hypothe
13	39	75.0	449	2 H88022	protein T27A1.5 [i
14	38	73.1	153	1 S15621	E6 protein - human
15	38	73.1	454	2 A72267	astB/chuk-related
16	37	71.2	291	2 JQ0060	hypothetical 32.7K
17	37	71.2	328	2 E71863	phenylalanine-tRNA
18	37	71.2	328	2 C64570	phenylalanine-tRNA
19	37	71.2	381	1 C64416	conserved hypotet
20	37	71.2	442	2 G72269	astB/chuk-related
21	36	69.2	155	1 W6WL43	E6 protein - human
22	36	69.2	158	2 S36561	E6 protein - human
23	36	69.2	185	2 H90816	hypothetical prote
24	36	69.2	210	2 D85676	unknown protein en
25	36	69.2	274	2 C69444	conserved hypotet
26	36	69.2	343	2 AF1783	polyol dehydrogena
27	36	69.2	400	1 I59360	homeotic protein 1
28	36	69.2	456	2 AE0521	aromatic amino aci
29	36	69.2	457	1 QRECAA	aromatic amino aci

ALIGNMENTS

RESULT 1

W6WLS

protein E6 - human papillomavirus type 16

C;Species: human papillomavirus type 16

C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C;Accession: A03682; T10427

R;Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virolgy 145, 181-185, 1985

A;Title: Human papillomavirus type 16 DNA sequence.

A;Reference number: A22355; MUID:85246220; PMID:2990099

A;Accession: A03682

A;Molecule type: DNA

A;Residues: 1-158 <SEE>

A;Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333033

R;Kennedy, I.M.; Hadow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A;Title: A negative element in the human poapillomavirus type 16 genome acts at the lev

A;Reference number: Z17014; MUID:91162763; PMID:1848319

A;Accession: T10427

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-158 <KEN>

A;Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

C;Genetics:

A;Gene: E6

C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; zinc finger

F;37-73/Region: zinc finger CCCC motif

F;110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 52; DB 1; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.095; 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0;

QY 1 CVYCKQQLL 9

|||||

Db 37 CVYCKQQLL 45

RESULT 2

W6WL35

E6 protein - human papillomavirus type 35

C;Species: human papillomavirus type 35

A;Note: Host Homo sapiens (man)

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C;Accession: E40824; S36521

R;Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.

Virolgy 186, 770-776, 1992

A;Title: The phylogenetic relationship and complete nucleotide sequence of human papill

A;Reference number: A40824; MUID:92124753; PMID:1310198

A;Accession: E40824

A;Status: translation not shown

us-08-170-344-9_rpr

A;Molecule type: DNA
A;Residues: 1-149 <MAR>
A;Cross-references: UNIPROT:P27228; GB:M74117; NID:g333050; PIDN:AAA46966.1; PID:g333051
R;DeLius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36521
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-149
A;Cross-references: EMBL:X74477; NID:g396997; PIDN:CAA52561.1; PID:g396998
A;Experimental source: strain 35H
A;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif

Query Match 86.5%; Score 45; DB 1; Length 149;
Best Local Similarity 87.5%; Pred. No. 1.3; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 1;
QY 1 CVYCKQQL 8
|||||:
Db 30 CVYCKQEL 37

RESULT 3
W6WL31
E6 protein - human papillomavirus type 31
C;Species: human papillomavirus type 31
A;Note: host Homo sapiens (man)
R;Goldsbrough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.
Virology 171, 306-311, 1989
A;Title: Nucleotide sequence of human papillomavirus type 31: a Cervical neoplasia-associ

C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: A32444
A;Reference number: A94398; MUID:89299478; PMID:2545036
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-149 <GOL>
A;Cross-references: UNIPROT:P17386; GB:J04353; NID:g333048; PIDN:AAA46950.1; PID:g459916
C;Comment: This protein may be involved in the oncogenic potential of this virus.
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif

Query Match 78.8%; Score 41; DB 1; Length 149;
Best Local Similarity 87.5%; Pred. No. 6.2; Mismatches 0; Indels 1; Gaps 0;
Matches 7; Conservative 0;
QY 1 CVYCKQQL 8
|||||:
Db 30 CVYCKQQL 37

RESULT 4
W6WL51
E6 protein - human papillomavirus type 51
C;Species: human papillomavirus type 51
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: E40415
R;Lungu, O.; Crum, C.P.; Silverstein, S.J.
J. Virol. 65, 4216-4225, 1991
A;Title: Biologic properties and nucleotide sequence analysis of human papillomavirus ty

A;Reference number: A40415; MUID:91303675; PMID:1649326
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-151 <LUN>

A;Cross-references: UNIPROT:P26554; GB:M62877
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif

Query Match 78.8%; Score 41; DB 1; Length 151;
Best Local Similarity 75.0%; Pred. No. 6.3; Mismatches 2; Indels 0; Gaps 0;
Matches 6; Conservative 2;
QY 1 CVYCKQQL 8
|||||:
Db 30 CVYCKQEL 37

RESULT 5

S36503
E6 protein - human papillomavirus type 30
C;Species: human papillomavirus type 30
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36503
R;DeLius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36503
A;Molecule type: DNA
A;Residues: 1-153
A;Cross-references: UNIPROT:P36809; EMBL:X74474; NID:g396973; PIDN:CAA52543.1; PID:g396973
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 78.8%; Score 41; DB 2; Length 153;
Best Local Similarity 75.0%; Pred. No. 6.3; Mismatches 2; Indels 0; Gaps 0;
Matches 6; Conservative 2;
QY 1 CVYCKQQL 8
|||||:
Db 33 CVYCKQEL 40

RESULT 6

W6WL56
E6 protein - human papillomavirus type 56
C;Species: human papillomavirus type 56
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: A33377; S36579
R;Loerincz, A.T.; Quinn, A.P.; Goldsbrough, M.D.; McAllister, P.; Temple, G.F.
J. Gen. Virol. 70, 3099-3104, 1989
A;Title: Human papillomavirus type 56: a new virus detected in cervical cancers.
A;Reference number: A33377; MUID:90063558; PMID:2555440
A;Accession: A33377
A;Molecule type: DNA
A;Residues: 1-155 <LOE>
A;Cross-references: UNIPROT:P24836
R;DeLius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.

A;Reference number: S36469
A;Accession: S36579
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-155
A;Cross-references: EMBL:X74483; NID:g397053; PIDN:CAA52596.1; PID:g397054
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;33-69/Region: zinc finger CCCC motif
F;106-142/Region: zinc finger CCCC motif

Query Match 78.8%; Score 41; DB 1; Length 155;
Best Local Similarity 75.0%; Pred. No. 6.4; Mismatches 2; Indels 0; Gaps 0;
Matches 6; Conservative 2;

Qy 1 CVYCKQQL 8
Db 33 CVYCKKEL 40

RESULT 7
A44890
E6 protein - human papillomavirus type 66
C;Species: human papillomavirus type 66
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C;Accession: A44890
R;Tawheed, A.R.; Beaudenon, S.; Favre, M.; Orth, G.
J. Clin. Microbiol. 29, 2656-2660, 1991
A;Title: Characterization of human papillomavirus type 66 from an invasive carcinoma of
A;Reference number: A44890; MUID:92129556; PMID:1663515
A;Accession: A44890
A;Molecule type: DNA
A;Residues: 1-155 <TAW>
A;Cross-references: UNIPROT:Q80955
A;Note: sequence extracted from NCBI backbone (NCBIN:78637, NCBI:P:78638)
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;33-69/Region: zinc finger CCCC motif
F;106-142/Region: zinc finger CCCC motif

Query Match 78.8%; Score 41; DB 2; Length 155;
Best Local Similarity 75.0%; Pred. No. 6.4;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVYCKQQL 8
Db 33 CVYCKKEL 40

RESULT 8
W6WLP
E6 protein - human papillomavirus type ME180 (provirus)
C;Species: human papillomavirus type ME180
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: C40509
R;Reuter, S.; Delius, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.
J. Virol. 65, 5564-5568, 1991
A;Title: Characterization of a novel human papillomavirus DNA in the cervical carcinoma
A;Reference number: A40509; MUID:91374616; PMID:1716694
A;Accession: C40509
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-158 <REU>
A;Cross-references: UNIPROT:P27962; GB:M73258
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;32-68/Region: zinc finger CCCC motif
F;105-141/Region: zinc finger CCCC motif

Query Match 78.8%; Score 41; DB 1; Length 158;
Best Local Similarity 75.0%; Pred. No. 6.5;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVYCKQQL 8
Db 32 CVYCKRQL 39

RESULT 9
S36515
E6 protein - human papillomavirus type 34
C;Species: human papillomavirus type 34
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36515
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.

A;Reference number: S36469
A;Accession: S36515
A;Molecule type: DNA
A;Residues: 1-148
A;Cross-references: UNIPROT:P36811; EMBL:X74476; NID:G396989; PIDN:CAAS2555.1; PID:G396
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 76.9%; Score 40; DB 2; Length 148;
Best Local Similarity 75.0%; Pred. No. 9.1;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVYCKQQL 8
Db 31 CVYCKRQL 38

RESULT 10
S57108
hypothetical protein YJR089w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein J1880
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
C;Accession: S57108; S71708
R;Manus, V.; Huang, M.E.; Galibert, F.
submitted to the Protein Sequence Database, September 1995
A;Reference number: S57085
A;Accession: S57108
A;Molecule type: DNA
A;Residues: 1-954 <MAN>
A;Cross-references: UNIPROT:P47134; EMBL:Z49589; NID:g1015781; PIDN:CAAS89616.1; PID:g10
R;Huang, M.E.; Manus, V.; Chuat, J.C.; Galibert, F.
Yeast 12, 869-875, 1996
A;Title: Analysis of a 62 kb DNA sequence of chromosome X reveals 36 open reading frame
A;Reference number: S71676; MUID:96437976; PMID:8840504
A;Accession: S71708
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-954 <HUA>
A;Cross-references: EMBL:L47993; NID:g1019675; PIDN:AAB39312.1; PID:g1019708
C;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1995
C;Genetics:
A;Gene: SGD:BIR1
A;Cross-references: SGD:S0003849
A;Map position: 10R

Query Match 76.9%; Score 40; DB 2; Length 954;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CVYCKQQL 8
Db 208 CVYCKQL 215

RESULT 11
S36544
E6 protein - human papillomavirus type 26
C;Species: human papillomavirus type 26
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36544
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36544
A;Molecule type: DNA
A;Residues: 1-150
A;Cross-references: UNIPROT:P36807; EMBL:X74472; NID:G396956; PIDN:CAAS2530.1; PID:G396
C;Superfamily: papillomavirus E6 protein
C;Keywords: early protein; zinc finger

Query Match 75.0%; Score 39; DB 2; Length 150;

```
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CVYCKQQL 8
Db 30 CVYCKETL 37

RESULT 12
ORF MSV251 hypothetical protein containing C3H2C3 RING finger - Melanoplus sanguinipes e
T28412
C;Species: Melanoplus sanguinipes entomopoxvirus
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T28412
R;Afonso, C.L.; Tuilman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A;Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A;Reference number: Z20484; MUID:99102612; PMID:9847359
A;Accession: T28412
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-329 <AFO>
A;Cross-references: UNIPROT:Q9YVJ1; EMBL:AF063866; NID:g4049647; PIDN:AAC97727.1; PID:g4
C;Genetics:
A;Note: MSV251

Query Match 75.0%; Score 39; DB 2; Length 329;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CVYCKQQL 9
Db 305 CPYCKQNIL 313

RESULT 13
H88022
Protein T27A1.5 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: H88022
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: H88022
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-449 <STO>
A;Cross-references: UNIPROT:O17275; GB:chr_II; PIDN:AB71045.1; PID:g2429516; GSPDB:GN000
C;Genetics:
A;Gene: T27A1.5
A;Map position: 2
C;Superfamily: Arabidopsis amino acid transport protein I

Query Match 75.0%; Score 39; DB 2; Length 449;
Best Local Similarity 55.6%; Pred. No. 31;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CVYCKQQL 9
Db 83 CICYTRQLI 91

RESULT 14
S15621
E6 protein - human papillomavirus type 57
C;Species: human papillomavirus type 57
A;Note: host Homo sapiens (man)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: S15621
```

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R;Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.
Virus Res. 18, 81-98, 1990
A;Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and
A;Reference number: S15614; MUID:91188699; PMID:1964523
A;Accession: S15621
A;Molecule type: DNA
A;Residues: 1-153 <HIR>
A;Cross-references: UNIPROT:P22158; EMBL:X55965; NID:g60882; PIDN:CAA39430.1; PID:g6088
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;29-65/Region: zinc finger CCCC motif
F;102-138/Region: zinc finger CCCC motif

Query Match 73.1%; Score 38; DB 1; Length 153;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CVYCKQQL 8
Db 29 CVYCKRPL 36

RESULT 15
A72267
astB/chuR-related protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: A72267
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hicke
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.
C.M.
Nature 399, 323-329, 1999
A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: A72267
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-454 <ARN>
A;Cross-references: UNIPROT:Q9X148; GB:AE001787; GB:AE000512; NID:g4981882; PIDN:AAD363
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TM1325

Query Match 73.1%; Score 38; DB 2; Length 454;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CVYCKQQL 9
Db 102 CVYCYQKVL 110

Search completed: June 28, 2005, 19:23:23
Job time : 12.2 secs
```

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OM protein - protein search, using sw model

Run on: June 28, 2005, 17:44:26 ; Search time 55.3 Seconds
(without alignments)
83.340 Million cell updates/sec

Title: US-08-170-344-9
Perfect score: 52
Sequence: 1 CVYCKQQLL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	26	2 Q81956	Q81956 human papil
2	52	100.0	99	2 Q919B2	Q919B2 human papil
3	52	100.0	130	2 Q919B4	Q919B4 human papil
4	52	100.0	130	2 Q919B8	Q919B8 human papil
5	52	100.0	130	2 Q919C0	Q919C0 human papil
6	52	100.0	130	2 Q919C2	Q919C2 human papil
7	52	100.0	130	2 Q919C8	Q919C8 human papil
8	52	100.0	130	2 Q919D0	Q919D0 human papil
9	52	100.0	138	2 Q919D2	Q919D2 human papil
10	52	100.0	143	2 Q919B6	Q919B6 human papil
11	52	100.0	143	2 Q919C4	Q919C4 human papil
12	52	100.0	151	2 Q12335	Q12335 human papil
13	52	100.0	151	2 Q12336	Q12336 human papil
14	52	100.0	151	2 Q76TS0	Q76TS0 human papil
15	52	100.0	151	2 Q778T6	Q778T6 human papil
16	52	100.0	151	2 Q778L6	Q778L6 human papil
17	52	100.0	151	2 Q77JC7	Q77JC7 human papil
18	52	100.0	151	2 Q77ZJ5	Q77ZJ5 human papil
19	52	100.0	151	2 Q80963	Q80963 human papil
20	52	100.0	151	2 Q80966	Q80966 human papil
21	52	100.0	151	2 Q89640	Q89640 human papil
22	52	100.0	151	2 Q89648	Q89648 human papil
23	52	100.0	151	2 Q89708	Q89708 human papil
24	52	100.0	151	2 Q89755	Q89755 human papil
25	52	100.0	151	2 Q89852	Q89852 human papil
26	52	100.0	151	2 Q89887	Q89887 human papil
27	52	100.0	151	2 Q8B564	Q8B564 human papil
28	52	100.0	151	2 Q8BB19	Q8BB19 human papil
29	52	100.0	151	2 Q8BB20	Q8BB20 human papil
30	52	100.0	151	2 Q8BB21	Q8BB21 human papil
31	52	100.0	151	2 Q9W8C3	Q9W8C3 human papil

32 52 100.0 151 2 Q9W931
33 52 100.0 151 2 Q9WMP2
34 52 100.0 151 2 Q9WMP3
35 52 100.0 151 2 Q9WMP4
36 52 100.0 151 2 Q9WMP5
37 52 100.0 158 1 VE6_HPV16
38 52 100.0 158 2 Q8JMU8
39 52 100.0 158 2 Q8QHN0
40 52 100.0 158 2 Q8QHP5
41 52 100.0 158 2 Q8QHT0
42 52 100.0 158 2 Q8QRD5
43 52 100.0 158 2 Q8QRD6
44 52 100.0 158 2 Q8QRD7
45 52 100.0 158 2 Q8QRD8

Q9W931 human papil
Q9WMP2 human papil
Q9WMP3 human papil
Q9WMP4 human papil
Q9WMP5 human papil
FO3116 human papil
Q8JMU8 human papil
Q8QHN0 human papil
Q8QHP5 human papil
Q8QHT0 human papil
Q8QRD5 human papil
Q8QRD6 human papil
Q8QRD7 human papil
Q8QRD8 human papil

ALIGNMENTS

RESULT 1

Q81956 PRELIMINARY; PRT; 26 AA.
AC Q81956;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6E7 (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SIHA.
RA Shipky R., Siwkowski A., Hampel A.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U59900; AAB03505.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 26 AA; 3208 MW; F06EBBE995EB67D5 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.021; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 CVYCKQQLL 9
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DB 13 CVYCKQQLL 21
|||

RESULT 2

Q919B2 PRELIMINARY; PRT; 99 AA.
AC Q919B2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RL "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404704; AAL01365.1; -.

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DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 99 AA; 12005 MW; C2B96025EC370E38 CRC64;
Query Match 100.0%; Score 52; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CVYCKQQLL 9
Db |||||
6 CVYCKQQLL 14
RESULT 3
Q919B4 PRELIMINARY; PRT; 130 AA.
AC Q919B4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404703; AAL01353.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227EEDDC CRC64;
Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CVYCKQQLL 9
Db |||||
9 CVYCKQQLL 17
RESULT 4
Q919B8 PRELIMINARY; PRT; 130 AA.
AC Q919B8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404701; AAL01359.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CVYCKQQLL 9
Db |||||
9 CVYCKQQLL 17
RESULT 5
Q919C0 PRELIMINARY; PRT; 130 AA.
AC Q919C0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404700; AAL01357.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CVYCKQQLL 9
Db |||||
9 CVYCKQQLL 17
RESULT 6
Q919C2 PRELIMINARY; PRT; 130 AA.
AC Q919C2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404699; AAL01355.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
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Query Match 100.0%; Score 52; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.091;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVYCKQQLL 9
 |||||
 Db 9 CVYCKQQLL 17

RESULT 7
 Q919C8 PRELIMINARY; PRT; 130 AA.
 AC Q919C8; (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DE E6 protein (Fragment)
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF040495; AAL01347.1; -
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.091;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVYCKQQLL 9
 |||||
 Db 9 CVYCKQQLL 17

RESULT 8
 Q919D0 PRELIMINARY; PRT; 130 AA.
 AC Q919D0; (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DE E6 protein (Fragment)
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF040495; AAL01347.1; -
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 130 AA; 15735 MW; 9EFB30EEDCA21AF3 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.091;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CVYCKQQLL 9
 |||||
 Db 9 CVYCKQQLL 17

RESULT 9
 Q919D2 PRELIMINARY; PRT; 138 AA.
 AC Q919D2; (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DE E6 protein (Fragment)
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF040494; AAL01345.1; -
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 138 AA; 16696 MW; 481E5AEA90895FC2 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 138;
 Best Local Similarity 100.0%; Pred. No. 0.096;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVYCKQQLL 9
 |||||
 Db 17 CVYCKQQLL 25

RESULT 10
 Q919B6 PRELIMINARY; PRT; 143 AA.
 AC Q919B6; (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DE E6 protein (Fragment)
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF0404702; AAL01361.1; -
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3B5E2AC CRC64;

Query Match 100.0%; Score 52; DB 2; Length 143;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVYCKQQLL 9

Db 22 CVYCKQQL 30
|||||

RESULT 11

Q919C4 PRELIMINARY; PRT; 143 AA.
ID O12335
AC O12335
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF0404698; AAL01353.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 143 AA; 17274 MW; 5PB0F7E1EC6DBA82 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 143;

Best Local Similarity 100.0%; Pred. No. 0.1; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVYCKQQL 9
|||||

Db 22 CVYCKQQL 30
|||||

RESULT 12

O12335 PRELIMINARY; PRT; 151 AA.
ID O12335
AC O12335
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003015; AAB70732.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18238 MW; BFF32A8B016CC88B CRC64;

Query Match 100.0%; Score 52; DB 2; Length 151;

Best Local Similarity 100.0%; Pred. No. 0.1; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVYCKQQL 9
|||||

Db 30 CVYCKQQL 38
|||||

RESULT 13

O12336 PRELIMINARY; PRT; 151 AA.
ID O12336
AC O12336
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003016; AAB70733.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;

Query Match 100.0%; Score 52; DB 2; Length 151;

Best Local Similarity 100.0%; Pred. No. 0.1; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVYCKQQL 9
|||||

Db 30 CVYCKQQL 38
|||||

RESULT 14

Q76TSO PRELIMINARY; PRT; 151 AA.
ID Q76TSO
AC Q76TSO
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
DR EMBL; U34114; AAA91661.1; -.
DR EMBL; U34125; AAA91672.1; -.
DR EMBL; U34130; AAA91677.1; -.
DR EMBL; U34131; AAA91678.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVYCKQQLL 9
| | | | |
Db 30 CVYCKQQLL 38

RESULT 15

Q77816 PRELIMINARY; PRT; 151 AA.
AC Q77816;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388056; CAB45104.1; -.
DR EMBL; AJ388061; CAB45114.1; -.
DR EMBL; AJ388066; CAB45124.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR01334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18334 MW; FF8F2A2FCEBA6C02 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVYCKQQLL 9
| | | | |
Db 30 CVYCKQQLL 38

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Job time : 55.3 secs

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OM protein - protein search, using sw model

Run on: June 29, 2005, 01:35:30 ; Search time 57.55 Seconds
(without alignments)

60.138 Million cell updates/sec

Title: US-08-170-344-9

Perfect score: 52

Sequence: 1 CVYCKQQLL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	10	17	US-10-484-063-3
2	52	100.0	15	16	US-10-476-570-24
3	52	100.0	15	16	US-10-476-570-25
4	52	100.0	21	16	US-10-476-570-10
5	52	100.0	32	16	US-10-476-570-9
6	52	100.0	33	16	US-10-476-570-19
7	52	100.0	151	14	US-10-177-390-6
8	52	100.0	151	17	US-10-484-063-20
9	52	100.0	151	17	US-10-484-063-27
10	52	100.0	158	17	US-10-858-384-2
11	52	100.0	158	17	US-10-367-057-16

12	52	100.0	171	16	US-10-472-724-2	Sequence 2, Appli
13	52	100.0	266	9	US-09-367-309A-1	Sequence 1, Appli
14	52	100.0	273	13	US-10-000-903-4	Sequence 4, Appli
15	52	100.0	273	17	US-10-899-771-4	Sequence 4, Appli
16	52	100.0	292	13	US-10-000-903-10	Sequence 10, Appli
17	52	100.0	292	17	US-10-899-771-10	Sequence 10, Appli
18	52	100.0	371	13	US-10-000-903-6	Sequence 6, Appli
19	52	100.0	371	17	US-10-899-771-6	Sequence 6, Appli
20	52	100.0	390	13	US-10-000-903-14	Sequence 14, Appli
21	52	100.0	390	17	US-10-899-771-14	Sequence 14, Appli
22	52	100.0	536	15	US-10-367-095-10	Sequence 10, Appli
23	52	100.0	536	15	US-10-368-046-10	Sequence 10, Appli
24	52	100.0	536	16	US-10-367-367-10	Sequence 10, Appli
25	52	100.0	536	17	US-10-918-337-10	Sequence 10, Appli
26	48	92.3	30	16	US-10-476-570-53	Sequence 53, Appli
27	48	92.3	30	17	US-10-858-384-4	Sequence 4, Appli
28	40	76.9	135	16	US-10-437-963-106779	Sequence 106779, Appli
29	39	75.0	15	16	US-10-476-570-23	Sequence 23, Appli
30	39	75.0	147	15	US-10-369-493-11069	Sequence 11069, A
31	39	75.0	157	15	US-10-424-599-229548	Sequence 229548, A
32	39	75.0	185	16	US-10-425-115-312020	Sequence 312020, A
33	39	75.0	398	14	US-10-291-737-6	Sequence 6, Appli
34	39	75.0	398	14	US-10-365-564-6	Sequence 6, Appli
35	39	75.0	449	14	US-10-225-810-35	Sequence 35, Appli
36	39	75.0	449	15	US-10-369-493-5326	Sequence 5326, Ap
37	38	73.1	145	16	US-10-425-115-199640	Sequence 199640, A
38	38	73.1	343	15	US-10-369-493-300	Sequence 300, App
39	38	73.1	774	15	US-10-425-114-43519	Sequence 43519, A
40	38	73.1	798	16	US-10-425-115-185751	Sequence 185751, A
41	38	73.1	1724	16	US-10-437-963-159035	Sequence 159035, A
42	37	71.2	45	16	US-10-425-115-234065	Sequence 234065, A
43	37	71.2	79	16	US-10-437-963-145353	Sequence 145353, A
44	37	71.2	88	14	US-10-023-896-135	Sequence 135, App
45	37	71.2	96	16	US-10-437-963-202331	Sequence 202331, A

ALIGNMENTS

RESULT 1
US-10-484-063-3
; Sequence 3, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-3

Query Match 100.0%; Score 52; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CVYCKQQLL 9
Db 1 CVYCKQQLL 9

RESULT 2
US-10-476-570-24
; Sequence 24, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 24
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 31-45
US-10-476-570-24

Query Match 100.0%; Score 52; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.08; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVYCKQQLL 9
Db 7 CVYCKQQLL 15
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RESULT 3
US-10-476-570-25
; Sequence 25, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 25
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 36-50
US-10-476-570-25

Query Match 100.0%; Score 52; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.08; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVYCKQQLL 9
Db 2 CVYCKQQLL 10
|||

RESULT 4
US-10-476-570-10
; Sequence 10, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 21
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 30-50
US-10-476-570-10

Query Match 100.0%; Score 52; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.11; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVYCKQQLL 9
Db 8 CVYCKQQLL 16
|||

RESULT 5
US-10-476-570-9
; Sequence 9, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 32
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-45
US-10-476-570-9

Query Match 100.0%; Score 52; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVYCKQQLL 9
Db 24 CVYCKQQLL 32

RESULT 6
US-10-476-570-19
; Sequence 19, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 33
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-46
US-10-476-570-19

Query Match 100.0%; Score 52; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVYCKQQLL 9
Db 24 CVYCKQQLL 32

RESULT 7
US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerp Innovatisecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6

Query Match 100.0%; Score 52; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVYCKQQLL 9
Db 30 CVYCKQQLL 38

RESULT 8
US-10-484-063-20
; Sequence 20, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-20

Query Match 100.0%; Score 52; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVYCKQQLL 9
Db 30 CVYCKQQLL 38

RESULT 9
US-10-484-063-27
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-484-063-27

Query Match 100.0%; Score 52; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVYCKQQLL 9
Db 30 CVYCKQQLL 38

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RESULT 10
US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCES
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match      100.0%; Score 52; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CVYCKQQLL 9
Db      37 CVYCKQQLL 45

RESULT 11
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match      100.0%; Score 52; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CVYCKQQLL 9
Db      37 CVYCKQQLL 45

RESULT 12
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Artegui, Angel

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; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match      100.0%; Score 52; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CVYCKQQLL 9
Db      42 CVYCKQQLL 50

RESULT 13
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match      100.0%; Score 52; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CVYCKQQLL 9
Db      37 CVYCKQQLL 45

RESULT 14
US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903

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; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4

Query Match      100.0%; Score 52; DB 13; Length 273;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CVYCKQQLL 9
Db      143 CVYCKQQLL 151

RESULT 15
US-10-899-771-4
; Sequence 4, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeic protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and B6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-4

Query Match      100.0%; Score 52; DB 17; Length 273;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CVYCKQQLL 9
Db      143 CVYCKQQLL 151

Search completed: June 29, 2005, 03:24:08
Job time : 58.55 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:27:48 ; Search time 17.15 Seconds
(without alignments)

39.174 Million cell updates/sec

Title: US-08-170-344-9

Perfect score: 52

Sequence: 1 CVYCKQQLL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	10	3	US-08-159-339A-575
2	52	100.0	20	2	US-08-934-915-160
3	52	100.0	158	4	US-09-980-523A-2
4	52	100.0	162	1	US-08-316-239B-3
5	52	100.0	162	1	US-08-316-239B-4
6	52	100.0	172	3	US-08-860-165-14
7	52	100.0	172	3	US-09-359-382-14
8	52	100.0	182	1	US-08-117-083-10
9	52	100.0	266	3	US-08-860-165-10
10	52	100.0	266	3	US-09-359-382-10
11	52	100.0	266	4	US-09-367-309A-1
12	52	100.0	273	3	US-09-485-885-4
13	52	100.0	292	3	US-09-485-885-10
14	52	100.0	371	3	US-09-485-885-6
15	52	100.0	390	3	US-09-485-885-14
16	48	92.3	30	4	US-09-980-523A-4
17	41	78.8	80	4	US-09-252-991A-31270
18	41	78.8	347	4	US-09-248-796A-24285
19	38	73.1	156	3	US-09-134-001C-4260
20	37	71.2	344	4	US-09-134-000C-5935
21	37	71.2	959	4	US-09-270-767-39036
22	37	71.2	959	4	US-09-270-767-54253
23	36	69.2	151	4	US-10-101-464A-984
24	36	69.2	441	4	US-09-949-016-9659
25	36	69.2	462	4	US-09-489-039A-12427
26	35	67.3	158	2	US-08-247-904B-10
27	35	67.3	158	3	US-08-767-942A-19

28	35	67.3	271	1	US-08-117-083-14
29	35	67.3	278	3	US-09-485-885-21
30	35	67.3	383	3	US-09-485-885-23
31	35	67.3	472	4	US-09-328-352-4537
32	35	67.3	558	4	US-09-138-277C-1
33	34	65.4	9	3	US-08-159-339A-226
34	34	65.4	9	3	US-08-159-339A-238
35	34	65.4	9	3	US-08-159-339A-253
36	34	65.4	9	3	US-08-159-339A-570
37	34	65.4	10	3	US-08-159-339A-573
38	34	65.4	15	3	US-08-159-339A-1176
39	34	65.4	32	1	US-08-466-285-2
40	34	65.4	32	3	US-08-164-768-2
41	34	65.4	64	4	US-09-732-210-488
42	34	65.4	118	4	US-09-270-767-60607
43	34	65.4	168	4	US-09-248-796A-14459
44	34	65.4	273	4	US-09-270-767-40146
45	34	65.4	273	4	US-09-270-767-55362

ALIGNMENTS

RESULT 1
US-08-159-339A-575
; Sequence 575, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 575:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

Sequence 14, Appl
Sequence 21, Appl
Sequence 23, Appl
Sequence 437, Ap
Sequence 1, Appl
Sequence 226, App
Sequence 238, App
Sequence 253, App
Sequence 570, App
Sequence 573, App
Sequence 1176, Ap
Sequence 2, Appl
Sequence 488, App
Sequence 60607, A
Sequence 14459, A
Sequence 40146, A
Sequence 55362, A

US-08-159-339A-575

Query Match 100.0%; Score 52; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVYCKQQLL 9
| | | | | | | |
Db 1 CVYCKQQLL 9

RESULT 2

US-08-934-915-160
; Sequence 160, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Fouch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 160:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-160

Query Match 100.0%; Score 52; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVYCKQQLL 9
| | | | | | | |
Db 6 CVYCKQQLL 14

RESULT 3

US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:

; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO81 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 52; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVYCKQQLL 9
| | | | | | | |
Db 37 CVYCKQQLL 45

RESULT 4

US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant

; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 100.0%; Score 52; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVYCKQQLL 9
| | | | |
Db 37 CVYCKQQLL 45

RESULT 5

US-08-316-239B-4
Sequence 4, Application US/08316239B
Patent No. 5679509

GENERAL INFORMATION:

; APPLICANT: Wheeler, Cosette M.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNNE-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO

US-08-316-239B-4

Query Match 100.0%; Score 52; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVYCKQQLL 9
| | | | |
Db 37 CVYCKQQLL 45

RESULT 6

US-08-860-165-14
Sequence 14, Application US/08860165A
Patent No. 6004557

GENERAL INFORMATION:

; APPLICANT: EDWARDS, Stirling John

; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14

Query Match 100.0%; Score 52; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.088;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVYCKQQLL 9
| | | | |
Db 106 CVYCKQQLL 114

RESULT 7

US-09-359-382-14
Sequence 14, Application US/09359382
Patent No. 6306397

GENERAL INFORMATION:

; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match 100.0%; Score 52; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.088;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVYCKQQLL 9
| | | | |
Db 106 CVYCKQQLL 114

RESULT 8

US-08-117-083-10
Sequence 10, Application US/08117083
Patent No. 5719054

GENERAL INFORMATION:

; APPLICANT: Bournsnel, Michael E.
; APPLICANT: Inglis, Stephen C.

; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
; OTHER INFORMATION: /note= "Xaa refers to stop codon in
; OTHER INFORMATION: the open reading frame."
US-08-117-083-10

Query Match 100.0%; Score 52; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVYCKQQLL 9
Db 38 CVYCKQQLL 46

RESULT 9
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 52; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVYCKQQLL 9
Db 37 CVYCKQQLL 45

RESULT 10
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 52; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CVYCKQQLL 9
Db 37 CVYCKQQLL 45

RESULT 11
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 52; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.13; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 CVYCKQQLL 9
Db 37 CVYCKQQLL 45
|||||

RESULT 12
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485.885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match 100.0%; Score 52; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.14; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 CVYCKQQLL 9
Db 143 CVYCKQQLL 151
|||||

RESULT 13
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485.885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10

Query Match 100.0%; Score 52; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.14; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 CVYCKQQLL 9
Db 162 CVYCKQQLL 170
|||||

RESULT 14
US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485.885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6

Query Match 100.0%; Score 52; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.18; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 CVYCKQQLL 9
Db 143 CVYCKQQLL 151
|||||

RESULT 15
US-09-485-885-14
; Sequence 14, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485.885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-14

Query Match 100.0%; Score 52; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 0.19; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 CVYCKQQLL 9
|||||

Db 162 CVYCKQQL 170

Search completed: June 28, 2005, 19:29:12
Job time : 18.15 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:32:21 ; Search time 11.2747 Seconds
(without alignments)
76.805 Million cell updates/sec

Title: US-08-170-344-80
Perfect score: 51
Sequence: 1 AYIDNYNKF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	76.5	469	2 S44193	tubulin gamma chai
2	39	76.5	472	2 S39553	tubulin gamma chai
3	39	76.5	474	2 T50558	tubulin gamma-2 ch
4	39	76.5	474	2 T47957	tubulin gamma-1 ch
5	38	74.5	218	2 S36835	glutathione transf
6	38	74.5	240	2 T50831	superoxide dismuta
7	38	74.5	943	2 T24707	hypothetical prote
8	38	74.5	1102	2 T12681	hypothetical prote
9	37	72.5	233	2 T09788	probable superoxid
10	37	72.5	298	2 E97096	Zn-binding lipopro
11	37	72.5	482	2 T49079	serine-type carbox
12	37	72.5	611	2 T03872	hypothetical prote
13	37	72.5	2295	2 B71621	probable membrane
14	36	70.6	95	2 T41855	AcMNPV orf117 - Bo
15	36	70.6	136	2 E70182	hypothetical prote
16	36	70.6	199	2 AC3120	superoxide dismuta
17	36	70.6	200	2 AC2173	iron superoxide di
18	36	70.6	227	2 A39267	superoxide dismuta
19	36	70.6	234	2 JC4611	superoxide dismuta
20	36	70.6	240	2 D98167	superoxide dismuta
21	36	70.6	320	2 T10549	hypothetical prote
22	36	70.6	328	2 F95158	glycosyl transfera
23	36	70.6	328	2 F98024	raffinose-raffinof
24	36	70.6	456	2 S14924	hypothetical prote
25	36	70.6	734	2 S37998	probable serine/th
26	36	70.6	866	2 I79267	traB protein - Esc
27	36	70.6	3225	2 D81702	adherence factor T
28	35.5	69.6	441	2 T28411	ORF MSV250 hypothe
29	35	68.6	194	2 A35235	adenylate kinase (

30	35	68.6	316	2 B75435	ferrochelatase - D
31	35	68.6	389	2 T20811	hypothetical prote
32	35	68.6	395	2 D84102	flagellar hook-ass
33	35	68.6	435	2 A36813	hypothetical prote
34	35	68.6	545	2 S59143	NADH2 dehydrogenas
35	35	68.6	601	2 F84979	sulfite reductase
36	35	68.6	730	2 T44313	hypothetical prote
37	35	68.6	730	2 S70954	otng protein - Vib
38	35	68.6	796	2 S66769	probable membrane
39	35	68.6	895	2 A45554	rhopty complex po
40	35	68.6	911	2 T18451	hypothetical prote
41	35	68.6	1352	2 T01808	hypothetical prote
42	35	68.6	1415	2 T08945	hypothetical prote
43	35	68.6	1515	2 T04204	hypothetical prote
44	34	66.7	125	2 E59106	hypothetical prote
45	34	66.7	135	2 H72663	hypothetical prote

ALIGNMENTS

RESULT 1
S44193
tubulin gamma chain - maize
C;Species: Zea mays (maize)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S44193
R;Canada, J.; Stoppin, V.; Endle, M.C.; Lambert, A.M.
submitted to the EMBL Data Library, April 1994
A;Description: Sequence of a maize cDNA encoding gamma-tubulin.
A;Reference number: S44193
A;Accession: S44193
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-469 <CAN>
A;Cross-references: UNIPROT:Q41808; EMBL:X78891; NID:g474405; PIDN:CAA55488.1; PID:g474
C;Superfamily: tubulin

Query Match 76.5%; Score 39; DB 2; Length 469;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AYIDNYNKF 9
Db 405 AFLDNYRKF 413
|:|:|:|:|:|

RESULT 2
S39553
tubulin gamma chain - fern (Anemia phyllitidis)
C;Species: Anemia phyllitidis
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S39553
R;Fuchs, U.; Moepps, B.; Maucher, H.P.; Schraudolf, H.
Plant Mol. Biol. 23, 595-603, 1993
A;Title: Isolation, characterization and sequence of a cDNA encoding gamma-tubulin prot
A;Reference number: S39553; MUID:94033338; PMID:8219092
A;Accession: S39553
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-472 <FUC>
A;Cross-references: UNIPROT:P34785; EMBL:X69188; NID:g429150; PIDN:CAA48932.1; PID:g429
C;Superfamily: tubulin

Query Match 76.5%; Score 39; DB 2; Length 472;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AYIDNYNKF 9
Db 406 AFLDNYRKF 414
|:|:|:|:|:|

RESULT 3

T50558
tubulin gamma-2 chain [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C;Accession: T50558
R;Liu, B.; Joshi, H.C.; Wilson, T.J.; Silflow, C.D.; Palevitz, B.A.; Snustad, D.P.
Plant Cell 6, 303-314, 1994
A;Title: gamma-tubulin in Arabidopsis: gene sequence, immunoblot, and immunofluorescence
A;Reference number: 222994; PMID:8148650; PMID:8148650
A;Accession: T50558
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-474 <LIU>
A;Cross-references: UNIPROT:P38558; EMBL:U03990; PIDN:AAA20654.1
A;Experimental source: Columbia
C;Genetics:
A;Gene: TUBG2
A;Introns: 43/3; 148/1; 281/3; 299/3; 334/3; 359/3; 374/3; 417/3; 452/3
C;Function:
A;Description: structural component of cytoskeleton
C;Superfamily: tubulin

Query Match 76.5%; Score 39; DB 2; Length 474;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AYIDNYNKF 9
|:|||||
Db 405 AFLDNYRKF 413

RESULT 4

T47957
tubulin gamma-1 chain [similarity] - Arabidopsis thaliana
N;Alternate names: protein P15G16.40
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47957; T50559
R;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quet
submitted to the Protein Sequence Database, January 2000
A;Reference number: 224480
A;Accession: T47957
A;Molecule type: DNA
A;Residues: 1-474 <DEH>
A;Cross-references: UNIPROT:P38557; EMBL:AL132959
A;Experimental source: cultivar Columbia; BAC clone F15G16
R;Liu, B.; Joshi, H.C.; Wilson, T.J.; Silflow, C.D.; Palevitz, B.A.; Snustad, D.P.
Plant Cell 6, 303-314, 1994
A;Title: gamma-tubulin in Arabidopsis: gene sequence, immunoblot, and immunofluorescence
A;Reference number: 222994; PMID:8148650; PMID:8148650
A;Accession: T50559
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-474 <LIU>
A;Cross-references: EMBL:U02069; PIDN:AAA20653.1
A;Experimental source: Columbia
C;Genetics:
A;Gene: TUBG1
A;Map position: 3
A;Introns: 43/3; 148/1; 281/3; 299/3; 334/3; 359/3; 374/3; 417/3; 452/3
A;Note: F15G16.40
C;Superfamily: tubulin
C;Keywords: microtubule

Query Match 76.5%; Score 39; DB 2; Length 474;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AYIDNYNKF 9
|:|||||
Db 405 AFLDNYRKF 413

RESULT 5

S36835
glutathione transferase (EC 2.5.1.18) (clone PM239x14) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: S36835; S31968
R;Bartling, D.; Radzio, R.; Steiner, U.; Weiler, E.W.
Eur. J. Biochem. 216, 579-586, 1993
A;Title: A glutathione S-transferase with glutathione-peroxidase activity from Arabidop
A;Reference number: S36835; PMID:93387310; PMID:8375395
A;Accession: S36835
A;Molecule type: mRNA
A;Residues: 1-218 <BAR>
A;Cross-references: UNIPROT:P42769; EMBL:X68304; NID:g22653; PIDN:CAA48376.1; PID:g2266
C;Superfamily: glutathione transferase
C;Keywords: transferase

Query Match 74.5%; Score 38; DB 2; Length 218;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AYIDNYNKF 9
|:|||||
Db 45 AYLDNYHVP 53

RESULT 6

T50831
superoxide dismutase (EC 1.15.1.1) (Mn) [similarity] - Zantedeschia aethiopica
C;Species: Zantedeschia aethiopica
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 09-Jul-2004
C;Accession: T50831
R;Lino-Neto, T.; Tavares, R.M.; Palme, K.; Pais, M.S.S.
submitted to the EMBL Data Library, September 1998
A;Description: Expression of superoxide dismutases during senescence and regreening of
A;Reference number: Z25250
A;Accession: T50831
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-240 <LIN>
A;Cross-references: UNIPROT:O82584; EMBL:AF094832; PIDN:AAC63379.1
C;Genetics:
A;Gene: Masod
C;Superfamily: superoxide dismutase (Mn)
C;Keywords: manganese; metalloprotein; oxidoreductase
F;64,112,201,205/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match 74.5%; Score 38; DB 2; Length 240;
Best Local Similarity 87.5%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AYIDNYNKF 8
|:|||||
Db 71 AYITNYNK 78

RESULT 7

T24707
hypothetical protein T08G3.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24707
R;Lloyd, C.
submitted to the EMBL Data Library, December 1996
A;Reference number: Z19926
A;Accession: T24707
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-943 <WIL>
A;Cross-references: UNIPROT:Q9XU47; EMBL:Z83238; PIDN:CAB05800.1; GSPDB:GN00023; CESP:T
A;Experimental source: clone T08G3
C;Genetics:

Query Match 74.5%; Score 38; DB 2; Length 943;
Best Local Similarity 87.5%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AYIDNYNKF 9
|:|||||
Db 405 AFLDNYRKF 413

A;Gene: CESP:T08G3.7

A;Map position: 5

A;Introns: 48/3; 302/3; 342/3; 480/1; 605/3; 644/1; 719/1; 850/1; 896/3

C;Superfamily: Caenorhabditis elegans hypothetical protein F36D3.5

Query Match 74.5%; Score 38; DB 2; Length 943;

Best Local Similarity 77.8%; Pred. No. 88;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AYIDNKNK 9

|||: ||||

Db 637 AYINAYNKF 645

RESULT 8

T12681 hypothetical protein 63B12.9 - fruit fly (*Drosophila melanogaster*)

C;Species: *Drosophila melanogaster*

C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004

C;Accession: T12681

R;Ferraz, C.; Vidal, S.; Brun, C.; Bucheton, A.; Demaille, J.G.

submitted to the EMBL Data Library, January 1998

A;Description: Sequencing the distal X chromosome of *Drosophila melanogaster*.

A;Reference number: Z17572

A;Accession: T12681

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1102 <PER>

A;Cross-references: UNIPROT:Q9W553; EMBL:AL021106; PIDN:CAA15938.1

A;Experimental source: clone cosmid 63B12

C;Genetics:

A;Cross-references: FlyBase:FBgn0000117

A;Introns: 107/2; 301/1

A;Note: 63B12.9

C;Superfamily: fruit fly hypothetical protein 63B12.9

Query Match

Best Local Similarity 74.5%; Score 38; DB 2; Length 1102;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AYIDNKNK 8

|||: ||||

Db 421 AYVDYRNK 428

RESULT 9

T09788

probable superoxide dismutase (EC 1.15.1.1) (Mn) - papaya

N;Alternate names: manganese superoxide dismutase

C;Species: *Carica papaya* (papaya)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C;Accession: T09788

R;Lin, C.T.; Lin, M.T.

submitted to the EMBL Data Library, June 1996

A;Reference number: Z16854

A;Accession: T09788

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-233 <LIN>

A;Cross-references: UNIPROT:Q42672; EMBL:L77078; NID:g1369764; PID:g1369765

A;Experimental source: cultivar Tainong 2; callus

C;Genetics:

A;Gene: Mn-SOD

C;Function:

A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen

C;Superfamily: superoxide dismutase (Mn)

C;Keywords: manganese; metalloprotein; oxidoreductase

F;51,99,188,192/Binding site: manganese (His, His, Asp, His) #status predicted

Query Match

Best Local Similarity 72.5%; Score 37; DB 2; Length 233;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AYIDNKNK 8

|||: ||||

Db 58 AYVTNKNK 65

RESULT 10

E97096

Zn-binding lipoprotein related (surface adhesin A), ADHS [imported] - *Clostridium acetobutylicum*

C;Species: *Clostridium acetobutylicum*

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004

C;Accession: E97096

R;Molling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee

; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: E97096

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-298 <KUR>

A;Cross-references: UNIPROT:Q97IP7; GB:AE001437; PIDN:AAK79560.1; PID:g15024548; GSPDB:

A;Experimental source: *Clostridium acetobutylicum* ATCC824

C;Genetics:

A;Gene: CAC1593

C;Superfamily: adhesin B

Query Match

Best Local Similarity 72.5%; Score 37; DB 2; Length 298;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YIDNKNKF 9

|||: ||||

Db 165 YIDNKNKF 172

RESULT 11

T49079

serine-type carboxypeptidase like protein - *Arabidopsis thaliana*

N;Alternate names: Protein F4F15.110

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004

C;Accession: T49079

R;Alcaraz, J.P.; Clabault, G.; Cottet, A.; Mache, R.; Mewes, H.W.; Rudd, S.; Lemcke, K.

submitted to the Protein Sequence Database, April 2000

A;Reference number: Z25015

A;Accession: T49079

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-482 <ALC>

A;Cross-references: UNIPROT:Q9SV04; EMBL:AL049711; GSPDB:GN00061; ATSP:F4F15.110

A;Experimental source: cultivar Columbia; BAC clone F4F15

C;Genetics:

A;Gene: ATSP:F4F15.110

A;Map position: 3

A;Introns: 116/1; 151/1

C;Superfamily: serine carboxypeptidase

Query Match

Best Local Similarity 72.5%; Score 37; DB 2; Length 482;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 IDNKNKF 9

|||: ||||

Db 268 MDNKNKF 274

RESULT 12

T03872

hypothetical protein C49G7.1 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C;Accession: T03872

R;Bradshaw, H.; Graves, T.; Fronick, W.

submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid C49G7.

A;Reference number: Z16068

A;Accession: T03872

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-611 <WIL>

A;Cross-references: UNIPROT:O16229; EMBL:AF016418; NID:g2291147; PIDN:AAB55284.1; PID:92

C;Genetics:

A;Map position: V

A;Introns: 32/3; 109/3; 141/1; 264/3; 303/1; 378/1; 411/3; 517/1; 563/3

A;Note: C49G7.1

Query Match 72.5%; Score 37; DB 2; Length 611;

Best Local Similarity 66.7%; Pred. No. 86;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AYIDNKNK 9

Db 296 AFVDVYNK 304

|||||

|||||

RESULT 13

B71621 Probable membrane associated protein PFB0190c - malaria parasite (Plasmodium falciparum)

C;Species: Plasmodium falciparum

C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004

C;Accession: B71621

R; Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;

Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.

Science 292, 1126-1132, 1998

A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.

A;Reference number: A71600; MUID:99021743; PMID:9804551

A;Accession: B71621

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-2295 <GAR>

A;Cross-references: UNIPROT:Q9TY98; GB:AE001379; GB:AE001362; NID:g3845118; PIDN:AAC7182

A;Experimental source: clone 3D7

C;Genetics:

A;Gene: PFB0190c

Query Match 72.5%; Score 37; DB 2; Length 2295;

Best Local Similarity 85.7%; Pred. No. 3.2e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 IDNKNK 9

Db 318 IDNKNK 324

|||||

|||||

RESULT 14

T41855

AcMNPV orf117 - Bombyx mori nuclear polyhedrosis virus (isolate T3)

C;Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV

A;Variety: isolate T3

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C;Accession: T41855

R;Gomi, S.; Majima, K.;

J. Gen. Virol. 80, 1323-1337, 1999

A;Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.

A;Reference number: 222020; MUID:99281911; PMID:103555780

A;Accession: T41855

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-95 <KAM>

A;Cross-references: UNIPROT:O92474; EMBL:L33180; PIDN:AAC63784.1

C;Genetics:

A;Note: Orf_96

Query Match 70.6%; Score 36; DB 2; Length 95;

Best Local Similarity 71.4%; Pred. No. 20;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 IDNKNK 9

Db 83 VDNKNK 89

|||||

|||||

RESULT 15

E70182

hypothetical protein B80662 - Lyme disease spirochete

C;Species: Borrelia burgdorferi (Lyme disease spirochete)

C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004

C;Accession: E70182

R; Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Whit-

son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt

; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997

A;Authors: Smith, H.O.; Venter, J.C.

A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.

A;Reference number: A70100; MUID:98055943; PMID:9403685

A;Accession: E70182

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-136 <KLE>

A;Cross-references: UNIPROT:O51606; GB:AE001167; GB:AE000783; NID:g2688585; PIDN:AAC670

A;Experimental source: strain B31

Query Match 70.6%; Score 36; DB 2; Length 136;

Best Local Similarity 75.0%; Pred. No. 28;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AYIDNKNK 8

Db 129 SYISNKNK 136

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|||||

Search completed: June 29, 2005, 01:38:56

Job time : 12.2747 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2005, 23:28:22 ; Search time 54.2473 Seconds
(without alignments)
84.958 Million cell updates/sec

Title: US-08-170-344-80
Perfect score: 51
Sequence: 1 AYIDNKNKF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	84.3	206	Q6MHD3	Q6mhd3 bdellovibrio
2	42	82.4	304	Q73Y74	Q73Y74 mycobacteri
3	42	82.4	664	Q972B2	Q972b2 sulfolobus
4	40	78.4	365	Q8A9I1	Q8a9i1 bacteroides
5	39	76.5	275	Q6FRS4	Q6frs4 candida gla
6	39	76.5	399	Q9FZR1	Q9fzr1 mycoplasma
7	39	76.5	421	1 TBG3 MAIZE	Q41874 zea mays (m
8	39	76.5	454	2 Q75M06	Q75m06 oryza sativ
9	39	76.5	469	1 TBG1 MAIZE	Q41807 zea mays (m
10	39	76.5	469	1 TBG2 MAIZE	Q41808 zea mays (m
11	39	76.5	469	1 TBG2 ORYZA	Q49068 oryza sativ
12	39	76.5	469	2 Q9M421	Q9m421 hordeum vul
13	39	76.5	472	1 TBG ANEPH	R34785 anemia phyl
14	39	76.5	472	2 Q8GZ70	Q8gzt0 lupinus alb
15	39	76.5	474	1 TBG1 ARATH	R38557 arabidopsis
16	39	76.5	474	1 TBG2 ARATH	R38558 arabidopsis
17	39	76.5	475	1 TBG PHYPA	Q9xf93 physcomitre
18	39	76.5	475	2 Q8LKL1	Q8lkl1 conocephalu
19	39	76.5	475	2 Q7XJCI	Q7xjc1 haplomitriu
20	39	76.5	836	2 Q8ID71	Q8id71 plasmodium
21	39	76.5	920	2 Q94165	Q94i65 oryza sativ
22	38	74.5	136	2 Q660K8	Q660k8 borrelia ga
23	38	74.5	147	2 Q93YG5	Q93yg5 lactuca sat
24	38	74.5	218	1 GTH5 ARATH	R42769 arabidopsis
25	38	74.5	224	2 Q9FV33	Q9fv33 digitalis l
26	38	74.5	240	2 Q82584	Q82584 zantedeschi
27	38	74.5	371	2 Q7RD59	Q7rd59 plasmodium
28	38	74.5	666	1 TKT_BUCBP	Q89ay2 buchnera ap
29	38	74.5	943	2 Q9XU47	Q9xu47 caenorhabdi
30	38	74.5	1037	2 Q6MDS4	Q6mds4 parachlamyd
31	38	74.5	1058	2 Q8A3L3	Q8a3l3 bacteroides

32 38 74.5 1102 2 O46089
33 37.5 73.5 916 1 ODOI_BUCBP
34 37 72.5 104 2 Q6YCA8
35 37 72.5 150 2 Q7R6V6
36 37 72.5 170 2 Q6CRN2
37 37 72.5 233 2 Q975S7
38 37 72.5 233 2 Q42672
39 37 72.5 240 2 Q6BUZ8
40 37 72.5 298 2 Q97IP7
41 37 72.5 398 2 Q8ISM0
42 37 72.5 482 2 Q9SV04
43 37 72.5 563 2 Q6FVX0
44 37 72.5 581 2 Q8I585
45 37 72.5 611 2 O16229

ALIGNMENTS

RESULT 1
Q6MHD3 PRELIMINARY; PRT; 206 AA.
AC Q6MHD3;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Sodb protein (EC 1.15.1.1).
GN Name=sodb; OrderedLocusNames=Bd3617;
OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164; DOI=10.1126/science.1093027;
RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
RA Keller H., Lambert C., Evans K.J., Goessmann A., Meyer F.,
RA Sockett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
RT genomic perspective.";
RL Science 303:689-692(2004).
CC -|- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems (By similarity).
CC -|- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -|- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
DR EMBL; BX842656; CAE80994.1; -.
DR HSSP; P04179; 1AP6.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0004784; F:superoxide dismutase activity; IEA.
DR GO; GO:0006801; P:superoxide metabolism; IEA.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF02777; SOD_Fe_C; 1.
DR Pfam; PF00081; SOD_Fe_N; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_MN; 1.
KW Complete proteome; Oxidoreductase.
SQ SEQUENCE 206 AA; 23077 MW; 80A93190CAFE37D7 CRC64;

Query Match 84.3%; Score 43; DB 2; Length 206;
Best Local Similarity 88.9%; Pred.No. 8.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AYIDNKNKF 9
|||||
Db 33 AYIDNKNKF 41

RESULT 2
Q73Y74 PRELIMINARY; PRT; 304 AA.
ID Q73Y74

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AC Q73Y74;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
GN OrderedLocuNames=MAP2083c;
OS Mycobacterium paratuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1770;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=k10;
RA Li L., Bannantine J., Zhang Q., Amosin A., Alt D., Kapur V.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017234; AA04400.1; -.
DR InterPro; IPR007621; DUF477.
DR Pfam; PF04536; DUF477; 1.
KW Complete proteome.
SQ SEQUENCE 304 AA; 32857 MW; BBCEA19B226F0D98 CRC64;

Query Match 82.4%; Score 42; DB 2; Length 304;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YIDNKNKF 9
Db 70 YVDNFKF 77

RESULT 3
Q972B2 PRELIMINARY; PRT; 664 AA.
AC Q972B2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 664aa long hypothetical DNA topoisomerase.
GN OrderedLocuNames=ST1216;
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RX MEDLINE=21456156; PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yanagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermoacidophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7.";
RL DNA Res. 8:123-140(2001).
CC -!- FUNCTION: The reaction catalyzed by topoisomerases leads to the
CC conversion of one topological isomer of DNA to another (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: ATP-independent breakage of single-stranded
CC DNA, followed by passage and rejoining.
CC -!- SIMILARITY: Belongs to the prokaryotic type I/III topoisomerase
CC family.
CC EMBL; AP000985; BAB66257.1; -.
DR HSSP; O29238; 1GL9.
DR GO; GO:0005694; C:chromosome; IEA.
DR GO; GO:0003917; F:DNA topoisomerase type I activity; IEA.
DR GO; GO:0006304; P:DNA modification; IEA.
DR GO; GO:0006285; P:DNA topological change; IEA.
DR GO; GO:0006268; P:DNA unwinding; IEA.
DR InterPro; IPR003601; DNATopi ATP bind.
DR InterPro; IPR003602; DNATopi DNA bind.
DR InterPro; IPR000380; DNA_topoisomrase.
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DR InterPro; IPR005739; Topoi_arch.
DR InterPro; IPR006171; Toprim_dom.
DR InterPro; IPR006154; Toprim_sub.
DR Pfam; PF01131; Topoisom_bac; 1.
DR Pfam; PF01751; Toprim; 1.
DR PRINTS; PR00417; PRTPISMRASE1.
DR SMART; SM00437; TOP1AC; 1.
DR SMART; SM00436; TOP1BC; 1.
DR SMART; SM00493; TOP1RM; 1.
DR TIGRFAMs; TIGR01057; topA_arch; 1.
KW Complete proteome; DNA-binding; Hypothetical protein; Isomerase;
KW Topoisomerase.
SQ SEQUENCE 564 AA; 76602 MW; 051FF24D876C5A7B CRC64;

Query Match 82.4%; Score 42; DB 2; Length 664;
Best Local Similarity 75.0%; Pred. No. 41;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YIDNKNKF 9
Db 574 YLDNKNKY 581

RESULT 4
Q8A9I1 PRELIMINARY; PRT; 365 AA.
AC Q8A9I1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN OrderedLocuNames=BT0834;
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VP1-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
RL Science 299:2074-2076(2003).
DR EMBL; AE016929; AA075941.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR005495; Yjgp_YjgQ.
DR Pfam; PF03739; Yjgp_YjgQ; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 365 AA; 42000 MW; A9B40726B279AB46 CRC64;

Query Match 78.4%; Score 40; DB 2; Length 365;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYIDNYN 7
Db 165 AYIDNYN 171

RESULT 5
Q6FRS4 PRELIMINARY; PRT; 275 AA.
AC Q6FRS4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Similarities with sp|P31377 Saccharomyces cerevisiae YAL014c
DE FUN34.
DR ORFNames=CAGL0H06325g;
OS Candida glabrata CBS138.
OC Eukaryota; Fungi; Ascomycota; Saccharomycota; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
```

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OX NCBI_TaxID=284593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS138;
RG Genolevures;
RA DuJon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talia E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisarane A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantrave F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenn S., Potter S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44 (2004).
DR EMBL; CR380954; CAG60003.1; -.
DR InterPro; IPR010989; t-snare.
DR InterPro; IPR000727; T-SNARE.
DR Pfam; PF05739; SNARE; 1.
DR SMART; SM00397; t-SNARE; 1.
DR PROSITE; PS0192; T-SNARE; 1.
SQ SEQUENCE 275 AA; 31113 MW; E9A225E6BE766CFE CRC64;

Query Match 76.5%; Score 39; DB 2; Length 275;
Best Local Similarity 87.5%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 AYIDNYNK 8
||| |||
Db 62 AYIDEYNK 69

RESULT 6
O9FZR1 PRELIMINARY; PRT; 399 AA.
AC O9FZR1;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE P46.
GN Name=orf8;
OS Mycoplasma virus P1.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae.
OX NCBI_TaxID=35238;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95273474; PubMed=7753907; DOI=10.1006/plas.1995.1005;
RA Zou N., Fark K., Dybvig K.;
RT "Mycoplasma virus P1 has a linear, double-stranded DNA genome with
RT inverted terminal repeats.";
RL Plasmid 33:41-49 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21223405; PubMed=11322826; DOI=10.1006/plas.2000.1501;
RA Tu A.H.T., Voelker L.L., Shen X., Dybvig K.;
RT "Complete nucleotide sequence of the mycoplasma virus P1 genome.";
RN [3]
RP SEQUENCE FROM N.A.
RA Tu A., Shen X., Voelker L.L., Dybvig K.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF246223; AAG01283.1; -.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR008161; Clg_helix.
DR InterPro; IPR008160; Collagen.
DR Pfam; PF01391; Collagen; 1.

DR ProDom; PD000007; Clg_helix; 2.
SQ SEQUENCE 399 AA; 46196 MW; 7D0284B08E13F6E5 CRC64;

Query Match 76.5%; Score 39; DB 2; Length 399;
Best Local Similarity 75.0%; Pred. No. 87;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 2 YIDNYNKF 9
||| |||
Db 330 YINNYNRF 337

RESULT 7
TBG3 MAIZE
ID TBG3 MAIZE STANDARD; PRT; 421 AA.
AC Q41874;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 03-JUN-2004 (Rel. 44, Last annotation update)
DE Tubulin gamma-3 chain (Gamma-3 tubulin) (Fragment).
GN Name=TUBG3; Synonyms=TUBC, TUBG;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Black Mexican Sweet;
RA Canaday J., Stoppin V., Endle M.C., Lambert A.M.;
RT "Identification of two maize cDNAs encoding gamma-tubulin.";
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Tubulin is the major constituent of microtubules. Gamma
CC tubulin is found at microtubule organizing centers (MTOC) such as
CC the spindle poles or the centrosome, suggesting that it is
CC involved in the minus-end nucleation of microtubule assembly.
CC -!- SIMILARITY: Belongs to the tubulin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X83696; CAA58671.1; -.
DR HSSP; P02554; ITUB.
DR InterPro; IPR002454; Gamma_tubulin.
DR InterPro; IPR008280; Tub_FtsZ_C.
DR InterPro; IPR000217; Tubulin_.
DR InterPro; IPR003008; Tubulin_FtsZ.
DR Pfam; PF00091; Tubulin; 1.
DR Pfam; PF03953; Tubulin C; 1.
DR PRINTS; PR01161; TUBULIN.
DR PROSITE; PS00227; TUBULIN; 1.
KW GTP-binding; Microtubule; Multigene family.
FT NON_TER 1
FT NP_BIND 94 100 GTP (Potential).
SQ SEQUENCE 421 AA; 47541 MW; 7C2BC3B91EC77523 CRC64;

Query Match 76.5%; Score 39; DB 1; Length 421;
Best Local Similarity 66.7%; Pred. No. 92;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 AYIDNYNKF 9
||| |||
Db 357 AFLDNYNKF 365

RESULT 8
Q75M06 PRELIMINARY; PRT; 454 AA.
ID Q75M06

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AC Q75W06;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative tubulin gamma-2 chain (Gamma-2 tubulin).
GN Name=P0676505.8;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Chow T.-Y., Hsiung Y.-I.-C., Chen C.-S., Chen H.-H., Liu S.-M.,
RA Chao Y.-T., Lee P.-F., Chang S.-J., Chen H.-C., Chen S.-K.,
RA Chen T.-R., Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y.,
RA Hsiao S.-H., Hsiung J.-N., Hsu C.-H., Kau P.-I., Lee M.-C., Leu H.-L.,
RA Li Y.-P., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
RA Wu H.-P., Shaw J.-P.,
RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RL -1- SIMILARITY: Belongs to the tubulin family.
CC EMBL; AC087425; AAS55777.1; -.
CC DR GO; GO:0045298; C:tubulin; IEA.
CC DR GO; GO:0005525; F:GTP binding; IEA.
CC DR GO; GO:0003924; F:GTPase activity; IEA.
CC DR GO; GO:0005198; F:structural molecule activity; IEA.
CC DR GO; GO:0046785; P:microtubule polymerization; IEA.
CC DR GO; GO:0007018; P:microtubule-based movement; IEA.
CC DR InterPro; IPR002454; Gamma tubulin.
CC DR InterPro; IPR000217; Tubulin.
CC DR InterPro; IPR003008; Tubulin_FtsZ.
CC DR Pfam; PF00091; Tubulin_C; 1.
CC DR PRINTS; PR01164; GAMMATUBULIN.
CC DR PRINTS; PR01161; TUBULIN.
CC DR PROSITE; PS00227; TUBULIN; UNKNOWN_1.
KW GTP-binding; Microtubule.
SQ SEQUENCE 454 AA; 51145 MW; CA341CC51EBABA41 CRC64;

Query Match 76.5%; Score 39; DB 2; Length 454;
Best Local Similarity 66.7%; Pred. No. 99;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AYIDNYNKF 9
Db 390 AFLDNYRKF 398

RESULT 9
TBG1 MAIZE
ID TBG1 MAIZE STANDARD; PRT; 469 AA.
AC Q41873;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Tubulin gamma-1 chain (Gamma-1 tubulin).
GN Name=TUBG1; Synonyms=TUBC, TUBG;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Black Mexican Sweet;
EX MEDLINE=95175624; PubMed=7870837; DOI=10.1104/pp.107.1.309;
RA Lopez I., Khan S., Sevik M., Cande W.Z., Hussey P.J.;
RT "Isolation of a full-length cDNA encoding Zea mays gamma-tubulin.";
RL Plant Physiol. 107:309-310(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Black Mexican Sweet;

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RA Canaday J., Stoppin V., Endle M.C., Lambert A.M.;
RT "Identification of two maize cDNAs encoding gamma-tubulin.";
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Tubulin is the major constituent of microtubules. Gamma
CC tubulin is found at microtubule organizing centers (MTOC) such as
CC the spindle poles or the centrosome, suggesting that it is
CC involved in the minus-end nucleation of microtubule assembly.
CC -1- SIMILARITY: Belongs to the tubulin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X80375; CAA56592.1; -.
CC EMBL; X83695; CAA58670.1; -.
CC DR HSPF; P02554; IFFX.
CC DR InterPro; IPR002454; Gamma tubulin.
CC DR InterPro; IPR008280; Tub_FtsZ_C.
CC DR InterPro; IPR000217; Tubulin.
CC DR InterPro; IPR003008; Tubulin_FtsZ.
CC DR Pfam; PF00091; Tubulin; 1.
CC DR Pfam; PF03953; Tubulin_C; 1.
CC DR PRINTS; PR01161; TUBULIN.
CC DR PROSITE; PS00227; TUBULIN; 1.
KW GTP-binding; Microtubule; Multigene family.
FT NP BIND 142 148 GTP (Potential).
FT CONFLICT 352 352 Y->D (in Ref. 2).
SQ SEQUENCE 469 AA; 52933 MW; 0B4C8857C527D19E CRC64;

Query Match 76.5%; Score 39; DB 1; Length 469;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AYIDNYNKF 9
Db 405 AFLDNYRKF 413

RESULT 10
TBG2 MAIZE
ID TBG2 MAIZE STANDARD; PRT; 469 AA.
AC Q41808;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tubulin gamma-2 chain (Gamma-2 tubulin).
GN Name=TUBG2; Synonyms=TUBC, TUBG;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Black Mexican Sweet;
RA Canaday J., Stoppin V., Endle M.C., Lambert A.M.;
RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Tubulin is the major constituent of microtubules. Gamma
CC tubulin is found at microtubule organizing centers (MTOC) such as
CC the spindle poles or the centrosome, suggesting that it is
CC involved in the minus-end nucleation of microtubule assembly.
CC -1- SIMILARITY: Belongs to the tubulin family.
CC -----
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CC -----
DR EMBL: X78891; CAA55488.1; -.
DR PIR: S44193; S44193.
DR HSP: P02554; IFFX.
DR MaizedB; 113512; -.
DR InterPro; IPR002454; Gamma tubulin.
DR InterPro; IPR008280; Tub_Ftsz_C.
DR InterPro; IPR000217; Tubulin_.
DR InterPro; IPR003008; Tubulin_Ftsz.
DR Pfam; PF00091; Tubulin; 1.
DR Pfam; PF03953; Tubulin_C; 1.
DR PRINTS; PR01161; TUBULIN.
DR PROSITE; PS00227; TUBULIN; 1.
DR KW GTP-binding; Microtubule; Multigene family.
DR NP BIND 142 148 GTP (Potential).
DR FT NP BIND 142 148
DR SQ SEQUENCE 469 AA; 76841 MW; 3F06E5848FA2B5D1 CRC64;

Query Match 76.5%; Score 39; DB 1; Length 469;
Best Local Similarity 66.7%; pred.No.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AYDNYNKF 9
Db |::||| ||
405 AFLDNYRKF 413

RESULT 11
TBG2_ORYSA STANDARD; PRT; 469 AA.
ID TBG2_ORYSA
AC 049068;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Tubulin gamma-2 chain (Gamma-2 tubulin).
GN Name=TUBG2; Synonyms=TUBC;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OC NCBI_TaxID=4530;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=cv. Japonica / Yeongnambyeo;
RA Kim Y.-K., Cha Y.-K., Jun H.-Y., Kim J.-D., Choi J.-S., Kim H.-R.,
RA Han I.-S.;
RT "Nucleotide sequence of a cDNA (Ostubg2) encoding a gamma-tubulin in
RT the rice plant (Oryza sativa).";
RL (er) Plant Gene Register PGR99-186.
CC -|- FUNCTION: Tubulin is the major constituent of microtubules. Gamma
CC tubulin is found at microtubule organizing centers (MTOC) such as
CC the spindle poles or the centrosome, suggesting that it is
CC involved in the minus-end nucleation of microtubule assembly.
CC -|- SIMILARITY: Belongs to the tubulin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF036957; AAB92557.1; -.
DR HSP: P02554; IFFX.
DR Gramene; 049068; -.
DR InterPro; IPR002454; Gamma tubulin.
DR InterPro; IPR008280; Tub_Ftsz_C.
DR InterPro; IPR000217; Tubulin_.
DR InterPro; IPR003008; Tubulin_Ftsz.
DR Pfam; PF00091; Tubulin; 1.
DR Pfam; PF03953; Tubulin_C; 1.
DR PRINTS; PR01161; TUBULIN.
DR
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OS Anemia phyllitidis (Fern).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Moniliformeae; Filicophyta; Filicopsida; Filicales; Schizaeaceae;
 OC Anemia.
 OX NCBI_TaxID=12940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9403338; PubMed=9219092;
 RA Fuchs U., Moepfs B., Maucher H.P., Schraudolph H.;
 RT "Isolation, characterization and sequence of a cDNA encoding gamma-
 RT tubulin protein from the fern Anemia phyllitidis L. Sw.";
 RL Plant Mol. Biol. 23:595-603(1993).
 CC -!- FUNCTION: Tubulin is the major constituent of microtubules. Gamma
 CC tubulin is found at microtubule organizing centers (MTOC) such as
 CC the spindle poles or the centrosome, suggesting that it is
 CC involved in the minus-end nucleation of microtubule assembly.
 CC -!- SIMILARITY: Belongs to the tubulin family.
 CC -----
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 CC -----
 DR EMBL; X69188; CAA48932.1; -.
 DR PIR; S39553; S39553.
 DR HSSP; P02554; 1FFX.
 DR InterPro; IPR002454; Gamma tubulin.
 DR InterPro; IPR008280; Tub_FtsZ_C.
 DR InterPro; IPR000217; Tubulin_PtsZ.
 DR InterPro; IPR003008; Tubulin_PtsZ.
 DR Pfam; PF00091; Tubulin_C; 1.
 DR Pfam; PF03953; Tubulin_C; 1.
 DR PRINTS; PR01161; TUBULIN.
 DR PROSITE; PS00227; TUBULIN; 1.
 KW GTP-binding; Microtubule.
 FT NP_BIND 142 148 GTP (Potential).
 SQ SEQUENCE 472 AA; 53138 MW; F1E76F51BCC3DA09 CRC64;
 Query Match 76.5%; Score 39; DB 1; Length 472;
 Best Local Similarity 66.7%; Pred. No. 1e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 AYIDNKNKF 9
 Db 406 AFLDNVRFK 414
 ID Q8GZT0 PRELIMINARY; PRT; 472 AA.
 AC Q8GZT0;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Gamma-tubulin.
 GN Name=TubG1;
 OS Lupinus albus (White lupine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Genisteae; Lupinus.
 OX NCBI_TaxID=3870;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Saibo N.J.M., Van Der Straeten D., Rodrigues-Pousada C.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the tubulin family.
 DR EMBL; AF376053; AAN87551.1; -.
 DR HSSP; P02554; 1TUB.
 DR GO; GO:0005813; C:centrosome; ISS.
 DR GO; GO:0000794; C:condensed nuclear chromosome; ISS.

DR GO; GO:0000930; C:gamma-tubulin complex; ISS.
 DR GO; GO:0005827; C:polar microtubule; ISS.
 DR GO; GO:0005515; F:protein binding; ISS.
 DR GO; GO:0005200; F:structural constituent of cytoskeleton; ISS.
 DR GO; GO:0000212; P:meiotic spindle assembly; ISS.
 DR GO; GO:0007020; P:microtubule nucleation; ISS.
 DR GO; GO:0007052; P:mitotic spindle assembly; ISS.
 DR GO; GO:0007088; P:regulation of mitosis; ISS.
 DR InterPro; IPR002454; Gamma tubulin.
 DR InterPro; IPR000217; Tubulin.
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 DR InterPro; IPR008280; Tub_FtsZ_C.
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 DR Pfam; PF03953; Tubulin_C; 1.
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 DR PRINTS; PR01161; TUBULIN.
 DR PROSITE; PS00227; TUBULIN; UNKNOWN_1.
 KW GTP-binding; Microtubule.
 SQ SEQUENCE 472 AA; 53183 MW; 968965CF870844B CRC64;
 Query Match 76.5%; Score 39; DB 2; Length 472;
 Best Local Similarity 66.7%; Pred. No. 1e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 AYIDNKNKF 9
 Db 405 AFLDNVRFK 413
 ID TBG1_ARATH STANDARD; PRT; 474 AA.
 AC TBG1_ARATH
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Tubulin gamma-1 chain (Gamma-1 tubulin).
 GN Name=TUBG1; OrderedLocNames=At3g61650; ORFNames=F15G16.40;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=94198600; PubMed=8148650;
 RA Liu B., Joshi H.C., Wilson T.J., Silflow C.D., Palevitz B.A.,
 RA Snustad D.P.;
 RA "Gamma-tubulin in Arabidopsis: gene sequence, immunoblot, and
 RT immunofluorescence studies."
 RL Plant Cell 6:303-314(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016720; PubMed=11130713; DOI=10.1038/35048706;
 RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unsel M.,
 RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
 RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
 RA De Simone V., Choiane N., Artiguenave F., Robert C., Brottier P.,
 RA Wincker P., Cattolico L., Weissbach J., Saurin W., Quetier F.,
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
 RA Wurmelbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
 RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
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 RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordiek G.,
 RA Reichelt J., Scharfe M., Schoen O., Bagues M., Terol J., Clement J.,
 RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
 RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
 RA de Haan M., Maarso A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
 RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
 RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P.,
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,

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RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:820-822(2000).
CC
CC -1- FUNCTION: Tubulin is the major constituent of microtubules. Gamma
CC tubulin is found at microtubule organizing centers (MTOC) such as
CC the spindle poles or the centrosome, suggesting that it is
CC involved in the minus-end nucleation of microtubule assembly.
CC
CC -1- SIMILARITY: Belongs to the tubulin family.
CC
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CC PIR; T47957; T47957.
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CC InterPro; IPR002454; Gamma_tubulin.
CC InterPro; IPR008280; Tub_FtsZ_C.
CC InterPro; IPR000217; Tubulin_.
CC InterPro; IPR003008; Tubulin_FtsZ.
CC Pfam; PF00091; Tubulin; 1.
CC Pfam; PF03953; Tubulin_C; 1.
CC PRINTS; PR01161; TUBULIN.
CC PROSITE; PS00227; TUBULIN; 1.
CC GTP-binding; Microtubule; Multigene family.
KW NP BIND 142 148 GTP (Potential).
FT SEQUENCE 474 AA; 53246 MW; EE7636FF6277209D CRC64;
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Query Match 76.5%; Score 39; DB 1; Length 474;
Best Local Similarity 66.7%; Pred.No. 1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 AYIDNYNKF 9
Db 405 AFLDNYRKF 413
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Job time : 56.2473 secs

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OM protein - protein search, using sw model

Run on: June 29, 2005, 05:18:25 ; Search time 53.8517 Seconds
(without alignments)
64.268 Million cell updates/sec

Title: US-08-170-344-80

Perfect score: 51

Sequence: 1 AYIDNKNK 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	9	8	US-08-344-824-13
2	51	100.0	9	15	US-10-149-138-4201
3	51	100.0	9	15	US-10-149-138-4357
4	51	100.0	9	15	US-10-149-135-2198
5	51	100.0	9	15	US-10-149-135-2297
6	51	100.0	9	16	US-10-149-138-4201
7	51	100.0	9	16	US-10-149-138-4357
8	51	100.0	9	17	US-10-654-601-2492
9	51	100.0	9	17	US-10-751-845-121
10	42	82.4	349	14	US-10-270-875-57
11	42	82.4	349	14	US-10-270-878-57

12	42	82.4	349	14	US-10-270-786-57	Sequence 57, Appl
13	42	82.4	349	14	US-10-270-710-57	Sequence 57, Appl
14	42	82.4	349	14	US-10-270-859-57	Sequence 57, Appl
15	42	82.4	349	14	US-10-270-846-57	Sequence 57, Appl
16	42	82.4	871	14	US-10-270-875-36	Sequence 36, Appl
17	42	82.4	871	14	US-10-270-878-36	Sequence 36, Appl
18	42	82.4	871	14	US-10-270-786-36	Sequence 36, Appl
19	42	82.4	871	14	US-10-270-710-36	Sequence 36, Appl
20	42	82.4	871	14	US-10-270-859-36	Sequence 36, Appl
21	42	82.4	871	14	US-10-270-846-36	Sequence 36, Appl
22	39	76.5	343	15	US-10-425-114-61984	Sequence 61984, A
23	39	76.5	421	16	US-10-425-115-249343	Sequence 249343, A
24	39	76.5	469	16	US-10-437-963-115148	Sequence 115148, A
25	39	76.5	469	16	US-10-425-115-249348	Sequence 249348, A
26	39	76.5	469	16	US-10-425-115-249350	Sequence 249350, A
27	39	76.5	469	16	US-10-739-930-8534	Sequence 8534, Ap
28	39	76.5	925	16	US-10-437-963-199923	Sequence 199923, A
29	37	72.5	568	15	US-10-282-122A-53606	Sequence 53606, A
30	36	70.6	215	16	US-10-425-115-347860	Sequence 347860, A
31	36	70.6	303	9	US-09-765-272-202	Sequence 202, App
32	36	70.6	328	10	US-09-769-744A-48	Sequence 48, Appl
33	36	70.6	328	15	US-10-282-122A-74030	Sequence 74030, A
34	36	70.6	328	17	US-10-472-928-2766	Sequence 2766, Ap
35	36	70.6	734	15	US-10-618-581-31	Sequence 31, Appl
36	35	68.6	71	15	US-10-282-122A-53134	Sequence 53134, A
37	35	68.6	160	15	US-10-282-122A-53134	Sequence 53134, A
38	35	68.6	257	9	US-09-071-035-32	Sequence 32, Appl
39	35	68.6	257	14	US-10-206-576-32	Sequence 32, Appl
40	35	68.6	257	17	US-10-912-362-32	Sequence 32, Appl
41	35	68.6	277	9	US-09-071-035-30	Sequence 30, Appl
42	35	68.6	277	14	US-10-206-576-30	Sequence 30, Appl
43	35	68.6	277	15	US-10-282-122A-57209	Sequence 57209, A
44	35	68.6	277	17	US-10-912-362-30	Sequence 30, Appl
45	35	68.6	316	15	US-10-369-493-569	Sequence 569, App

ALIGNMENTS

RESULT 1
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; Sequence 13, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:

```
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-344-824-13

Query Match 100.0%; Score 51; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYIDNKNKF 9
Db 1 AYIDNKNKF 9

RESULT 2
US-10-149-138-4201
; Sequence 4201, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4201
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4201

Query Match 100.0%; Score 51; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYIDNKNKF 9
Db 1 AYIDNKNKF 9

RESULT 3
US-10-149-138-4357
; Sequence 4357, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4201
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4201

Query Match 100.0%; Score 51; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYIDNKNKF 9
Db 1 AYIDNKNKF 9

RESULT 4
US-10-149-135-2188
; Sequence 2188, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US/10/149,135
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2188
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-2188

Query Match 100.0%; Score 51; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYIDNKNKF 9
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Db      1 AYIDNKNF 9
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RESULT 5
US-10-149-135-2297
; Sequence 2297, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 08/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2297
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-2297

Query Match      100.0%; Score 51; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AYIDNKNF 9
|||||
Db      1 AYIDNKNF 9
|||||
RESULT 6
US-10-149-138-4201
; Sequence 4201, Application US/10149138
; Publication No. US20040121946A9
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4357
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4201

Query Match      100.0%; Score 51; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AYIDNKNF 9
|||||
Db      1 AYIDNKNF 9
|||||
RESULT 7
US-10-149-138-4357
; Sequence 4357, Application US/10149138
; Publication No. US20040121946A9
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4357
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4357

Query Match      100.0%; Score 51; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AYIDNKNF 9
|||||
Db      1 AYIDNKNF 9
|||||
RESULT 8
US-10-654-601-2492
; Sequence 2492, Application US/10654601
; Publication No. US20050063983A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitiello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
```

```
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/10/654,601
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/09/239,043
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2492
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Standard peptide that binds to HLA A*2401
US-10-654-601-2492
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Query Match 100.0%; Score 51; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AYIDNKNKF 9
|:|||||
DB 1 AYIDNKNKF 9
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RESULT 9
US-10-751-845-121
; Sequence 121, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 121
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-751-845-121
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Query Match 100.0%; Score 51; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 AYIDNKNKF 9
|:|||||
DB 1 AYIDNKNKF 9
```

```
RESULT 10
US-10-270-875-57
; Sequence 57, Application US/10270875
; Publication No. US20030082741A1
; GENERAL INFORMATION:
; APPLICANT: Sigridur Hjorleifsdottir
; APPLICANT: Gudmundur O. Hreggvidsson
; APPLICANT: Olafur H. Fridjonsson
; APPLICANT: Arnthor Aevarsson
; APPLICANT: Jakob K. Kristjansson
; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
; TITLE OF INVENTION: Host Organism
; FILE REFERENCE: 2739.1001-001
; CURRENT APPLICATION NUMBER: US/10/270,875
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/585,858
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/137,120
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Bacteriophage RM378
US-10-270-875-57
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Query Match 82.4%; Score 42; DB 14; Length 349;
Best Local Similarity 77.8%; Pred. No. 35;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AYIDNKNKF 9
|:|||||
DB 118 AHIDNKNKF 126
```

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RESULT 11
US-10-270-878-57
; Sequence 57, Application US/10270878
; Publication No. US20030082790A1
; GENERAL INFORMATION:
; APPLICANT: Sigridur Hjorleifsdottir
; APPLICANT: Gudmundur O. Hreggvidsson
; APPLICANT: Olafur H. Fridjonsson
; APPLICANT: Arnthor Aevarsson
; APPLICANT: Jakob K. Kristjansson
; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
; TITLE OF INVENTION: Host Organism
; FILE REFERENCE: 2739.1001-001
; CURRENT APPLICATION NUMBER: US/10/270,878
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/585,858
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Bacteriophage RM378
US-10-270-878-57
```

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Query Match 82.4%; Score 42; DB 14; Length 349;
Best Local Similarity 77.8%; Pred. No. 35;
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Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYIDNKNKF 9
|:|:|:|:|
Db 118 AHIDNFKF 126

RESULT 12

US-10-270-786-57
; Sequence 57, Application US/10270786
; Publication No. US20030087392A1
; GENERAL INFORMATION:
; APPLICANT: Sigrður Hjørleifsdóttir
; APPLICANT: Guðmundur O. Hreggviðsson
; APPLICANT: Ólafur H. Friðjónsson
; APPLICANT: Arnthor Aevartsson
; APPLICANT: Jakob K. Kristjánsson
; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
; TITLE OF INVENTION: Host Organism
; FILE REFERENCE: 2739.1001-001
; CURRENT APPLICATION NUMBER: US/10/270,786
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/585,858
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/137,120
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Bacteriophage RM378
US-10-270-786-57

Query Match 82.4%; Score 42; DB 14; Length 349;
Best Local Similarity 77.8%; Pred. No. 35;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYIDNKNKF 9
|:|:|:|:|
Db 118 AHIDNFKF 126

RESULT 13

US-10-270-710-57
; Sequence 57, Application US/10270710
; Publication No. US20030092128A1
; GENERAL INFORMATION:
; APPLICANT: Sigrður Hjørleifsdóttir
; APPLICANT: Guðmundur O. Hreggviðsson
; APPLICANT: Ólafur H. Friðjónsson
; APPLICANT: Arnthor Aevartsson
; APPLICANT: Jakob K. Kristjánsson
; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
; TITLE OF INVENTION: Host Organism
; FILE REFERENCE: 2739.1001-001
; CURRENT APPLICATION NUMBER: US/10/270,710
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/585,858
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/137,120
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Bacteriophage RM378
US-10-270-710-57

Query Match 82.4%; Score 42; DB 14; Length 349;
Best Local Similarity 77.8%; Pred. No. 35;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYIDNKNKF 9
|:|:|:|:|
Db 118 AHIDNFKF 126

RESULT 14

US-10-270-859-57
; Sequence 57, Application US/10270859
; Publication No. US20030092134A1
; GENERAL INFORMATION:
; APPLICANT: Sigrður Hjørleifsdóttir
; APPLICANT: Guðmundur O. Hreggviðsson
; APPLICANT: Ólafur H. Friðjónsson
; APPLICANT: Arnthor Aevartsson
; APPLICANT: Jakob K. Kristjánsson
; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
; TITLE OF INVENTION: Host Organism
; FILE REFERENCE: 2739.1001-001
; CURRENT APPLICATION NUMBER: US/10/270,859
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/585,858
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/137,120
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Bacteriophage RM378
US-10-270-859-57

Query Match 82.4%; Score 42; DB 14; Length 349;
Best Local Similarity 77.8%; Pred. No. 35;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYIDNKNKF 9
|:|:~|:~|:~|
Db 118 AHIDNFKF 126

RESULT 15

US-10-270-846-57
; Sequence 57, Application US/10270846
; Publication No. US20030129727A1
; GENERAL INFORMATION:
; APPLICANT: Sigrður Hjørleifsdóttir
; APPLICANT: Guðmundur O. Hreggviðsson
; APPLICANT: Ólafur H. Friðjónsson
; APPLICANT: Arnthor Aevartsson
; APPLICANT: Jakob K. Kristjánsson
; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
; TITLE OF INVENTION: Host Organism
; FILE REFERENCE: 2739.1001-001
; CURRENT APPLICATION NUMBER: US/10/270,846
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/585,858
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/137,120
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Bacteriophage RM378
US-10-270-846-57

Query Match 82.4%; Score 42; DB 14; Length 349;
Best Local Similarity 77.8%; Pred. No. 35;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYIDNKNF 9
|:|:|:|
Db 118 AHIDNKNF 126

Search completed: June 29, 2005, 05:48:18
Job time : 53.8517 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:37:59 ; Search time 16.8626 Seconds
(without alignments)
39.842 Million cell updates/sec

Title: US-08-170-344-80

Perfect score: 51

Sequence: 1 AYTDNKNF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	9	3	US-08-159-339A-128
2	51	100.0	9	4	US-09-543-608A-48
3	51	100.0	9	4	US-09-239-043D-2492
4	42	82.4	349	4	US-09-585-858-57
5	42	82.4	349	4	US-10-270-878-57
6	42	82.4	871	4	US-09-585-858-36
7	42	82.4	871	4	US-10-270-878-36
8	39	76.5	300	4	US-09-248-796A-15551
9	36	70.6	250	4	US-09-248-796A-27542
10	36	70.6	303	3	US-08-961-083-202
11	36	70.6	303	4	US-09-536-784-202
12	36	70.6	328	4	US-09-583-110-3554
13	36	70.6	331	4	US-09-107-433-4710
14	35	68.6	9	3	US-08-159-339A-127
15	35	68.6	153	4	US-09-270-767-32948
16	35	68.6	153	4	US-09-270-767-48165
17	35	68.6	257	4	US-09-071-035-32
18	35	68.6	277	4	US-09-071-035-30
19	35	68.6	278	4	US-09-134-000C-4965
20	35	68.6	291	4	US-09-107-532A-7234
21	35	68.6	382	4	US-09-540-236-3108
22	35	68.6	445	4	US-09-543-681A-6637
23	35	68.6	731	4	US-09-134-000C-4355
24	34.5	67.6	144	4	US-09-248-796A-27829
25	34	66.7	205	4	US-09-248-796A-18009
26	34	66.7	245	1	US-08-015-985-8
27	34	66.7	245	4	US-09-280-597-8

28	34	66.7	263	2	US-08-685-992-5	Sequence 5, Appli
29	34	66.7	263	2	US-09-144-925-5	Sequence 5, Appli
30	34	66.7	290	4	US-09-585-858-49	Sequence 49, Appl
31	34	66.7	290	4	US-10-270-878-49	Sequence 49, Appl
32	34	66.7	471	4	US-09-107-532A-4629	Sequence 4629, Ap
33	34	66.7	706	4	US-09-949-016-7086	Sequence 7086, Ap
34	34	66.7	1006	4	US-09-949-016-7897	Sequence 7897, Ap
35	34	66.7	1442	1	US-08-015-986A-3	Sequence 3, Appli
36	34	66.7	1442	2	US-08-446-363-3	Sequence 2, Appli
37	34	66.7	1445	1	US-08-015-986A-2	Sequence 2, Appli
38	34	66.7	1445	2	US-08-446-363-2	Sequence 2, Appli
39	33	64.7	60	4	US-09-248-796A-25820	Sequence 25820, A
40	33	64.7	123	4	US-09-270-767-33977	Sequence 33977, A
41	33	64.7	123	4	US-09-270-767-49194	Sequence 49194, A
42	33	64.7	269	4	US-09-543-681A-5309	Sequence 5309, Ap
43	33	64.7	282	4	US-09-248-796A-14879	Sequence 14879, A
44	33	64.7	297	4	US-09-248-796A-22761	Sequence 22761, A
45	33	64.7	320	2	US-08-245-511-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-159-339A-128
; Sequence 128, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ For Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 128:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-128

Query Match 100.0%; Score 51; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYIDNKNKF 9
 |||||
 Db 1 AYIDNKNKF 9

RESULT 2

US-09-543-608A-48
 ; Sequence 48, Application US/09543608A

; Patent No. 6602510

; GENERAL INFORMATION:

; APPLICANT: Fikes, John D.

; APPLICANT: Sette, Alessandro

; APPLICANT: Sidney, John

; APPLICANT: Southwood, Scott

; APPLICANT: Celis, Sateban

; APPLICANT: Keogh, Elissa A.

; APPLICANT: Chesnut, Robert

; APPLICANT: Epimmune Inc.

; TITLE OF INVENTION: HLA Class I A2 Tumor Associated Antigen

; TITLE OF INVENTION: Peptides and Vaccine Compositions

; FILE REFERENCE: 018623-015710US

; CURRENT APPLICATION NUMBER: US/09/543.608A

; CURRENT FILING DATE: 2002-04-05

; NUMBER OF SEQ ID NOS: 52

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 48

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Standard Peptide 979.02

US-09-543-608A-48

Query Match 100.0%; Score 51; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYIDNKNKF 9
 |||||
 Db 1 AYIDNKNKF 9

RESULT 3

US-09-239-043D-2492

; Sequence 2492, Application US/09239043D

; Patent No. 6689363

; GENERAL INFORMATION:

; APPLICANT: Sette, Alessandro

; APPLICANT: Sidney, John

; APPLICANT: Southwood, Scott

; APPLICANT: Vitiello, Maria A.

; APPLICANT: Livingston, Brian D.

; APPLICANT: Celis, Esteban

; APPLICANT: Kubo, Ralph T.

; APPLICANT: Grey, Howard M.

; APPLICANT: Chesnut, Robert

; APPLICANT: Epimmune Inc.

; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus

; TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions

; FILE REFERENCE: 2060.0060007

; CURRENT APPLICATION NUMBER: US/09/239.043D

; CURRENT FILING DATE: 1999-01-27

; PRIOR APPLICATION NUMBER: US 09/189, 702

; PRIOR FILING DATE: 1998-11-10

; PRIOR APPLICATION NUMBER: US 08/978, 291

; PRIOR FILING DATE: 1997-11-25

; PRIOR APPLICATION NUMBER: US 08/820, 360

; PRIOR FILING DATE: 1997-03-12
 ; PRIOR APPLICATION NUMBER: US 60/013, 363
 ; PRIOR FILING DATE: 1996-03-13
 ; PRIOR APPLICATION NUMBER: US 08/461, 603
 ; PRIOR FILING DATE: 1995-06-05
 ; PRIOR APPLICATION NUMBER: US 08/347, 610
 ; PRIOR FILING DATE: 1994-12-01
 ; PRIOR APPLICATION NUMBER: US 08/344, 824
 ; PRIOR FILING DATE: 1994-11-23
 ; PRIOR APPLICATION NUMBER: US 08/278, 634
 ; PRIOR FILING DATE: 1994-07-21
 ; PRIOR APPLICATION NUMBER: US 08/205, 713
 ; PRIOR FILING DATE: 1994-03-04
 ; PRIOR APPLICATION NUMBER: US 08/197, 484
 ; PRIOR FILING DATE: 1994-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 2579
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2492
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Standard peptide that binds to HLA A*2401
 US-09-239-043D-2492

Query Match 100.0%; Score 51; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYIDNKNKF 9
 |||||
 Db 1 AYIDNKNKF 9

RESULT 4

US-09-585-858-57

; Sequence 57, Application US/09585858

; Patent No. 6492161

; GENERAL INFORMATION:

; APPLICANT: Sigridur Hjorleifsdottir

; APPLICANT: Gudmundur O. Hreggvidsson

; APPLICANT: Olafur H. Fridjonsson

; APPLICANT: Arthor Aevansson

; APPLICANT: Jakob K. Kristjansson

; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic

; TITLE OF INVENTION: Host Organism

; FILE REFERENCE: 2739.1001-001

; CURRENT APPLICATION NUMBER: US/09/585,858

; CURRENT FILING DATE: 2000-12-18

; PRIOR APPLICATION NUMBER: 60/137,120

; PRIOR FILING DATE: 1999-06-02

; NUMBER OF SEQ ID NOS: 73

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 57

; LENGTH: 349

; TYPE: PRT

; ORGANISM: Bacteriophage RM378

US-09-585-858-57

Query Match 82.4%; Score 42; DB 4; Length 349;
 Best Local Similarity 77.8%; Pred. No. 12;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AYIDNKNKF 9
 |||||
 Db 118 AHIDNPNKF 126

RESULT 5

US-10-270-878-57

; Sequence 57, Application US/10270878

; Patent No. 6818425

; GENERAL INFORMATION:
; APPLICANT: Sigríður Hjörleifsdóttir
; APPLICANT: Guðmundur O. Hreggviðsson
; APPLICANT: Olafur H. Fridjónsson
; APPLICANT: Arnthor Aevarsson
; APPLICANT: Jakob K. Kristjánsson
; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
; FILE REFERENCE: 2739.1001-001
; CURRENT APPLICATION NUMBER: US/10/270,878
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/585,858
; PRIOR FILING DATE: 2000-12-18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 349
; TYPE: PRT
; ORGANISM: Bacteriophage RM378
US-10-270-878-57

Query Match 82.4%; Score 42; DB 4; Length 349;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYIDNYNKF 9
|:|:|:|
Db 118 AHIDNFKF 126

RESULT 6
US-09-585-858-36
; Sequence 36, Application US/09585858
; Patent No. 6492161
; GENERAL INFORMATION:
; APPLICANT: Sigríður Hjörleifsdóttir
; APPLICANT: Guðmundur O. Hreggviðsson
; APPLICANT: Olafur H. Fridjónsson
; APPLICANT: Arnthor Aevarsson
; APPLICANT: Jakob K. Kristjánsson
; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
; FILE REFERENCE: 2739.1001-001
; CURRENT APPLICATION NUMBER: US/09/585,858
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/137,120
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Bacteriophage RM378
US-09-585-858-36

Query Match 82.4%; Score 42; DB 4; Length 871;
Best Local Similarity 77.8%; Pred. No. 30;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYIDNYNKF 9
|:|:|:|
Db 118 AHIDNFKF 126

RESULT 7
US-10-270-878-36
; Sequence 36, Application US/10270878
; Patent No. 6818425
; GENERAL INFORMATION:
; APPLICANT: Sigríður Hjörleifsdóttir
; APPLICANT: Guðmundur O. Hreggviðsson
; APPLICANT: Olafur H. Fridjónsson
; APPLICANT: Arnthor Aevarsson

; APPLICANT: Jakob K. Kristjánsson
; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
; FILE REFERENCE: 2739.1001-001
; CURRENT APPLICATION NUMBER: US/10/270,878
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/585,858
; PRIOR FILING DATE: 2000-12-18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 871
; TYPE: PRT
; ORGANISM: Bacteriophage RM378
US-10-270-878-36

Query Match 82.4%; Score 42; DB 4; Length 871;
Best Local Similarity 77.8%; Pred. No. 30;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AYIDNYNKF 9
|:|:|:|
Db 118 AHIDNFKF 126

RESULT 8
US-09-248-796A-15551
; Sequence 15551, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15551
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-15551

Query Match 76.5%; Score 39; DB 4; Length 300;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YIDNYNKF 9
|:|:|:|
Db 104 YLDNYGKF 111

RESULT 9
US-09-248-796A-27542
; Sequence 27542, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBIC
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 27542

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; LENGTH: 250
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-27542

Query Match          70.6%; Score 36; DB 4; Length 250;
Best Local Similarity 85.7%; Pred. No. 90;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      3 IDVYNKF 9
Db      186 IDNFKF 192

RESULT 10
US-08-961-083-202
; Sequence 202, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,083
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 202:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 303 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-961-083-202

Query Match          70.6%; Score 36; DB 3; Length 303;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AYIDVYNKF 9
Db      200 AYIDIYQKF 208

RESULT 11
US-09-536-784-202
; Sequence 202, Application US/09536784
; Patent No. 6573082
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
```

```
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 202:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 303 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 202:
US-09-536-784-202

Query Match          70.6%; Score 36; DB 4; Length 303;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AYIDVYNKF 9
Db      200 AYIDIYQKF 208

RESULT 12
US-09-583-110-3554
; Sequence 3554, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 3554
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-3554

Query Match          70.6%; Score 36; DB 4; Length 328;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 AYIDNYNKF 9
Db 225 AYIDIYQKF 233

RESULT 13

US-09-107-433-4710
; Sequence 4710, Application US/09107433
; Patent No. 6800744

; GENERAL INFORMATION:

; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNO
; THERAPEUTICS

; NUMBER OF SEQUENCES: 5206

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GENOME THERAPEUTICS CORPORATION

; STREET: 100 Beaver Street

; CITY: Waltham

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02354

; COMPUTER READABLE FORM:

; MEDIUM TYPE: CD-ROM ISO9660

; COMPUTER: <Unknown>

; OPERATING SYSTEM: <Unknown>

; SOFTWARE: <Unknown>

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/107,433

; FILING DATE: 30-Jun-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/ 085131

; FILING DATE: May 12, 1998

; APPLICATION NUMBER: 60/051553

; FILING DATE: July 2, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Ariniello, Pamela Deneke

; REGISTRATION NUMBER: 40,489

; REFERENCE/DOCKET NUMBER: GTC-011

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (781)893-5007

; TELEFAX: (781)893-8277

; INFORMATION FOR SEQ ID NO: 4710:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 331 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: YES

; ORIGINAL SOURCE:

; ORGANISM: Streptococcus pneumoniae

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (B) LOCATION 1...331

; SEQUENCE DESCRIPTION: SEQ ID NO: 4710:

US-09-107-433-4710

Query Match

Best Local Similarity 70.6%; Score 36; DB 4; Length 331;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AYIDNYNKF 9

Db 228 AYIDIYQKF 236

RESULT 14

US-08-159-339A-127

; Sequence 127, Application US/08159339A

; Patent No. 6037135

; GENERAL INFORMATION:

; APPLICANT: Kubo, Ralph T.

; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/159,339A

; FILING DATE: 29-NOV-1993

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/926,666

; FILING DATE: 07-AUG-1992

; APPLICATION NUMBER: US 08/027,746

; FILING DATE: 05-MAR-1993

; APPLICATION NUMBER: US 08/103,396

; FILING DATE: 06-AUG-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Weber, Ellen Lauver

; REGISTRATION NUMBER: 32,762

; REFERENCE/DOCKET NUMBER: 018623-005030US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; TELEX:

; INFORMATION FOR SEQ ID NO: 127:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-159-339A-127

Query Match

Best Local Similarity 68.6%; Score 35; DB 3; Length 9;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AYIDNYNKF 9

Db 1 AYIDNVYKF 9

RESULT 15

US-09-270-767-32948

; Sequence 32948, Application US/09270767

; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 32948

; LENGTH: 153

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

US-09-270-767-32948

Query Match 68.6%; Score 35; DB 4; Length 153;
Best Local Similarity 71.4%; Pred. No. 82;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 IDNKNF 9
:||||:
Db 76 LDNKNRF 82

Search completed: June 29, 2005, 01:44:33
Job time : 17.9126 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:23:48 ; Search time 11.2 Seconds
(without alignments)
77.317 Million cell updates/sec

Title: US-08-170-344-8
Perfect score: 48
Sequence: 1 IHDIIIECV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	158	1 W6WLS	protein E6 - human
2	38	79.2	1140	2 F88349	protein F15D4.7 [i
3	38	79.2	1140	2 T20984	hypothetical prote
4	38	79.2	1496	2 T19833	hypothetical prote
5	37	77.1	1428	2 S62419	hypothetical prote
6	36	75.0	75	2 A13163	hypothetical prote
7	36	75.0	519	2 T24772	hypothetical prote
8	36	75.0	1164	2 T03814	tumor suppressor p
9	35	72.9	145	2 H83709	small heat shock p
10	35	72.9	158	1 W6WLP	E6 protein - human
11	35	72.9	307	2 H70214	antigen, P35 homol
12	35	72.9	321	1 XXBYF1	ATP adenyllyltransf
13	35	72.9	704	2 T19942	hypothetical prote
14	34	70.8	146	2 T32255	hypothetical prote
15	34	70.8	148	2 S36515	E6 protein - human
16	34	70.8	149	1 W6WLS	E6 protein - human
17	34	70.8	221	2 A87284	hydrolase, haloaci
18	34	70.8	249	2 B32352	molybdopterin bios
19	34	70.8	306	2 T45586	hypothetical prote
20	34	70.8	358	2 D82485	transcription regu
21	34	70.8	505	1 S24550	protein-tyrosine k
22	34	70.8	523	2 T04742	hypothetical prote
23	34	70.8	1073	2 F89467	protein R09H3.1 [i
24	34	70.8	1177	2 T16594	hypothetical prote
25	34	70.8	1201	2 G86441	unknown protein [i
26	33	68.8	32	2 S19006	E6-II protein - hu
27	33	68.8	35	2 S19909	E6-III protein - h
28	33	68.8	47	2 S23825	E6-I protein - hum
29	33	68.8	148	2 A61237	E6 protein - human

ALIGNMENTS

RESULT 1
W6WLS

protein E6 - human papillomavirus type 16

C;Species: human papillomavirus type 16

C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C;Accession: A03682; T10427

R;Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virolgy 145, 181-185, 1985

A;Title: Human papillomavirus type 16 DNA sequence.

A;Reference number: A22355; MUID:85246220; PMID:2990099

A;Accession: A03682

A;Molecule type: DNA

A;Residues: 1-158 <SEE>

A;Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333030

R;Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A;Title: A negative element in the human poapillomavirus type 16 genome acts at the lev

A;Reference number: Z17014; MUID:91162763; PMID:1848319

A;Accession: T10427

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-158 <KEN>

A;Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G3330302

C;Genetics:

A;Gene: E6

C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; zinc finger

F;37-73/Region: zinc finger CCCC motif

F;110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 48; DB 1; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.043;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIIIECV 9

|||||

Db 30 IHDIIIECV 38

RESULT 2

F88349

protein F15D4.7 [imported] - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C;Accession: F88349

R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo

A;Reference number: A75000; MUID:99069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/Projects/C.e

A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an

A;Accession: F88349

```
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1140 <STO>
A;Cross-references: UNIPROT:Q93515; GB:chr_II; PIDN:CAB02490.1; PID:g3875970; GSPDB:GN0000020; CESP:F15D4.7
C;Genetics:
A;Gene: F15D4.7
A;Map position: 2

Query Match          79.2%; Score 38; DB 2; Length 1140;
Best Local Similarity 55.6%; Pred. No. 30;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 IHDIIIECV 9
|||::||:
551 IHDWVAECI 559

RESULT 3
T20984
hypothetical protein F15D4.7 - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20984
R;Smye, R.
submitted to the EMBL Data Library, September 1996
A;Reference number: Z19354
A;Accession: T20984
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-1140 <WIL>
A;Cross-references: UNIPROT:Q93515; EMBL:Z80344; PIDN:CAB02490.1; GSPDB:GN000020; CESP:F15D4.7
A;Gene: CESP:F15D4.7
A;Map position: 2
A;Introns: 747/73

Query Match          79.2%; Score 38; DB 2; Length 1140;
Best Local Similarity 55.6%; Pred. No. 30;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 IHDIIIECV 9
|||::||:
551 IHDWVAECI 559

RESULT 4
T19833
hypothetical protein C38D9.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19833
R;Ainscough, R.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19184
A;Accession: T19833
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-1496 <WIL>
A;Cross-references: UNIPROT:Q9XVC3; EMBL:Z81481; PIDN:CAB03949.1; GSPDB:GN000023; CESP:C38D9.3
C;Genetics:
A;Gene: CESP:C38D9.3
A;Map position: 5
A;Introns: 786/73

Query Match          79.2%; Score 38; DB 2; Length 1496;
Best Local Similarity 55.6%; Pred. No. 39;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 IHDIIIECV 9
|||::||:
590 IHDWVAECI 598
```

```
RESULT 5
S62419
hypothetical protein SPAC22F3.04 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: T38187; S62419
R;Iye, G.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, October 1995
A;Reference number: Z21776
A;Accession: T38187
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-1428 <LY2>
A;Cross-references: UNIPROT:Q09773; EMBL:Z54285; NID:gl008429; PIDN:CAA91069.1; PID:gl008429
A;Experimental source: strain 972h-; cosmid c22F3
C;Genetics:
A;Gene: SPAC22F3.04
A;Map position: 1L
A;Introns: 1042/1; 1114/1; 1187/3; 1308/2; 1381/2

Query Match          77.1%; Score 37; DB 2; Length 1428;
Best Local Similarity 75.0%; Pred. No. 58;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 HDIIIECV 9
||:||||:
1344 HEIILDCV 1351

RESULT 6
AI3163
hypothetical protein Atu5034 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AI3163
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
erge, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayin, T.; Levy, R.; Li, M.; McClellan,
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, B.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AI3163
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-75 <KUR>
A;Cross-references: UNIPROT:Q8UK35; GB:AE008687; PIDN:AAL45727.1; PID:gl7743458; GSPDB:
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu5034
A;Genome: plasmid

Query Match          75.0%; Score 36; DB 2; Length 75;
Best Local Similarity 71.4%; Pred. No. 4.8;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 HDIIIECV 8
||:||||
22 HDIIIECV 28
```

```
RESULT 7
T24772
hypothetical protein T10B10.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24772
R;Sims, M.
submitted to the EMBL Data Library, May 1996
A;Reference number: Z19934
```

A:Accession: T24772
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-519 <WIL>
A:Cross-references: UNIPROT:Q22374; EMBL:272514; PIDN:CAA96679.1; GSPDB:GN00028; CESP:TI
A:Experimental source: clone T10B10
C:Genetics:
A:Gene: CESP:T10B10.7
A:Map position: X
A:Introns: 47/3; 139/1; 183/1; 215/2; 249/2; 385/3; 440/3

Query Match 75.0%; Score 36; DB 2; Length 519;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIIIEC 8
|:|:|:|
Db 335 IYDIIEC 342

RESULT 8
T03814
tumor suppressor protein hamartin - human
C:Species: Homo sapiens (man)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T03814
R:van Slegtenhorst, M.; de Hoogt, R.; Hermans, C.; Nellist, M.; Janssen, B.; Verhoef, S.;
Fox, M.; Ekong, R.; Osborne, J.; Wolfe, J.; Povey, S.; Snell, R.G.; Cheadle, J.P.; Jo
Science 277, 805-808, 1997
A:Authors: Richardson, P.; Wilmer, F.; Munro, C.; Hawkins, T.L.; Sepp, T.; Ali, J.B.M.;
Iatkowski, D.J.
A:Title: Identification of the tuberous sclerosis gene TSC1 on chromosome 9q34.
A:Reference number: 215098; MUID:97390505; PMID:9242607
A:Accession: T03814
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1164 <VAN>
A:Cross-references: UNIPROT:Q92574; EMBL:AF013168; NID:g23331280; PIDN:AACS1674.1; PID:g2
C:Genetics:
A:Gene: TSC1
A:Map position: 9q34

Query Match 75.0%; Score 36; DB 2; Length 1164;
Best Local Similarity 57.1%; Pred. No. 75;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HDIIIEC 8
|:|:|:|
Db 253 HDVVIEC 259

RESULT 9
H83709
small heat shock protein BH0480 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: H83709
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: H83709
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-145 <STO>
A:Cross-references: UNIPROT:Q9KEFJ9; GB:AF001508; GB:BA000004; NID:g10172890; PIDN:BAB041
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH0480
C:Superfamily: alpha-crystallin-related small heat shock protein

Query Match 72.9%; Score 35; DB 2; Length 145;
Best Local Similarity 71.4%; Pred. No. 15;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HDIIIEC 8
|:|:|:|
Db 48 HEVILEC 54

RESULT 10
W6WLP
E6 protein - human papillomavirus type ME180 (provirus)
C:Species: human papillomavirus type ME180
A>Note: host Homo sapiens (man)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: C40509
R:Reuter, S.; Delius, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.
J. Virol. 65, 5564-5568, 1991
A:Title: Characterization of a novel human papillomavirus DNA in the cervical carcinoma
A:Reference number: A40509; MUID:91374616; PMID:1716694
A:Accession: C40509
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-158 <REU>
A:Cross-references: UNIPROT:P27962; GB:W73258
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:32-68/Region: zinc finger CCCC motif
F:105-141/Region: zinc finger CCCC motif

Query Match 72.9%; Score 35; DB 1; Length 158;
Best Local Similarity 44.4%; Pred. No. 16;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IHDIIIECV 9
|:|:|:|
Db 25 LHDVTIDCV 33

RESULT 11
H70214
antigen, p35 homolog - Lyme disease spirochete plasmid A/lp54
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C>Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
C:Accession: H70214
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Whit
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: H70214
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-307 <KLE>
A:Cross-references: UNIPROT:Q9R7J2; GB:AE000790; NID:g2690224; PIDN:AAC66255.1; PID:g26
A:Experimental source: strain B31
C:Genetics:
C:Genome: plasmid
C:Superfamily: Borrelia burgdorferi hypothetical protein BB138

Query Match 72.9%; Score 35; DB 2; Length 307;
Best Local Similarity 77.8%; Pred. No. 31;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IHDIIIECV 9
|:|:|:|
Db 288 IHDIIIDLV 296

RESULT 12
XXBYPI
ATP adenyllyltransferase (EC 2.7.7.53) I - yeast (Saccharomyces cerevisiae)
N:Alternate names: diadenosinetetraphosphate alpha-beta-phosphorylase I; protein YCL050

N;Contains: sulfate adenylyltransferase (ADP) (EC 2.7.7.5)
C;Species: Saccharomyces cerevisiae
C;Date: 31-Mar-1991 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: S12946; S17970; S19380; S07847; A37535; JQ0793
R;Kaushal, V.; Avila, D.M.; Hardies, S.C.; Barnes, L.D.
Gene 95, 79-84, 1990
A;Title: Sequencing and enhanced expression of the gene encoding diadenosine 5',5'''-P(1)
A;Reference number: JQ0793; MUID:91071609; PMID:2174812
A;Accession: S12946
A;Molecule type: DNA
A;Residues: 1-321 <KAU>
A;Cross-references: UNIPROT:P16550; GB:M35204; NID:g171425; PIDN:AAA34581.1; PID:g171426
A;Accession: S17970
A;Molecule type: protein
A;Residues: 49-78,'W',80-84;281-321 <KAU2>
R;Fuller, L.J.; Kelly, A.; Lewis, C.; McKee, R.A.; Pearson, B.M.
submitted to the Protein Sequence Database, March 1992
A;Reference number: S19380
A;Accession: S19380
A;Molecule type: DNA
A;Residues: 1-321 <FUL>
A;Cross-references: EMBL:X59720; NID:g1907116; PIDN:CAA42394.1; PID:g5311; GSPDB:GN00003
R;Plateau, P.; Fromant, M.; Schmitter, J.M.; Buhler, J.M.; Blanquet, S.
J. Bacteriol. 171, 6437-6445, 1989
A;Title: Isolation, characterization, and inactivation of the APA1 gene encoding yeast
A;Reference number: S07847; MUID:90076083; PMID:2556364
A;Accession: S07847
A;Molecule type: DNA
A;Residues: 1-99,'E',101-321 <PLA>
A;Cross-references: GB:M31791; NID:g171063; PIDN:AAA34427.1; PID:g171064
A;Accession: A37535
A;Molecule type: protein
A;Residues: 15-33;39-99,'E',101-260;263-321 <PLA2>
C;Genetics:
A;Gene: SGD:APAL; DTP1; MIPS:YCL050C
A;Cross-references: SGD:S0000555; MIPS:YCL050C
A;Map position: 3L
C;Superfamily: ATP adenylyltransferase
C;Keywords: acetylated amino end; blocked amino end; nucleotidyltransferase
F;2-321/Product: ATP adenylyltransferase I #status predicted <MAT>
F;2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted

Query Match 72.9%; Score 35; DB 1; Length 321;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IHDIIILEC 8
|:|:|:|:|
DB 299 INDIIILEC 306

RESULT 13
T19942
hypothetical protein C44H4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19942
R;Smye, R.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z19200
A;Accession: T19942
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-704 <WIL>
A;Cross-references: UNIPROT:Q93376; EMBL:Z79598; PIDN:CAB01868.1; GSPDB:GN00028; CESP:C4
A;Experimental source: clone C44H4
C;Genetics:
A;Gene: CESP:C44H4.4
A;Map position: X
A;Introns: 15/2; 50/3; 82/3; 107/2; 146/3; 183/3; 229/1; 335/1; 401/1; 514/3; 540/3; 629
C;Superfamily: Caenorhabditis elegans hypothetical protein C44H4.4

Query Match 72.9%; Score 35; DB 2; Length 704;

Best Local Similarity 44.4%; Pred. No. 71;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 IHDIIILECV 9
|:|:|:|:|
DB 424 VHDLTITQCV 432

RESULT 14
T32255
hypothetical protein T15B7.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32255
R;Pauley, A.; Gattung, S.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid T15B7.
A;Reference number: Z21139
A;Accession: T32255
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-146 <PAU>
A;Cross-references: UNIPROT:O17043; EMBL:AF022985; PIDN:AAB69973.1; GSPDB:GN00023; CESP:
A;Experimental source: strain Bristol N2; clone T15B7
C;Genetics:
A;Gene: CESP:T15B7.1
A;Map position: 5
A;Introns: 13/2; 87/3

Query Match 70.8%; Score 34; DB 2; Length 146;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 IHDIIILECV 9
|:|:|:|:|
DB 132 IHPVKECV 140

RESULT 15
S36515
E6 protein - human papillomavirus type 34
C;Species: human papillomavirus type 34
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36515
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36515
A;Molecule type: DNA
A;Residues: 1-148
A;Cross-references: UNIPROT:P36811; EMBL:X74476; NID:g396989; PIDN:CAA52555.1; PID:g396
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 70.8%; Score 34; DB 2; Length 148;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 IHDIIILECV 9
|:|:|:|:|
DB 24 IHEIIEIDCV 32

Search completed: June 28, 2005, 19:23:22
Job time : 12.2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 17:44:26 ; Search time 55.3 Seconds
(without alignments)
83.340 Million cell updates/sec

Title: US-08-170-344-8
Perfect score: 48
Sequence: 1 IHDIILECV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	26	2 Q81956	Q81956 human papil
2	48	100.0	130	2 Q919B8	Q919B8 human papil
3	48	100.0	130	2 Q919C0	Q919C0 human papil
4	48	100.0	130	2 Q919C2	Q919C2 human papil
5	48	100.0	130	2 Q919D0	Q919D0 human papil
6	48	100.0	138	2 Q919D2	Q919D2 human papil
7	48	100.0	143	2 Q919B6	Q919B6 human papil
8	48	100.0	143	2 Q919C4	Q919C4 human papil
9	48	100.0	151	2 Q12335	Q12335 human papil
10	48	100.0	151	2 Q12336	Q12336 human papil
11	48	100.0	151	2 Q76TS0	Q76TS0 human papil
12	48	100.0	151	2 Q77E16	Q77E16 human papil
13	48	100.0	151	2 Q77E16	Q77E16 human papil
14	48	100.0	151	2 Q77JC7	Q77JC7 human papil
15	48	100.0	151	2 Q77ZJ5	Q77ZJ5 human papil
16	48	100.0	151	2 Q80963	Q80963 human papil
17	48	100.0	151	2 Q80966	Q80966 human papil
18	48	100.0	151	2 Q89648	Q89648 human papil
19	48	100.0	151	2 Q89708	Q89708 human papil
20	48	100.0	151	2 Q89755	Q89755 human papil
21	48	100.0	151	2 Q89852	Q89852 human papil
22	48	100.0	151	2 Q89887	Q89887 human papil
23	48	100.0	151	2 Q9W8C3	Q9W8C3 human papil
24	48	100.0	151	2 Q9W931	Q9W931 human papil
25	48	100.0	151	2 Q9WMP2	Q9WMP2 human papil
26	48	100.0	151	2 Q9WMP4	Q9WMP4 human papil
27	48	100.0	158	1 VE6_HPV16	VE6_HPV16 human papil
28	48	100.0	158	2 Q8JMH8	Q8JMH8 human papil
29	48	100.0	158	2 Q8QHNO	Q8QHNO human papil
30	48	100.0	158	2 Q8QHP5	Q8QHP5 human papil
31	48	100.0	158	2 Q8QRD5	Q8QRD5 human papil

32 48 100.0 158 2 Q8QRD6
33 48 100.0 158 2 Q8QRD7
34 48 100.0 158 2 Q8QRD8
35 48 100.0 158 2 Q71BI7
36 48 100.0 158 2 Q9WH13
37 48 100.0 161 2 Q919C6
38 48 100.0 161 2 Q919D4
39 46 95.8 151 2 Q9WMP5
40 45 93.8 151 2 Q8B920
41 44 91.7 151 2 Q89640
42 44 91.7 158 2 Q8QHT0
43 44 91.7 158 2 Q8QRD9
44 44 91.7 158 2 Q8QRE0
45 44 91.7 158 2 Q8QRE1

Q8qrds human papil
Q8qrds human papil
Q8qrds human papil
Q71bi7 human papil
Q9wh13 human papil
Q919c6 human papil
Q919d4 human papil
Q9wmp5 human papil
Q8bb20 human papil
Q89640 human papil
Q8qht0 human papil
Q8qrds human papil
Q8qre0 human papil
Q8qre1 human papil

ALIGNMENTS

RESULT 1

Q81956 PRELIMINARY; PRT; 26 AA.
AC Q81956;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE E6E7 (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SIHA.
RA Shippy R., Siwkowski A., Hampel A.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U59900; AAB03505.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; B6.
DR Pfam; PF00518; B6; 1.
FT NON_TER 1 1
SQ SEQUENCE 26 AA; 3208 MW; F06EBBE995EB67D5 CRC64;
Query Match 100.0%; Score 48; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIILECV 9
Db 6 IHDIILECV 14

RESULT 2

Q919B8 PRELIMINARY; PRT; 130 AA.
AC Q919B8;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RL "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404701; AAL01359.1; -.

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DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15775 MW; 92D3C07BF96B092F CRC64;
  Query Match 100.0%; Score 48; DB 2; Length 130;
  Best Local Similarity 100.0%; Pred. No. 0.14;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIIIECV 9
Db 2 IHDIIIECV 10

RESULT 3
Q919C0 PRELIMINARY; PRT; 130 AA.
AC Q919C0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040700; AAL01357.1; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
  Query Match 100.0%; Score 48; DB 2; Length 130;
  Best Local Similarity 100.0%; Pred. No. 0.14;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIIIECV 9
Db 2 IHDIIIECV 10

RESULT 4
Q919C2 PRELIMINARY; PRT; 130 AA.
AC Q919C2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040699; AAL01355.1; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.

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FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
  Query Match 100.0%; Score 48; DB 2; Length 130;
  Best Local Similarity 100.0%; Pred. No. 0.14;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIIIECV 9
Db 2 IHDIIIECV 10

RESULT 5
Q919D0 PRELIMINARY; PRT; 130 AA.
AC Q919D0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040695; AAL01347.1; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15735 MW; 9EFB30EEDCA21AF3 CRC64;
  Query Match 100.0%; Score 48; DB 2; Length 130;
  Best Local Similarity 100.0%; Pred. No. 0.14;
  Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIIIECV 9
Db 2 IHDIIIECV 10

RESULT 6
Q919D2 PRELIMINARY; PRT; 138 AA.
AC Q919D2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040694; AAL01345.1; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 138 AA; 16696 MW; 481E5AEA90895FC2 CRC64;

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Query Match 100.0%; Score 48; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIIILECV 9
Db 10 IHDIIILECV 18

RESULT 7
Q919B6 PRELIMINARY; PRT; 143 AA.
AC Q919B6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404702; AAL01361.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;

Query Match 100.0%; Score 48; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIIILECV 9
Db 15 IHDIIILECV 23

RESULT 8
Q919C4 PRELIMINARY; PRT; 143 AA.
AC Q919C4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404698; AAL01353.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 IHDIIILECV 9
Db 15 IHDIIILECV 23

RESULT 9
O12335 PRELIMINARY; PRT; 151 AA.
AC O12335;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003015; AAB70732.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18238 MW; BEF32A8B016CC88B CRC64;

Query Match 100.0%; Score 48; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIIILECV 9
Db 23 IHDIIILECV 31

RESULT 10
O12336 PRELIMINARY; PRT; 151 AA.
AC O12336;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003016; AAB70733.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;

Query Match 100.0%; Score 48; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 IHDIIIECV 9
Db 23 IHDIIIECV 31

RESULT 11
Q76TSO PRELIMINARY; PRT; 151 AA.
ID Q76TSO
AC Q76TSO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34114; AAA91661.1; -.
DR EMBL; U34125; AAA91672.1; -.
DR EMBL; U34130; AAA91677.1; -.
DR EMBL; U34131; AAA91678.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18292 MW; 35012A9E0193C35 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIIIECV 9
Db 23 IHDIIIECV 31

RESULT 12
Q77816 PRELIMINARY; PRT; 151 AA.
ID Q77816
AC Q77816;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388056; CAB45104.1; -.
DR EMBL; AJ388061; CAB45114.1; -.
DR EMBL; AJ388066; CAB45124.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.

Qy 1 IHDIIIECV 9
Db 23 IHDIIIECV 31

RESULT 13
Q77E16 PRELIMINARY; PRT; 151 AA.
ID Q77E16
AC Q77E16;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 oncoprotein (E6 protein).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AF469197; AA015691.1; -.
DR EMBL; AJ388063; CAB45118.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CF1F CRC64;

Query Match 100.0%; Score 48; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIIIECV 9
Db 23 IHDIIIECV 31

RESULT 14
Q77JC7 PRELIMINARY; PRT; 151 AA.
ID Q77JC7
AC Q77JC7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6 variant (Transforming protein E6).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Xinjiang;
RA Ma Z., Qian D., Ma J., Lin R., Ming W., Zhong Z., Zhang Q., Zhang F.;
RT "Cloning and Sequencing of HPV16 E6 gene from Cervical Carcinoma
RT Biopsies in Xinjiang.";

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RL  Sheng Wu Hua Xue Yu Sheng Wu Wu Li Jin Zhan 0:0-0(2001).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=20112892; PubMed=10644829;
RA  van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA  Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT  "Analysis of human papillomavirus type 16 E6 variants in relation to
RL  p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RN  J. Gen. Virol. 81:317-325(2000).
RN  [3]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=22242222; PubMed=12355268; DOI=10.1007/s00239-002-2344-y;
RA  Derilippis V.R., Ayala F.G., Villarreal L.P.;
RT  "Evidence of diversifying selection in human papillomavirus type 16 E6
RL  but not E7 oncogenes.";
RN  J. Mol. Evol. 55:491-499(2002).
RN  [4]
RP  SEQUENCE FROM N.A.
RA  Cruz Mr., Cerqueira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,
RA  Martins C.R.F.;
RL  Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN  [5]
RP  SEQUENCE FROM N.A.
RA  Cruz M.R., Martins C.R.F.;
RL  Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AF327851; AAG45940.1; -
DR  EMBL; AJ388057; CAB45106.1; -
DR  EMBL; AJ388069; CAB45130.1; -
DR  EMBL; AY089951; AAM11875.1; -
DR  EMBL; AY089954; AAM11881.1; -
DR  EMBL; AY112663; AAM51854.1; -
DR  GO; GO:0042025; C:host cell nucleus; IEA.
DR  GO; GO:0003677; F:DNA binding; IEA.
DR  InterPro; IPR01334; E6.
DR  Pfam; PF00518; E6; 1.
DR  SEQUENCE 151 AA; 18320 MW; 617D2A2FDB4F8C17 CRC64;
SQ

Query Match          100.0%; Score 48; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 IHDIILECV 9
Db  23 IHDIILECV 31

RESULT 15
Q77ZJ5
ID  Q77ZJ5      PRELIMINARY;      PRT;    151 AA.
AC  Q77ZJ5;
DT  05-JUL-2004 (TrEMBLrel. 27, Created)
DT  05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT  05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE  E6 protein.
OS  Human papillomavirus type 16.
OC  Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC  Papillomavirus.
OX  NCBI_TaxID=10581;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=97437474; PubMed=9292007;
RA  Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA  Beth-Giraldo E., Giraldo G.;
RT  "Sequence variations and viral genomic state of human papillomavirus
RL  type 16 in penile carcinomas from Ugandan patients.";
RN  J. Gen. Virol. 78:2199-2208(1997).
DR  EMBL; AF003018; AAB70735.1; -
DR  GO; GO:0042025; C:host cell nucleus; IEA.
DR  GO; GO:0003677; F:DNA binding; IEA.
DR  InterPro; IPR001334; E6.
DR  Pfam; PF00518; E6; 1.
DR  SEQUENCE 151 AA; 18221 MW; 60CD2A34DAF48CB7 CRC64;
SQ
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Query Match          100.0%; Score 48; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 IHDIILECV 9
Db  23 IHDIILECV 31
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Search completed: June 28, 2005, 19:19:22
Job time : 56.3 secs

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OM protein - protein search, using sw model

Run on: June 29, 2005, 01:35:30 ; Search time 57.55 Seconds
(without alignments)

60.138 Million cell updates/sec

Title: US-08-170-344-8

Perfect score: 48

Sequence: 1 IHDIIIECV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	48	100.0	10	14	US-10-128-711-72
2	48	100.0	10	14	US-10-133-210-280
3	48	100.0	15	16	US-10-476-570-22
4	48	100.0	15	16	US-10-476-570-23
5	48	100.0	21	16	US-10-476-570-10
6	48	100.0	30	16	US-10-476-570-53
7	48	100.0	30	17	US-10-476-384-4
8	48	100.0	32	16	US-10-476-570-9
9	48	100.0	33	16	US-10-476-570-19
10	48	100.0	151	14	US-10-177-390-6
11	48	100.0	151	17	US-10-484-063-20
					Sequence 72, Appl
					Sequence 280, Appl
					Sequence 22, Appl
					Sequence 23, Appl
					Sequence 10, Appl
					Sequence 53, Appl
					Sequence 4, Appl
					Sequence 9, Appl
					Sequence 19, Appl
					Sequence 6, Appl
					Sequence 20, Appl

12 48 100.0 151 17 US-10-484-063-27 Sequence 27, Appl
13 48 100.0 158 17 US-10-858-384-2 Sequence 2, Appl
14 48 100.0 158 17 US-10-367-057-16 Sequence 16, Appl
15 48 100.0 171 16 US-10-472-724-2 Sequence 2, Appl
16 48 100.0 266 9 US-09-367-309A-1 Sequence 1, Appl
17 48 100.0 273 13 US-10-000-903-4 Sequence 4, Appl
18 48 100.0 273 17 US-10-899-771-4 Sequence 4, Appl
19 48 100.0 292 13 US-10-000-903-10 Sequence 10, Appl
20 48 100.0 292 17 US-10-899-771-10 Sequence 10, Appl
21 48 100.0 371 13 US-10-000-903-6 Sequence 6, Appl
22 48 100.0 371 17 US-10-899-771-6 Sequence 6, Appl
23 48 100.0 390 13 US-10-000-903-14 Sequence 14, Appl
24 48 100.0 390 17 US-10-899-771-14 Sequence 14, Appl
25 48 100.0 536 15 US-10-367-095-10 Sequence 10, Appl
26 48 100.0 536 15 US-10-368-046-10 Sequence 10, Appl
27 48 100.0 536 16 US-10-367-367-10 Sequence 10, Appl
28 48 100.0 536 17 US-10-918-337-10 Sequence 10, Appl
29 44 91.7 9 16 US-10-777-053-547 Sequence 547, App
30 44 91.7 9 16 US-10-837-217-547 Sequence 547, App
31 44 91.7 15 16 US-10-476-570-24 Sequence 275411,
32 39 81.2 297 15 US-10-424-599-275411 Sequence 168507,
33 39 81.2 298 15 US-10-424-599-168507 Sequence 168507,
34 38 79.2 428 16 US-10-425-115-193535 Sequence 193535,
35 37 77.1 554 16 US-10-739-930-10846 Sequence 10846, A
36 37 77.1 601 16 US-10-437-963-195430 Sequence 195430,
37 36 75.0 58 15 US-10-424-599-219049 Sequence 219049,
38 36 75.0 70 14 US-10-029-386-33593 Sequence 33593, A
39 36 75.0 83 16 US-10-425-115-205547 Sequence 205547, A
40 36 75.0 274 15 US-10-425-114-58813 Sequence 58813, A
41 36 75.0 274 15 US-10-425-114-65774 Sequence 65774, A
42 36 75.0 291 16 US-10-437-963-145297 Sequence 145297,
43 36 75.0 294 15 US-10-424-599-187372 Sequence 187372,
44 36 75.0 294 15 US-10-425-114-52907 Sequence 52907, A
45 36 75.0 297 16 US-10-767-701-36891 Sequence 36891, A

ALIGNMENTS

RESULT 1
US-10-128-711-72
; Sequence 72, Application US/10128711
; Publication No. US20030099634A1
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; CHESTNUT, Robert W.
; SETTE, Alessandro D.
; CELIS, Esteban
; GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10128,711
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992

; APPLICATION NUMBER: US 07/874,491
 ; FILING DATE: 27-APR-1992
 ; APPLICATION NUMBER: US 07/827,682
 ; FILING DATE: 29-JAN-1992
 ; APPLICATION NUMBER: US 07/749,568
 ; FILING DATE: 26-AUG-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Parmelee, Steven W.
 ; REGISTRATION NUMBER: 31,990
 ; REFERENCE/DOCKET NUMBER: 14137-26-4
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 467-9600
 ; TELEFAX: (206) 623-6793
 ; INFORMATION FOR SEQ ID NO: 72:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 72:
 US-10-128-711-72

Query Match 100.0%; Score 48; DB 14; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIILECV 9
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 Db 2 IHDIILECV 10

RESULT 2

US-10-133-210-280
 ; Sequence 280, Application US/10133210
 ; Publication No. US20030101964A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Delisi, Charles
 ; APPLICANT: Berzofsky, Jay
 ; APPLICANT: Gulukota, Kamalakur
 ; APPLICANT: Vaccaro, Dennis
 ; APPLICANT: Weng, Zhiping
 ; APPLICANT: Zhang, Chao
 ; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
 ; TITLE OF INVENTION: COMPOSITIONS THEREOF
 ; FILE REFERENCE: BU-035AX
 ; CURRENT APPLICATION NUMBER: US/10/133,210
 ; CURRENT FILING DATE: 2002-04-26
 ; NUMBER OF SEQ ID NOS: 281
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 280
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-10-133-210-280

Query Match 100.0%; Score 48; DB 14; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.031;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIILECV 9
 | | | | | | | |
 Db 2 IHDIILECV 10

RESULT 3

US-10-476-570-22
 ; Sequence 22, Application US/10476570
 ; Publication No. US20040170644A1
 ; GENERAL INFORMATION:
 ; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE

; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
 ; APPLICANT: MAILLIERE, Bernard
 ; APPLICANT: BOURGAULT-VILLADA, Isabelle
 ; APPLICANT: POUVELLE-MORATILLE, Sandra
 ; APPLICANT: GUILLET, Jean-Gerard
 ; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
 ; TITLE OF INVENTION: papillomavirus proteins and uses thereof
 ; FILE REFERENCE: 45636-5071-US
 ; CURRENT APPLICATION NUMBER: US/10/476,570
 ; CURRENT FILING DATE: 2003-11-04
 ; PRIOR APPLICATION NUMBER: PCT/FR02/01533
 ; PRIOR FILING DATE: 2002-05-03
 ; PRIOR APPLICATION NUMBER: FR 01 05980
 ; PRIOR FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 22
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of the artificial sequence: peptide E6 24-38
 US-10-476-570-22

Query Match 100.0%; Score 48; DB 16; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.047;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIILECV 9
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 Db 7 IHDIILECV 15

RESULT 4

US-10-476-570-23
 ; Sequence 23, Application US/10476570
 ; Publication No. US20040170644A1
 ; GENERAL INFORMATION:
 ; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
 ; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
 ; APPLICANT: MAILLIERE, Bernard
 ; APPLICANT: BOURGAULT-VILLADA, Isabelle
 ; APPLICANT: POUVELLE-MORATILLE, Sandra
 ; APPLICANT: GUILLET, Jean-Gerard
 ; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
 ; TITLE OF INVENTION: papillomavirus proteins and uses thereof
 ; FILE REFERENCE: 45636-5071-US
 ; CURRENT APPLICATION NUMBER: US/10/476,570
 ; CURRENT FILING DATE: 2003-11-04
 ; PRIOR APPLICATION NUMBER: PCT/FR02/01533
 ; PRIOR FILING DATE: 2002-05-03
 ; PRIOR APPLICATION NUMBER: FR 01 05980
 ; PRIOR FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 23
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of the artificial sequence: peptide E6 28-42
 US-10-476-570-23

Query Match 100.0%; Score 48; DB 16; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.047;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIILECV 9
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 Db 3 IHDIILECV 11

RESULT 5

US-10-476-570-10
; Sequence 10, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 21
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 30-50
US-10-476-570-10
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Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IHDIIIECV 9
Db 1 IHDIIIECV 9
RESULT 6
US-10-476-570-53
; Sequence 53, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 30
; TYPE: PRT
; ORGANISM: artificial sequence
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; OTHER INFORMATION: Description of the artificial sequence: peptide E6 15-44
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Best Local Similarity 100.0%; Pred. No. 0.097;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IHDIIIECV 9

Db 16 IHDIIIECV 24
RESULT 7
US-10-858-384-4
; Sequence 4, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
US-10-858-384-4
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Best Local Similarity 100.0%; Pred. No. 0.097;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 IHDIIIECV 9
Db 16 IHDIIIECV 24
RESULT 8
US-10-476-570-9
; Sequence 9, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 32
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-45
US-10-476-570-9
Query Match 100.0%; Score 48; DB 16; Length 32;

Best Local Similarity 100.0%; Pred. No. 0.1; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 IHDIILECV 9
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Db 17 IHDIILECV 25

RESULT 9
US-10-476-570-19
; Sequence 19, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from B6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 33
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-46
US-10-476-570-19

Query Match 100.0%; Score 48; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIILECV 9
| | | | |
Db 17 IHDIILECV 25

RESULT 10
US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerp Innovatiscentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6

Query Match 100.0%; Score 48; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIILECV 9
| | | | |

Db 23 IHDIILECV 31

RESULT 11
US-10-484-063-20
; Sequence 20, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-20

Query Match 100.0%; Score 48; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIILECV 9
| | | | |
Db 23 IHDIILECV 31

RESULT 12
US-10-484-063-27
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-484-063-27

Query Match 100.0%; Score 48; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIILECV 9
| | | | |
Db 23 IHDIILECV 31

RESULT 13
US-10-858-384-2

; Sequence 2, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match 100.0%; Score 48; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIIILECV 9
Db 30 IHDIIILECV 38

RESULT 14

US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Cui, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match 100.0%; Score 48; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIIILECV 9
Db 30 IHDIIILECV 38

RESULT 15

US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination

; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match 100.0%; Score 48; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIIILECV 9
Db 35 IHDIIILECV 43

Search completed: June 29, 2005, 03:24:07
Job time : 57.55 sec

is Page Blank (uspto)

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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:27:48 ; Search time 17.15 Seconds
(without alignments)

39.174 Million cell updates/sec

Title: US-08-170-344-8

Perfect score: 48

Sequence: 1 IHDIIIECV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	10	3	US-08-159-339A-73
2	48	100.0	10	4	US-08-197-484-72
3	48	100.0	10	4	US-09-601-729-273
4	48	100.0	10	5	PCT-US95-02121-72
5	48	100.0	30	4	US-09-980-523A-4
6	48	100.0	59	3	US-09-390-027-6
7	48	100.0	158	4	US-09-980-523A-2
8	48	100.0	162	1	US-08-316-239B-3
9	48	100.0	162	1	US-08-316-239B-4
10	48	100.0	172	3	US-08-860-165-14
11	48	100.0	172	3	US-09-359-382-14
12	48	100.0	182	1	US-08-117-083-10
13	48	100.0	266	3	US-08-860-165-10
14	48	100.0	266	3	US-09-359-382-10
15	48	100.0	266	4	US-09-367-309A-1
16	48	100.0	273	3	US-09-485-885-4
17	48	100.0	292	3	US-09-485-885-10
18	48	100.0	371	3	US-09-485-885-6
19	48	100.0	390	3	US-09-485-885-14
20	44	91.7	14	1	US-07-909-122-3
21	44	91.7	30	1	US-08-363-586-4
22	41	85.4	620	4	US-09-248-796A-15013
23	36	75.0	10	3	US-08-159-339A-573
24	36	75.0	374	4	US-09-638-337-2
25	36	75.0	1164	3	US-09-457-708-2
26	36	75.0	1164	4	US-09-950-046A-2
27	36	75.0	1164	4	US-09-976-594-989

Sequence 5595, Ap
Sequence 33608, A
Sequence 48825, A
Sequence 13381, A
Sequence 4, Appl
Sequence 6713, Ap
Sequence 17124, A
Sequence 24727, A
Sequence 5486, Ap
Sequence 568, Ap
Sequence 60201, A
Sequence 29181, A
Sequence 8022, Ap
Sequence 22434, A
Sequence 44745, A
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-08-159-339A-73
Sequence 73, Application US/08159339A
Patent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-159-339A-73

Query Match 100.0%; Score 48; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIIIECV 9
| | | | | | | | | |
Db 1 IHDIIIECV 9

RESULT 2

US-08-197-484-72
; Sequence 72, Application US/08197484
; Patent No. 6419931
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Esteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/197,484
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-197-484-72

Query Match 100.0%; Score 48; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIIIECV 9

Db 2 IHDIIIECV 10
| | | | | | | | | |

RESULT 3

US-09-601-729-273
; Sequence 273, Application US/09601729
; Patent No. 6681052
; GENERAL INFORMATION:
; APPLICANT: THIAM, KADER
; APPLICANT: AURIAULT, CLAUDE
; APPLICANT: GRAS-MASSE, HELENE
; APPLICANT: LOING, ESTELLE
; APPLICANT: VERWAERDE, CLAUDIE
; APPLICANT: GUILLET, JEAN GERARD
; TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES
; TITLE OF INVENTION: THEREOF IN PHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: USB-97-AU-IN
; CURRENT APPLICATION NUMBER: US/09/601,729
; PRIOR APPLICATION NUMBER: PCT/FR99/00259
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 98 01439
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 273
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-601-729-273

Query Match 100.0%; Score 48; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIIIECV 9
| | | | | | | | | |
Db 2 IHDIIIECV 10

RESULT 4

PCT-US95-02121-72
; Sequence 72, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US95-02121-72

Query Match 100.0%; Score 48; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIIILECV 9
| | | | | | | | | |
Db 2 IHDIIILECV 10

RESULT 5
US-09-980-523A-4
; Sequence 4, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: WO/1 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-4

Query Match 100.0%; Score 48; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIIILECV 9
| | | | | | | | | |
Db 16 IHDIIILECV 24

RESULT 6
US-09-390-027-6
; Sequence 6, Application US/09390027
; Patent No. 6235523
; GENERAL INFORMATION:
; APPLICANT: GAJEWCZYK, Diane M.
; APPLICANT: PERSSON, Roy
; APPLICANT: YAO, Fei-Long

; APPLICANT: CAO, Shi-Xian
; APPLICANT: KLEIN, Michel H.
; APPLICANT: TARTAGLIA, James
; APPLICANT: MOINGEON, Philippe
; APPLICANT: ROVINSKI, Benjamin
; TITLE OF INVENTION: TREATMENT OF CERVICAL CANCER
; FILE REFERENCE: 1038-982 MIS:jb
; CURRENT APPLICATION NUMBER: US/09/390,027
; CURRENT FILING DATE: 1999-09-03
; EARLIER APPLICATION NUMBER: 60/099,291
; EARLIER FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-390-027-6

Query Match 100.0%; Score 48; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIIILECV 9
| | | | | | | | | |
Db 51 IHDIIILECV 59

RESULT 7
US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: WO/1 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 48; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIIILECV 9
| | | | | | | | | |
Db 30 IHDIIILECV 38

RESULT 8
US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.

```

; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/316,239B
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-316-239B-3

Query Match 100.0%; Score 48; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIILECV 9
Db 30 IHDIILECV 38

RESULT 9
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```

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; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-316-239B-4

Query Match 100.0%; Score 48; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIILECV 9
Db 30 IHDIILECV 38

RESULT 10
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
; US-08-860-165-14

Query Match 100.0%; Score 48; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIILECV 9
Db 99 IHDIILECV 107

RESULT 11
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann

```

```
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match      100.0%; Score 48; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIILECV 9
Db 99 IHDIILECV 107

RESULT 12
US-08-117-083-10
; Sequence 10, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Boursnell, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
```

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; OTHER INFORMATION: /note= "Xaa refers to stop codon in
; OTHER INFORMATION: the open reading frame."
US-08-117-083-10

Query Match      100.0%; Score 48; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIILECV 9
Db 31 IHDIILECV 39

RESULT 13
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match      100.0%; Score 48; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIILECV 9
Db 30 IHDIILECV 38

RESULT 14
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
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; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match      100.0%; Score 48; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIILECV 9
Db 30 IHDIILECV 38

RESULT 15
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match      100.0%; Score 48; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IHDIILECV 9
Db 30 IHDIILECV 38
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Search completed: June 28, 2005, 19:29:11
Job time : 17.15 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:32:21 ; Search time 11.2747 Seconds
(without alignments)
76.805 Million cell updates/sec

Title: US-08-170-344-79
Perfect score: 48
Sequence: 1 AVDLYHFLK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	81.2	110	2 C75038	hypothetical prote
2	39	81.2	182	2 S03247	nef protein (clone
3	39	81.2	204	2 S03246	nef protein (clone
4	39	81.2	204	2 S24985	nef protein - huma
5	39	81.2	205	1 ASLJH3	nef protein - huma
6	39	81.2	205	2 S43467	nef protein - huma
7	39	81.2	205	2 JC7975	HIV accessory prot
8	39	81.2	206	1 ASLJ12	nef protein - huma
9	39	81.2	206	1 ASLJFV	nef protein - huma
10	39	81.2	206	1 ASLJVL	nef protein - huma
11	39	81.2	206	2 S03245	nef protein (clone
12	39	81.2	206	2 S33986	nef protein - huma
13	39	81.2	206	2 S03244	nef protein (clone
14	39	81.2	206	2 JC5400	nef protein - Huma
15	39	81.2	207	1 QQLJND	nef protein - huma
16	39	81.2	212	1 QQLJZR	nef protein - huma
17	39	81.2	218	1 ASLJBR	nef protein - huma
18	38	79.2	279	2 T34461	hypothetical prote
19	37	77.1	401	2 F88678	protein H06H21.1
20	36	75.0	97	2 S54385	nef protein - huma
21	36	75.0	214	1 I44001	nef protein - huma
22	36	75.0	1703	2 S15047	SNF2 protein - yea
23	35	72.9	107	2 T16784	hypothetical prote
24	35	72.9	132	1 E70434	conserved hypotet
25	35	72.9	209	2 S61204	NEF protein - simi
26	35	72.9	229	1 ASLJW4	nef protein - simi
27	35	72.9	238	2 S61205	NEF protein - simi
28	35	72.9	239	2 S61206	NEF protein - simi
29	35	72.9	239	2 S54852	nef protein - simi

30	35	72.9	240	2 S24572	nef protein - huma
31	35	72.9	244	2 S61208	NEF protein - simi
32	35	72.9	246	2 S54853	nef protein - simi
33	35	72.9	250	2 S61207	NEF protein - simi
34	35	72.9	255	1 ASLJGN	nef protein - huma
35	35	72.9	255	2 S53099	nef protein - huma
36	35	72.9	250	1 ASLJJC	nef protein - huma
37	35	72.9	429	2 A70949	hypothetical prote
38	35	72.9	477	2 C59098	hypothetical prote
39	35	72.9	526	1 A34164	cholesterol monoox
40	35	72.9	552	2 AC0609	conserved hypotet
41	35	72.9	641	2 A24075	lipase precursor -
42	35	72.9	688	2 E88197	protein him-14 [im
43	35	72.9	848	2 T28055	hypothetical prote
44	35	72.9	1425	2 T30811	hepatocyte growth
45	35	72.9	2018	2 T34274	hypothetical prote

ALIGNMENTS

RESULT 1

C75038

hypothetical protein PAB0853 - Pyrococcus abyssi (strain Orsay)

C;Species: Pyrococcus abyssi

C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C;Accession: C75038

R;anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str

A;Reference number: A75001

A;Accession: C75038

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-110 <KAW>

A;Cross-references: UNIPROT:Q9UZ59; GB:AJ248287; GB:AL096836; NID:g5458657; PIDN:CAB502

A;Experimental source: strain Orsay

C;Genetics:

A;Gene: PAB0853

Query Match 81.2%; Score 39; DB 2; Length 110;
Best Local Similarity 77.8%; Pred. No. 1.8;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVDLYHFLK 9
|||::||
DB 69 AVDLYVYLK 77

RESULT 2

S03247

nef protein (clone C15) - human immunodeficiency virus type 1 (fragment)

N;Alternate names: 3'-orf protein

C;Species: human immunodeficiency virus type 1, HIV-1

C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Jun-2000

C;Accession: S03247

R;Ratner, L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, E.P.; Livak, K.J.; Pettew

Nucleic Acids Res. 13, 8219-8229, 1985

A;Title: Polymorphism of the 3' open reading frame of the virus associated with the ac

A;Reference number: S03244; MUID:86067228; PMID:2999715

A;Accession: S03247

A;Molecule type: mRNA

A;Residues: 1-182 <RAT>

A;Cross-references: EMBL:X03189; NID:g61552; PIDN:CAA26948.1; PID:g1335562

C;Genetics:

A;Gene: nef; 3'-orf; orf-F

C;Superfamily: AIDS nef protein

Query Match 81.2%; Score 39; DB 2; Length 182;
Best Local Similarity 88.9%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVDLYHFLK 9

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Db          60 AVDLSHFLK 68
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nef protein (clone HAT3) - human immunodeficiency virus type 1
RESULT 3
S03246
N:Alternate names: 3'-orf protein
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Sep-1999
C:Accession: S03246
R:Ratner, L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, K.J.; Petteway
Nucleic Acids Res. 13, 8219-8229, 1985
A>Title: Polymorphism of the 3' open reading frame of the virus associated with the acqu
A:Reference number: S03244; MUID:86067228; PMID:2999715
A:Accession: S03246
A:Molecule type: DNA
A:Residues: 1-204 <RAT>
A:Cross-references: EMBL:X03190; NID:g61550; PIDN:CAA26949.1; PID:g61551
A>Note: the authors translated the codon AGT for residue 11 as Gly
C:Genetics:
A:Gene: nef; 3'-orf; orf-F
C:Superfamily: AIDS nef protein
Query Match      81.2%; Score 39; DB 2; Length 204;
Best Local Similarity 88.9%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 AVDLYHFLK 9
||||| |||||
Db 82 AVDLSHFLK 90

RESULT 4
S24985
nef protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S24985
R:Harris, M.; Hislop, S.; Patsilinasos, P.; Neil, J.C.
submitted to the EMBL Data Library, November 1991
A:Description: In vivo derived HIV-1 NEF genes are heterogeneous and lack detectable nuc
A:Reference number: S24985
A:Accession: S24985
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-204 <HAR>
A:Cross-references: UNIPROT:Q76352; EMBL:X63044; NID:g60123; PIDN:CAA44770.1; PID:g60124
C:Superfamily: AIDS nef protein
Query Match      81.2%; Score 39; DB 2; Length 204;
Best Local Similarity 88.9%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 AVDLYHFLK 9
||||| |||||
Db 82 AVDLSHFLK 90

RESULT 5
ASLJH3
nef protein - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N:Alternate names: 3'-orf protein; orf-F protein
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C>Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C:Accession: A04005
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dora
nberger, J.A.; Papas, T.S.; Graybe, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A>Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2578615
A:Accession: A04005
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A:Molecule type: DNA
A:Residues: 1-205 <RAT>
A:Cross-references: UNIPROT:P03404
C:Genetics:
A:Gene: nef; 3'-orf; orf-F
C:Superfamily: AIDS nef protein
C:Keywords: AIDS; immunodeficiency
Query Match      81.2%; Score 39; DB 1; Length 205;
Best Local Similarity 88.9%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 AVDLYHFLK 9
||||| |||||
Db 84 AVDLSHFLK 92

RESULT 6
S43467
nef protein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S43467
R:Freund, J.; Kellner, R.; Houthaeve, T.; Kalbitzer, H.R.
Eur. J. Biochem. 221, 811-819, 1994
A>Title: Stability and proteolytic domains of Nef protein from human immunodeficiency v
A:Reference number: S43467; MUID:94229079; PMID:8174561
A:Accession: S43467
A:Molecule type: protein
A>Status: preliminary
A:Residues: 1-205 <PRE>
A:Cross-references: UNIPROT:Q9YYU9; UNIPROT:Q9WM30; UNIPROT:Q9PXM9; UNIPROT:O40177; UNI
PROT:Q9WM24
C:Superfamily: AIDS nef protein
Query Match      81.2%; Score 39; DB 2; Length 205;
Best Local Similarity 88.9%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 AVDLYHFLK 9
||||| |||||
Db 83 AVDLSHFLK 91

RESULT 7
JC7975
HIV accessory protein Nef - mouse
C:Species: Mus musculus (house mouse)
C>Date: 25-Aug-2003 #sequence_revision 25-Aug-2003 #text_change 15-Sep-2003
C:Accession: JC7975
R;Secco, P.; Cotella, D.; Santoro, C.
Biochem. Biophys. Res. Commun. 305, 1061-1066, 2003
A>Title: Selection of peptides with affinity for the N-terminal domain of GATA-1: Ident
A:Reference number: JC7975; PMID:12767938
A:Accession: JC7975
A:Molecule type: DNA
A:Residues: 1-205 <SEC>
C:Comment: This protein, an accessory viral protein, acts as a nuclear regulatory facto
binds p53 via its amino-terminal domain and protects cell against p53-mediated apoptos
C:Keywords: GATA-1; Nef
Query Match      81.2%; Score 39; DB 2; Length 205;
Best Local Similarity 88.9%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 AVDLYHFLK 9
||||| |||||
Db 84 AVDLSHFLK 92

RESULT 8
ASLJ12
nef protein - human immunodeficiency virus type 1 (isolate HTLV-III, 12)
```


N;Alternate names: 3'-orf protein; orf-F protein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: A04006
R;Arya, S.K.; Gallo, R.C.
Proc. Natl. Acad. Sci. U.S.A. 83, 2209-2213, 1986
A;Title: Three novel genes of human T-lymphotropic virus type III: immune reactivity of
A;Reference number: A94093; MUID:86177573; PMID:3008154
A;Accession: A04006
A;Molecule type: DNA
A;Residues: 1-206 <ARY>
A;Cross-references: UNIPROT:P04324; EMBL:M11840; NID:G328453; PIDN:AAA45001.1; PID:G3284
C;Genetics:
A;Gene: nef; 3'-orf; orf-F
C;Superfamily: AIDS nef protein
C;Keywords: AIDS; immunodeficiency

Query Match 81.2%; Score 39; DB 1; Length 206;
Best Local Similarity 88.9%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
||| ||||
Db 84 AVDLSHFLK 92

RESULT 9

ASLJFV
nef protein - human immunodeficiency virus type 1 (isolate LAV-1a)
N;Alternate names: 3'-orf protein; orf-F protein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C;Accession: A04008; S14609
R;Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A;Title: Nucleotide sequence of the AIDS virus, LAV.
A;Reference number: A90866; MUID:85099333; PMID:2981635
A;Accession: A04008
A;Molecule type: DNA
A;Residues: 1-206 <WAI>
A;Cross-references: UNIPROT:P03406; GB:K02013; NID:G326417; PIDN:AAB59752.1; PID:G326425
A;Experimental source: isolate LAV-1a
R;Ciccarelli, R.B.
submitted to the EMBL Data Library, March 1991
A;Reference number: S14607
A;Accession: S14609
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-206 <CIC>
A;Cross-references: EMBL:X58780; NID:G60113; PIDN:CAA41585.1; PID:G60114
C;Genetics:
A;Gene: nef; 3'-orf; orf-F
C;Superfamily: AIDS nef protein
C;Keywords: AIDS; immunodeficiency; phosphoprotein

Query Match 81.2%; Score 39; DB 1; Length 206;
Best Local Similarity 88.9%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
||| ||||
Db 84 AVDLSHFLK 92

RESULT 10

ASLJVL
nef protein - human immunodeficiency virus type 1 (isolate LV)
N;Alternate names: 3'-orf protein; orf-F protein
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C;Accession: A04007

R;Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.
Nature 313, 450-458, 1985
A;Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrov
A;Reference number: A93355; MUID:85111157; PMID:2982104
A;Accession: A04007
A;Molecule type: DNA
A;Residues: 1-206 <MUE>
A;Cross-references: UNIPROT:P03405; GB:K02083; NID:G555008; PIDN:AAB59874.1; PID:G32856
C;Genetics:
A;Gene: nef; 3'-orf; orf-F
C;Superfamily: AIDS nef protein
C;Keywords: AIDS; immunodeficiency

Query Match 81.2%; Score 39; DB 1; Length 206;
Best Local Similarity 88.9%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
||| ||||
Db 84 AVDLSHFLK 92

RESULT 11

S03245
nef protein (clone HXB3) - human immunodeficiency virus type 1
N;Alternate names: 3'-orf protein
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 20-Sep-1999
C;Accession: S03245
R;Ratner, L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, E.P.; Livak, K.J.; Pettew
Nucleic Acids Res. 13, 8219-8229, 1985
A;Title: Polymorphism of the 3' open reading frame of the virus associated with the acq
A;Reference number: S03244; MUID:86067228; PMID:2999715
A;Accession: S03245
A;Molecule type: DNA
A;Residues: 1-206 <RAT>
A;Cross-references: EMBL:X03188; NID:G61556; PIDN:CAA26947.1; PID:G61557
C;Genetics:
A;Gene: nef; 3'-orf; orf-F
C;Superfamily: AIDS nef protein

Query Match 81.2%; Score 39; DB 2; Length 206;
Best Local Similarity 88.9%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
||| ||||
Db 84 AVDLSHFLK 92

RESULT 12

S33986
nef protein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S33986
R;Carlini, F.
submitted to the EMBL Data Library, November 1991
A;Reference number: S33979
A;Accession: S33986
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-206 <CAR>
A;Cross-references: UNIPROT:Q78244; EMBL:Z11530; NID:G60192; PIDN:CAA77629.1; PID:G60202
C;Superfamily: AIDS nef protein

Query Match 81.2%; Score 39; DB 2; Length 206;
Best Local Similarity 88.9%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
||| ||||
Db 84 AVDLSHFLK 92

RESULT 13

S03244
nef protein (clone HXB2) - human immunodeficiency virus type 1
N;Alternate names: 3'-orf protein
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S03244
R;Ratner, L.; Starcich, B.; Josephs, S.F.; Hahn, B.H.; Reddy, E.P.; Livak, K.J.; Petteway
Nucleic Acids Res. 13, 8219-8229, 1985
A;Title: Polymorphism of the 3' open reading frame of the virus associated with the acqu
A;Reference number: S03244; MUID:86067228; PMID:2999715
A;Accession: S03244
A;Molecule type: DNA
A;Residues: 1-206 <RAT>
A;Cross-references: UNIPROT:Q9PM30; UNIPROT:Q9PM30; UNIPROT:Q40177; UNIPROT:Q90179; UNIF
L:X03187
A;Note: the in-frame stop codon at residue 124, shown as 'X', may be suppressed
C;Genetics:
A;Gene: nef; 3'-orf; orf-F
C;Superfamily: AIDS nef protein

Query Match 81.2%; Score 39; DB 2; Length 206;
Best Local Similarity 88.9%; Pred. No. 3.6; Indels 1; Gaps 0;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
|||||
Db 84 AVDLSHFLK 92

RESULT 14

JC5400
nef protein - Human immunodeficiency virus type 1, HIV-1
C;Species: Human immunodeficiency virus type 1, HIV-1
C;Date: 07-Jul-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C;Accession: JC5400
R;Macreadie, I.G.; Lowe, M.G.; Curtain, C.C.; Hewish, D.; Azad, A.A.
Biochem. Biophys. Res. Commun. 232, 707-711, 1997
A;Title: Cytotoxicity resulting from addition of HIV-1 Nef N-terminal peptides to yeast
A;Reference number: JC5400; MUID:97271389; PMID:9126340
A;Accession: JC5400
A;Molecule type: protein
A;Residues: 1-206 <MAC>
A;Cross-references: UNIPROT:Q9YYU9; UNIPROT:Q9MM30; UNIPROT:Q9PM30; UNIPROT:Q40177; UNIF
C;Comment: The amino-terminal part possesses membrane-perturbing and fusogenic activitie
lla.
C;Superfamily: AIDS nef protein
F;2-206/Product: nef protein #status predicted <MAT>

Query Match 81.2%; Score 39; DB 2; Length 206;
Best Local Similarity 88.9%; Pred. No. 3.6; Indels 1; Gaps 0;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
|||||
Db 84 AVDLSHFLK 92

RESULT 15

Q00688
nef protein - human immunodeficiency virus type 1 (isolate NDK)
N;Alternate names: 3'-orf protein; orf-F protein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: Q00688
R;Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A.;
Gene 81, 275-284, 1989
A;Title: Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the human immunc
A;Reference number: JQ0065; MUID:90034200; PMID:2806917
A;Accession: JQ0068

A;Molecule type: DNA
A;Residues: 1-207 <SPI>

A;Cross-references: UNIPROT:P18801; GB:M27323; NID:g328154; PIDN:AAA44874.1; PID:g32816

C;Genetics:
A;Gene: nef

C;Superfamily: AIDS nef protein

C;Keywords: AIDS; immunodeficiency

Query Match 81.2%; Score 39; DB 1; Length 207;
Best Local Similarity 88.9%; Pred. No. 3.6; Indels 1; Gaps 0;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
|||||
Db 85 AVDLSHFLK 93

Search completed: June 29, 2005, 01:38:55

Job time : 12.2747 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:28:22 ; Search time 54.2473 Seconds
(without alignments)
84.958 Million cell updates/sec

Title: US-08-170-344-79
Perfect score: 48
Sequence: 1 AVDLYHFLK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	83.3	349	2 Q73HE7	Q73he7 wolbachia p
2	39	81.2	110	2 Q9UZ59	Q9uz59 pyrococcus
3	39	81.2	110	2 Q900A5	Q900a5 human immun
4	39	81.2	110	2 Q903T9	Q903t9 human immun
5	39	81.2	113	2 Q8U3E1	Q8u3e1 pyrococcus
6	39	81.2	115	2 Q97005	Q97005 human immun
7	39	81.2	115	2 Q8AQF7	Q8aqf7 human immun
8	39	81.2	116	2 Q40241	O40241 human immun
9	39	81.2	116	2 Q40242	O40242 human immun
10	39	81.2	120	2 Q41540	O41540 human immun
11	39	81.2	121	2 Q76348	Q76348 human immun
12	39	81.2	121	2 Q79786	Q79786 human immun
13	39	81.2	123	1 NEF_HV1B1	P03404 human immun
14	39	81.2	123	1 NEF_HV1H2	P04601 human immun
15	39	81.2	131	2 Q6UEV0	Q6uev0 human immun
16	39	81.2	131	2 Q6UEW8	Q6uew8 human immun
17	39	81.2	131	2 Q6UF95	Q6uf95 human immun
18	39	81.2	131	2 Q6UF83	Q6uf83 human immun
19	39	81.2	131	2 Q6UFD1	Q6ufd1 human immun
20	39	81.2	131	2 Q6UFF9	Q6uff9 human immun
21	39	81.2	131	2 Q6UFL9	Q6ufl9 human immun
22	39	81.2	134	2 Q8AU42	Q8au42 human immun
23	39	81.2	135	2 Q6UFC2	Q6ufc2 human immun
24	39	81.2	137	2 Q8AJZ9	Q8ajz9 human immun
25	39	81.2	137	2 Q8AK08	Q8ak08 human immun
26	39	81.2	139	2 Q6UFG6	Q6ufg6 human immun
27	39	81.2	141	2 Q8JE98	Q8je98 human immun
28	39	81.2	142	2 Q8JE95	Q8je95 human immun
29	39	81.2	142	2 Q8JE96	Q8je96 human immun
30	39	81.2	142	2 Q8JE97	Q8je97 human immun
31	39	81.2	142	2 Q8JE99	Q8je99 human immun

32 39 81.2 143 2 Q8AIJ8 Q8aij8 human immun
33 39 81.2 144 2 Q8ADN0 Q8adn0 human immun
34 39 81.2 145 2 Q80156 Q80156 human immun
35 39 81.2 146 2 Q8AU26 Q8au26 human immun
36 39 81.2 147 2 Q8AU28 Q8au28 human immun
37 39 81.2 153 2 Q74916 Q74916 human immun
38 39 81.2 155 2 P88431 P88431 human immun
39 39 81.2 162 2 Q89WX3 Q89wx3 bradyrhizob
40 39 81.2 166 2 Q8AU33 Q8au33 human immun
41 39 81.2 176 2 Q74918 Q74918 human immun
42 39 81.2 181 2 Q9DRP1 Q9drp1 human immun
43 39 81.2 182 2 Q80820 Q80820 human t-cel
44 39 81.2 182 2 Q85574 Q85574 aids-associ
45 39 81.2 185 2 Q9DRN9 Q9drn9 human immun

ALIGNMENTS

RESULT 1

Q73HE7 PRELIMINARY; PRT; 349 AA.
AC Q73HE7; 2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE L-allo-threonine aldolase, putative.
GN OrderedLocusNames=WD0617;
OS Wolbachia pipientis wMel.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
OC Rickettsiaceae; Wolbachiae; Wolbachia.
OX NCBI_TaxID=66077;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15024419;
RA Wu M., Sun L.V., Vamathevan J.J., Riegler M., DeBoy R.T.,
RA Brownlie J.C., McGraw E.A., Martin W., Esser C., Ahmadinejad N.,
RA Wiegand C., Madupu R., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA Durkin A.S., Kolonay J.F., Nelson W.C., Mohamoud Y., Lee P.,
RA Berry K.J., Young M.B., Utterback T.R., Weidman J.F., Niernan W.C.,
RA Paulsen I.T., Nelson K.E., Tettelin H., O'Neill S.L., Eisen J.A.;
RA "Phylogenomics of the reproductive parasite Wolbachia pipientis wMel:
RT a streamlined genome overrrun by mobile genetic elements.";
RL PLoS Biol. 2:327-341(2004).
DR EMBL; AS017258; AAS14318.1; -
DR TIGR; WD0617; -
DR InterPro; IPR011166; TNase.
DR Pfam; PF01212; Beta_elim_lyase; 1.
DR Complete proteome.
SQ SEQUENCE 349 AA; 39101 MW; 9ED6582ED6D8E1E9 CRC64;

Query Match 83.3%; Score 40; DB 2; Length 349;
Best Local Similarity 87.5%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VDLYHFLK 9
|:|||||
Db 157 VELYHFLK 164

RESULT 2

Q9UZ59 PRELIMINARY; PRT; 110 AA.
AC Q9UZ59; 2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE Hypothetical protein.
GN ORFNames=PA80853;
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;

```

RN  SEQUENCE FROM N.A.
RP  STRAIN=GES / Orsay;
RX  MEDLINE=22511545; PubMed=12622808;
RA  Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O.,
RA  Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
RA  Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;
RT  "An integrated analysis of the genome of the hyperthermophilic
RL  archaeon Pyrococcus abyssi.";
RL  Mol. Microbiol. 47:1495-1512(2003).
DR  EMBL; AJ248287; CAB50200.1; -.
DR  PIR; C75038; C75038.
DR  GO; GO:0003677; F:DNA binding; IEA.
DR  GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR  InterPro; IPK010985; Metrepress_like.
KW  Complete proteome; Hypothetical protein.
SQ  SEQUENCE 110 AA; 13075 MW; 7524B2A20C506924 CRC64;

Query Match 81.2%; Score 39; DB 2; Length 110;
Best Local Similarity 77.8%; Pred. No. 8.5;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
Db 69 AVDLYYLKL 77

RESULT 3
Q900A5 PRELIMINARY; PRT; 110 AA.
AC Q900A5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Truncated nef protein.
GN Name=nef;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;

[1]
RN  SEQUENCE FROM N.A.
RP  Rhodes D.I., Ashton L., Solomon A., Carr A., Cooper D., Kaldor J.,
RA  Deacon N.;
RL  Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RL  EMBL; AY006063; AAG15585.1; -.
DR  HSSP; P04324; 10A4.
DR  GO; GO:0005525; F:GTP binding; IEA.
DR  Pfam; PF00469; F-protein; 1.
DR  ProDom; PD000031; HIV_Nef; 1.
KW  AIDS; Lipoprotein; Myristate.
SQ  SEQUENCE 110 AA; 12193 MW; 767337C8FB21D3C4 CRC64;

Query Match 81.2%; Score 39; DB 2; Length 110;
Best Local Similarity 88.9%; Pred. No. 8.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
Db 82 AVDLSHFLK 90

RESULT 4
Q903T9 PRELIMINARY; PRT; 110 AA.
AC Q903T9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Truncated nef protein.
GN Name=nef;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;

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[1]
RN  SEQUENCE FROM N.A.
RP  Rhodes D.I., Ashton L., Solomon A., Carr A., Cooper D., Kaldor J.,
RA  Deacon N.;
RL  Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RL  EMBL; AY006062; AAG15584.1; -.
DR  HSSP; P04324; 10A4.
DR  GO; GO:0005525; F:GTP binding; IEA.
DR  Pfam; PF00469; F-protein; 1.
DR  ProDom; PD000031; HIV_Nef; 1.
KW  AIDS; Lipoprotein; Myristate.
SQ  SEQUENCE 110 AA; 12192 MW; 767997C8F181D3C4 CRC64;

Query Match 81.2%; Score 39; DB 2; Length 110;
Best Local Similarity 88.9%; Pred. No. 8.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
Db 82 AVDLSHFLK 90

RESULT 5
Q8U3E1 PRELIMINARY; PRT; 113 AA.
AC Q8U3E1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein PF0527.
GN OrderedLocusNames=PF0527;
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;

[1]
RN  SEQUENCE FROM N.A.
RP  STRAIN=Vcl / DSM 3638 / ATCC 43587 / JCM 8422;
RA  Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT  "The complete sequence of the Pyrococcus furiosus genome.";
RL  Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RL  EMBL; AE010175; AAL80651.1; -.
DR  GO; GO:0003677; F:DNA binding; IEA.
DR  GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR  Complete proteome.
KW Complete proteome.
SQ  SEQUENCE 113 AA; 13433 MW; F91E60CEFF81C47D CRC64;

Query Match 81.2%; Score 39; DB 2; Length 113;
Best Local Similarity 77.8%; Pred. No. 8.7;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
Db 73 AVDLYYLKL 81

RESULT 6
Q97005 PRELIMINARY; PRT; 115 AA.
AC Q97005;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nef protein (fragment).
GN Name=nef;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;

[1]
RN  SEQUENCE FROM N.A.
RP  MEDLINE=96190564; PubMed=8627686;
RA  Gao F., Morrison S.G., Robertson D.L., Thornton C.L., Craig S.,
RA  Karlsson G., Sodroski J., Morgado M., Galvao-Castro B.,

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RA von Briesen H., Beddows S., Weber J., Sharp P.M., Shaw G.M.,
 RA Hahn B.H.;
 RT "Molecular cloning and analysis of functional envelope genes from
 RT human immunodeficiency virus type 1 sequence subtypes A through G. The
 RT WHO and NIAID Networks for HIV Isolation and Characterization.";
 RL J. Virol. 70:1651-1667(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Allen E.E.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U27408; AAB06247.1; -;
 DR GO: GO:0005525; F:GTP binding; IEA.
 DR InterPro; IPR001558; HIV_Nef.
 DR Pfam; PF00469; F-protein; 1.
 DR ProDom; PD000031; HIV_Nef; 1.
 KW AIDS; Lipoprotein; Myristate.
 FT NON TER 115
 SQ SEQUENCE 115 AA; 12995 MW; 6C7AF0E1FF37D25D CRC64;

Query Match 81.2%; Score 39; DB 2; Length 115;
 Best Local Similarity 88.9%; Pred. No. 8.9;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
 |||||
 Db 84 AVDLSHFLK 92

RESULT 7
 Q8AQP7 PRELIMINARY; PRT; 115 AA.
 ID Q8AQP7
 AC Q8AQP7;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Truncated nef protein.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OC NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chakraborty R., Reinis M., John M., Philpott S., Rostron T.,
 RA Yang H.B., Palakudy T. Sr., Musoke R., D'Agostino A., Weiser B.,
 RA Burger H., Rowland-Jones S.L.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF538652; AAN40103.1; -;
 DR GO: GO:0005525; F:GTP binding; IEA.
 DR InterPro; IPR001558; HIV_Nef.
 DR Pfam; PF00469; F-protein; 1.
 DR ProDom; PD000031; HIV_Nef; 1.
 KW AIDS; Lipoprotein; Myristate.
 SQ SEQUENCE 115 AA; 12767 MW; 164A537B850666CB CRC64;

Query Match 81.2%; Score 39; DB 2; Length 115;
 Best Local Similarity 88.9%; Pred. No. 8.9;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
 |||||
 Db 87 AVDLSHFLK 95

RESULT 8
 O40241 PRELIMINARY; PRT; 116 AA.
 ID O40241
 AC O40241;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Nef protein (Fragment).
 GN Name=nef;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96190564; PubMed=8627686;
 RA Gao F., Morrison S.G., Robertson D.L., Thornton C.L., Craig S.,
 RA Karlsson G., Sodroski J., Morgado M., Galvao-Castro B.,
 RA von Briesen H., Beddows S., Weber J., Sharp P.M., Shaw G.M.,
 RA Hahn B.H.;
 RT "Molecular cloning and analysis of functional envelope genes from
 RT human immunodeficiency virus type 1 sequence subtypes A through G. The
 RT WHO and NIAID Networks for HIV Isolation and Characterization.";
 RL J. Virol. 70:1651-1667(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Allen E.E.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U27401; AAB06243.1; -;
 DR HSP; P04324; IZEC.
 DR GO: GO:0005525; F:GTP binding; IEA.
 DR InterPro; IPR001558; HIV_Nef.
 DR Pfam; PF00469; F-protein; 1.
 DR ProDom; PD000031; HIV_Nef; 1.
 KW AIDS; Lipoprotein; Myristate.
 FT NON TER 116
 SQ SEQUENCE 116 AA; 13023 MW; 678FD1EF6C1AAB62 CRC64;

Query Match 81.2%; Score 39; DB 2; Length 116;
 Best Local Similarity 88.9%; Pred. No. 8.9;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
 |||||
 Db 84 AVDLSHFLK 92

RESULT 9
 O40242 PRELIMINARY; PRT; 116 AA.
 ID O40242
 AC O40242;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Nef protein (Fragment).
 GN Name=nef;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OC NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96190564; PubMed=8627686;
 RA Gao F., Morrison S.G., Robertson D.L., Thornton C.L., Craig S.,
 RA Karlsson G., Sodroski J., Morgado M., Galvao-Castro B.,
 RA von Briesen H., Beddows S., Weber J., Sharp P.M., Shaw G.M.,
 RA Hahn B.H.;
 RT "Molecular cloning and analysis of functional envelope genes from
 RT human immunodeficiency virus type 1 sequence subtypes A through G. The
 RT WHO and NIAID Networks for HIV Isolation and Characterization.";
 RL J. Virol. 70:1651-1667(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Allen E.E.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U27404; AAB06245.1; -;
 DR GO: GO:0005525; F:GTP binding; IEA.
 DR InterPro; IPR001558; HIV_Nef.
 DR Pfam; PF00469; F-protein; 1.
 DR ProDom; PD000031; HIV_Nef; 1.
 KW AIDS; Lipoprotein; Myristate.
 FT NON TER 116
 SQ SEQUENCE 116 AA; 13162 MW; 76C1CDFC81AE3392 CRC64;

Query Match 81.2%; Score 39; DB 2; Length 116;
 Best Local Similarity 88.9%; Pred. No. 8.9;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
 |||||
 Db 84 AVDLSHFLK 92

RESULT 9
 O40242 PRELIMINARY; PRT; 116 AA.
 ID O40242
 AC O40242;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Nef protein (Fragment).
 GN Name=nef;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OC NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96190564; PubMed=8627686;
 RA Gao F., Morrison S.G., Robertson D.L., Thornton C.L., Craig S.,
 RA Karlsson G., Sodroski J., Morgado M., Galvao-Castro B.,
 RA von Briesen H., Beddows S., Weber J., Sharp P.M., Shaw G.M.,
 RA Hahn B.H.;
 RT "Molecular cloning and analysis of functional envelope genes from
 RT human immunodeficiency virus type 1 sequence subtypes A through G. The
 RT WHO and NIAID Networks for HIV Isolation and Characterization.";
 RL J. Virol. 70:1651-1667(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Allen E.E.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U27404; AAB06245.1; -;
 DR GO: GO:0005525; F:GTP binding; IEA.
 DR InterPro; IPR001558; HIV_Nef.
 DR Pfam; PF00469; F-protein; 1.
 DR ProDom; PD000031; HIV_Nef; 1.
 KW AIDS; Lipoprotein; Myristate.
 FT NON TER 116
 SQ SEQUENCE 116 AA; 13162 MW; 76C1CDFC81AE3392 CRC64;

Query Match 81.2%; Score 39; DB 2; Length 116;
 Best Local Similarity 88.9%; Pred. No. 8.9;

```

Matches      8;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

Qy      1  AVDLYHFLK 9
Db      84  AVDLSHFLK 92

RESULT 10
ID      041540      PRELIMINARY;      PRT;      120 AA.
AC      041540;
DT      01-JAN-1998 (TrEMBLrel. 05, Created)
DT      01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Nef protein (fragment).
GN      Name=nef;
OS      Human immunodeficiency virus 1.
OC      Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX      NCBI_TaxID=11676;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C10;
RX      MEDLINE=98105804; PubMed=9445059;
RA      Connor R.I., Korber B.T.M., Graham B.S., Hahn B.H., Ho D.D.,
RA      Walker B.D., Neumann A.U., Vermund S.H., Mestecky J., Jackson S.,
RA      Fenamore E., Cao Y., Gao F., Kalam S., Kunstman K.J., McDonald D.,
RA      McWilliams N., Trkola A., Moore J.P., Wolinsky S.M.;
RT      "Immunological and virological analyses of persons infected by human
RT      immunodeficiency virus type 1 while participating in trials of
RT      recombinant gp120 subunit vaccines.";
RL      J. Virol. 72:1552-1576(1998).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C10;
RX      MEDLINE=92385154; PubMed=1515209;
RA      Harris M., Hislop S., Patsilinas P., Neil J.C.;
RA      "In vivo derived HIV-1 Nef genes are heterogeneous and lack detectable
RA      nucleotide binding activity.";
RT      AIDS Res. Hum. Retroviruses 8:537-543(1992).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C10;
RX      MEDLINE=92385154; PubMed=1515209;
RA      Harris M., Hislop S., Patsilinas P., Neil J.C.;
RA      "In vivo derived HIV-1 Nef genes are heterogeneous and lack detectable
RA      nucleotide binding activity.";
RT      AIDS Res. Hum. Retroviruses 8:537-543(1992).
RL      AIDS Res. Hum. Retroviruses 8:537-543(1992).

Matches      8;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

Qy      1  AVDLYHFLK 9
Db      84  AVDLSHFLK 92

RESULT 11
ID      076348      PRELIMINARY;      PRT;      121 AA.
AC      076348;
DT      01-NOV-1996 (TrEMBLrel. 01, Created)
DT      01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Nef protein.
GN      Name=nef;
OS      Human immunodeficiency virus 1.
OC      Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX      NCBI_TaxID=11676;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C10;
RX      MEDLINE=92385154; PubMed=1515209;
RA      Harris M., Hislop S., Patsilinas P., Neil J.C.;
RA      "In vivo derived HIV-1 Nef genes are heterogeneous and lack detectable
RA      nucleotide binding activity.";
RT      AIDS Res. Hum. Retroviruses 8:537-543(1992).
RL      AIDS Res. Hum. Retroviruses 8:537-543(1992).

Matches      8;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

Qy      1  AVDLYHFLK 9
Db      88  AVDLSHFLK 96

RESULT 12
ID      079786      PRELIMINARY;      PRT;      121 AA.
AC      079786;
DT      01-NOV-1996 (TrEMBLrel. 01, Created)
DT      01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Nef protein.
GN      Name=nef;
OS      Human immunodeficiency virus 1.
OC      Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX      NCBI_TaxID=11676;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C10;
RX      MEDLINE=92385154; PubMed=1515209;
RA      Harris M., Hislop S., Patsilinas P., Neil J.C.;
RA      "In vivo derived HIV-1 Nef genes are heterogeneous and lack detectable
RA      nucleotide binding activity.";
RT      AIDS Res. Hum. Retroviruses 8:537-543(1992).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C10;
RX      MEDLINE=92385154; PubMed=1515209;
RA      Harris M., Hislop S., Patsilinas P., Neil J.C.;
RA      "In vivo derived HIV-1 Nef genes are heterogeneous and lack detectable
RA      nucleotide binding activity.";
RT      AIDS Res. Hum. Retroviruses 8:537-543(1992).
RL      AIDS Res. Hum. Retroviruses 8:537-543(1992).

Matches      8;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

Qy      1  AVDLYHFLK 9
Db      82  AVDLSHFLK 90

RESULT 13
ID      079786      PRELIMINARY;      PRT;      123 AA.
AC      079786;
DT      01-NOV-1996 (TrEMBLrel. 01, Created)
DT      01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Nef protein (negative factor) (F-protein) [Contains: C-terminal core protein].
GN      Name=nef;
OS      Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).

```

```

[2]
RN      SEQUENCE FROM N.A.
RP      Harris M.P.G.;
RA      Submitted (NOV-1991) to the EMBL/GenBank/DBJ databases.
RL      EMBL; X63040; CAA44766.1; -.
DR      HSSP; P04324; 1QA4.
DR      GO; GO:0005525; F:GTP binding; IEA.
DR      InterPro; IPR001558; HIV_Nef.
DR      Pfam; PF00469; F-protein; 1.
DR      ProDom; PD000031; HIV_Nef; 1.
DR      AIDS; Lipoprotein; Myristate.
KW      AIDS; Lipoprotein; Myristate.
SQ      SEQUENCE      121 AA;      13458 MW;      BB2417415263B423 CRC64;

Query Match      81.2%;      Score 39;      DB 2;      Length 121;
Best Local Similarity      88.9%;      Pred. No. 9.4;
Matches      8;      Conservative      0;      Mismatches      1;      Indels      0;      Gaps      0;

Qy      1  AVDLYHFLK 9
Db      82  AVDLSHFLK 90

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ID      079786      PRELIMINARY;      PRT;      121 AA.
AC      079786;
DT      01-NOV-1996 (TrEMBLrel. 01, Created)
DT      01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Nef protein.
GN      Name=nef;
OS      Human immunodeficiency virus 1.
OC      Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX      NCBI_TaxID=11676;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C10;
RX      MEDLINE=92385154; PubMed=1515209;
RA      Harris M., Hislop S., Patsilinas P., Neil J.C.;
RA      "In vivo derived HIV-1 Nef genes are heterogeneous and lack detectable
RA      nucleotide binding activity.";
RT      AIDS Res. Hum. Retroviruses 8:537-543(1992).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C10;
RX      MEDLINE=92385154; PubMed=1515209;
RA      Harris M., Hislop S., Patsilinas P., Neil J.C.;
RA      "In vivo derived HIV-1 Nef genes are heterogeneous and lack detectable
RA      nucleotide binding activity.";
RT      AIDS Res. Hum. Retroviruses 8:537-543(1992).
RL      AIDS Res. Hum. Retroviruses 8:537-543(1992).

Matches      8;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

Qy      1  AVDLYHFLK 9
Db      82  AVDLSHFLK 90

RESULT 13
ID      079786      PRELIMINARY;      PRT;      123 AA.
AC      079786;
DT      01-NOV-1996 (TrEMBLrel. 01, Created)
DT      01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Nef protein (negative factor) (F-protein) [Contains: C-terminal core protein].
GN      Name=nef;
OS      Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).

```

CC Viruses; Retrovirus; Retroviridae; Lentivirus.
 CC NCBI_TaxID=11678;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85111123; PubMed=2578615;
 RA Ratner L., Haseltine W.A., Patarca R., Livak K.J., Starcich B.R.,
 RA Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
 RA Baumanster K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
 RA Lautenberger J.A., Papas T.S., Ghayeb J., Chang N.T., Gallo R.C.,
 RA Wong-Staal F.;
 RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
 RL Nature 313:277-284(1985).
 CC -!- FUNCTION: Early protein that seems to play a role in optimizing
 CC the host cell environment for viral replication without causing
 CC cell death by apoptosis. Enhances virus infectivity and
 CC pathogenicity (By similarity).
 CC -!- PATHOGENICITY: Down-modulates surface MHC-I molecules. Internalized
 CC molecules are sequestered to the trans-Golgi network (TGN). Also
 CC decreases cell surface CD4 antigen by interacting with the Src
 CC family kinase LCK thereby inducing LCK-CD4 dissociation and by
 CC increasing clathrin-dependent endocytosis of this antigen to
 CC target it to lysosomal degradation. Peroxisomal acyl-coenzyme A
 CC thioester hydrolase 1 (PTE1) seems to be involved in this process.
 CC May serve as a direct bridge between CD4 and the cellular
 CC endocytic machinery by interacting with beta-COP and adaptins. In
 CC consequence, surface MHC-I and CD4 are decreased and infected
 CC cells are masked for immune recognition by cytotoxic T
 CC lymphocytes. Decreasing the number of viral receptors prevents
 CC infection by more HIV particles (By similarity).
 CC -!- FUNCTION: Bypasses host T-cell signaling by inducing a
 CC transcriptional program nearly identical to that of anti-CD3 cell
 CC activation. Interacts with the TCR-zeta chain to upregulate the
 CC Fas ligand (FasL). Increasing surface FasL molecules and
 CC decreasing surface MHC-I molecules send attacking cytotoxic T-cell
 CC into apoptosis (By similarity).
 CC -!- FUNCTION: Protects the infected cell from apoptosis in order to
 CC keep it alive until the next virus generation is ready to strike.
 CC Inhibits the Fas and TNFR-mediated death signals by blocking
 CC MAP3K5. Interacts with p53 and decreases the half-life of the
 CC latter, protecting the infected cell against p53-mediated
 CC apoptosis. Inhibits the apoptotic signals regulated by the Bcl-2
 CC family proteins through the formation of a Nef/P13-kinase/PAK
 CC complex that induces phosphorylation of Bad (By similarity).
 CC -!- SUBUNIT: Homodimer. Interacts with various cellular proteins
 CC including MAP3K5, beta-COP, PAK2, PACS1, the Src family kinases
 CC HCK and LCK, TCR-zeta chain, PTE1 and P13-kinase. Interaction with
 CC P13-kinase activates the Nef associated p21-activated kinase (PAK)
 CC and leads to increased production of HIV-1. This interaction
 CC depends on the C-terminus of both proteins. Interacts and inhibits
 CC kinase activity of LCK and MAPK3 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Associates with the inner
 CC plasma membrane through its N-terminal anchor domain. Also found
 CC in the paranuclear area, probably in the TGN. Correct localization
 CC requires PACS1. Also incorporated in virions at a rate of about 10
 CC molecules per virion, where it is cleaved (By similarity).
 CC -!- DOMAIN: The N-terminal anchor domain is composed of the N-
 CC myristoyl glycine and of a cluster of positively charged amino
 CC acids. It is required for inner plasma membrane targeting of Nef
 CC and virion incorporation, and thereby for infectivity. This domain
 CC is also involved in binding to p53 (By similarity).
 CC -!- DOMAIN: The acidic cluster contains sorting information as it
 CC binds to the TGN sorting protein PACS1 (By similarity).
 CC -!- DOMAIN: The SH3-binding domain constituted of pxxp motifs mediates
 CC binding to several Src family proteins thereby regulating their
 CC tyrosine kinase activity. The same motifs also mediates the
 CC association with MAPK3, P13-kinase and TCR-zeta (By similarity).
 CC -!- PTM: The virion-associated proteins are cleaved by the viral
 CC proteinase PR to release the soluble C-terminal core protein (By
 CC similarity).
 CC -!- PTM: Myristoylation is essential for inner plasma membrane
 CC targeting of Nef and virion incorporation and thereby for
 CC infectivity. Also required to reduce CD4 expression at the cell
 CC surface (By similarity).

CC -!- PTM: Phosphorylated on serine residues, probably by host PKC (By
 CC similarity).
 CC -!- MISCELLANEOUS: In this isolate a mutation in position 124 adds a
 CC stop codon and the protein is much shorter than in other isolates
 CC (210 AA).
 CC -!- SIMILARITY: Belongs to the lentiviruses Nef protein family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/annouce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M15654; AAA44206.1; -;
 CC PIR: A04005; ASLJH3.
 CC HSP: P03406; 10A4.
 CC HIV: M15654; NEFSBH102.
 CC InterPro: IPR001558; HIV Nef.
 CC Pfam: PF00469; F-protein; 1.
 CC ProDom: PD000031; HIV Nef; 1.
 CC KW AIDS; Apoptosis; Early protein; Lipoprotein; Membrane; Myristate;
 CC Phosphorylation; Repeat; SH3-binding; Viral immunoevasion; Virulence.
 CC CHAIN 1 123
 CC FT CHAIN 58 123
 CC FT DOMAIN 1 57
 CC FT DOMAIN 62 65
 CC FT DOMAIN 69 80
 CC FT REPEAT 69 71
 CC FT REPEAT 72 74
 CC FT REPEAT 75 77
 CC FT REPEAT 78 80
 CC FT DOMAIN 108 123
 CC FT
 CC SITE 20 20
 CC SITE 57 58
 CC SITE 69 78
 CC SITE 2 2
 CC SEQUENCE 123 AA; 13606 MW; 0811735345F0E98B CRC64;
 CC
 CC Query Match 81.2%; Score 39; DB 1; Length 123;
 CC Best Local Similarity 88.9%; Pred. No. 9.5;
 CC Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC Qy 1 AVDLYHFLK 9
 CC Db 84 AVDLSHFLK 92
 CC
 CC RESULT 14
 CC NEF_HV1H2 STANDARD; PRT; 123 AA.
 CC ID NEF_HV1H2
 CC AC P04601; O09780; Q85587;
 CC DT 13-AUG-1987 (Rel. 05, Created)
 CC DT 15-JUL-1999 (Rel. 38, Last sequence update)
 CC DT 25-OCT-2004 (Rel. 45, Last annotation update)
 CC DE Nef protein (Negative factor) (F-protein) (3-ORF) [Contains: C-
 CC terminal core protein].
 CC GN Name=nef;
 CC OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
 CC OC Viruses; Retrovirus; Retroviridae; Lentivirus.
 CC ON NCBI_TaxID=11706;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=86067228; PubMed=2999715;

are decreased and infected cells are masked for immune recognition by cytotoxic T lymphocytes. Decreasing the number of viral receptors prevents reinfection by more HIV particles.

-!- FUNCTION: Bypasses host T-cell signaling by inducing a transcriptional program nearly identical to that of anti-CD3 cell activation. Interacts with the TCR-zeta chain to upregulate the Fas ligand (FasL). Increasing surface FasL molecules and decreasing surface MHC-I molecules send attacking cytotoxic T-cell into apoptosis (By similarity).

-!- FUNCTION: Protects the infected cell from apoptosis in order to keep it alive until the next virus generation is ready to strike. Inhibits the Fas and TNFR-mediated death signals by blocking MAP3K5. Interacts with p53 and decreases the half-life of the latter, protecting the infected cell against p53-mediated apoptosis. Inhibits the apoptotic signals regulated by the Bcl-2 family proteins through the formation of a Nef/P13-kinase/PAK complex that induces phosphorylation of Bad (By similarity).

-!- SUBUNIT: Homodimer. Interacts with various cellular proteins including MAP3K5, beta-COP, PAK2, PACS1, the Src family kinases HCK and Lck, TCR-zeta chain, PTE1 and P13-kinase. Interaction with P13-kinase activates the Nef associated p21-activated kinase (PAK) and leads to increased production of HIV-1. This interaction depends on the C-terminus of both proteins. Interacts and inhibits kinase activity of LCK and MAPK3 (By similarity).

-!- SUBCELLULAR LOCATION: Cytoplasmic. Associates with the inner plasma membrane through its N-terminal anchor domain. Also found in the paranuclear area, probably in the TGN. Correct localization requires PACS1. Also incorporated in virions at a rate of about 10 molecules per virion, where it is cleaved (By similarity).

-!- DOMAIN: The N-terminal anchor domain is composed of the N-myristoyl glycine and of a cluster of positively charged amino acids. It is required for inner plasma membrane targeting of Nef and virion incorporation, and thereby for infectivity. This domain is also involved in binding to p53 (By similarity).

-!- DOMAIN: The acidic cluster contains sorting information as it binds to the TGN sorting protein PACS1.

-!- DOMAIN: The SH3-binding domain constitutes of PxxP motifs mediates binding to several Src family proteins thereby regulating their tyrosine kinase activity. The same motifs also mediates the association with MAPK3, P13-kinase and TCR-zeta (By similarity).

-!- PTM: The virion-associated proteins are cleaved by the viral proteinase PR to release the soluble C-terminal core protein (By similarity).

-!- PTM: Myristoylation is essential for inner plasma membrane targeting of Nef and virion incorporation and thereby for infectivity. Also required to reduce CD4 expression at the cell surface (By similarity).

-!- PTM: Phosphorylated on serine residues, probably by host PKC (By similarity).

-!- MISCELLANEOUS: In this isolate a mutation in position 124 adds a stop codon and the protein is much shorter than in other isolates (210 AA).

-!- SIMILARITY: Belongs to the lentiviruses Nef protein family.

-!- CAUTION: In clone pNL4-3 (AC P03406), it has been show that down-modulation of surface MHC class I molecules is independent of ARF6 endosomal pathway.

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EMBL; X03187; CAA26946.1; --
 EMBL; X03455; AAB50263.1; --
 EMBL; AF033819; AAC82597.1; --
 HSSP; P04324; 1ZEC.
 HIV; K03455; NEF\$HXB2.
 InterPro; IPR001558; HIV_Nef.
 Pfam; PF00469; F-protein; 1.
 ProDom; PD000031; HIV_Nef; 1.

RA Ratner L., Starcich B.R., Josephs S.F., Hahn B.H., Reddy E.P., Livak K.J., Petteway S.R. Jr., Pearson M.L., Haseltine W.A., Arya S.K., Wong-Staal F.;
 RT "Polymorphism of the 3' open reading frame of the virus associated with the acquired immune deficiency syndrome, human T-lymphotropic virus type III.";
 RL Nucleic Acids Res. 13:8219-8229(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87299196; PubMed=3040055;
 RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S., Gallo R.C., Wong-Staal F.;
 RT "Complete nucleotide sequences of functional clones of the AIDS virus.";
 RL AIDS Res. Hum. Retroviruses 3:57-69(1987).
 RN [3]
 RP REVISIONS.
 RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S., Gallo R.C., Wong-Staal F.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP FUNCTION.
 RC STRAIN=Isolate HXB2/Clone R7;
 RX PubMed=8124721;
 RA Aiken C., Komar J., Landau N.R., Lenburg M.E., Trono D.;
 RT "Nef induces CD4 endocytosis: requirement for a critical dileucine motif in the membrane-proximal CD4 cytoplasmic domain.";
 RL Cell 76:853-864(1994).
 RN [5]
 RP FUNCTION.
 RC STRAIN=Isolate HXB2/Clone R7;
 RX PubMed=9971776;
 RA Mangasarian A., Piguet V., Wang J.-K., Chen Y.-L., Trono D.;
 RT "Nef-induced CD4 and major histocompatibility complex class I (MHC-I) down-regulation are governed by distinct determinants: N-terminal alpha helix and proline repeat of Nef selectively regulate MHC-I trafficking.";
 RL J. Virol. 73:1964-1973(1999).
 RN [6]
 RP FUNCTION, AND SUBCELLULAR LOCATION.
 RC STRAIN=Isolate HXB2/Clone R7;
 RX PubMed=12526811;
 RA Blagoveschenskaya A.D., Thomas L., Feliciangeli S.F., Hung C.-H., Thomas G.;
 RT "HIV-1 Nef protein binds to the cellular protein PACS-1 to downregulate class I major histocompatibility complexes.";
 RL Nat. Cell Biol. 2:163-167(2000).
 RN [7]
 RP FUNCTION, AND MUTAGENESIS OF MET-20; 62-GLU--GLU-65; PRO-72 AND PRO-75.
 RC STRAIN=Isolate HXB2D;
 RX PubMed=12526811;
 RA Blagoveschenskaya A.D., Thomas L., Feliciangeli S.F., Hung C.-H., Thomas G.;
 RT "HIV-1 Nef downregulates MHC-I by a PACS-1- and P13K-regulated ARF6 endocytic pathway.";
 RL Cell 111:853-866(2002).
 CC -!- FUNCTION: Early protein that seems to play a role in optimizing the host cell environment for viral replication without causing cell death by apoptosis (By similarity). Enhances virus infectivity and pathogenicity.
 CC -!- FUNCTION: Down-modulates surface MHC-I molecules through the P13-kinase-mediated ARF6 endosomal pathway. Combines with PACS1 and accelerates the ARF6-dependent internalization of MHC-I molecules. Internalized molecules are sequestered to the trans-Golgi network (TGN). Also decreases cell surface CD4 antigen by interacting with the Src family kinase LCK thereby inducing LCK-CD4 dissociation and by increasing clathrin-dependent endocytosis of this antigen to target it to lysosomal degradation. Peroxisomal acyl-coenzyme A thioester hydrolase 1 (PTE1) seems to be involved in this process (By similarity). May serve as a direct bridge between CD4 and the cellular endocytic machinery by interacting with beta-COP and adaptins. In consequence, surface MHC-I and CD4

KW AIDS; Apoptosis; Early protein; Lipoprotein; Membrane; Myristate;
KW Phosphorylation; Repeat; SH3-binding; Viral immunoevasion; Virulence;
FT CHAIN 1 123 Nef protein (By similarity).
FT CHAIN 58 123 C-terminal core protein (By similarity).
FT DOMAIN 1 57 Anchor (By similarity).
FT DOMAIN 62 65 Acidic cluster.
FT DOMAIN 69 80 4 X 3 AA tandem repeats of P-X-X.
FT REPEAT 69 71 1.
FT REPEAT 72 74 2.
FT REPEAT 75 77 3.
FT REPEAT 78 80 4.
FT DOMAIN 108 123 Mediates dimerization, Nef-PTB1
interaction, Nef-induced CD4 and MHC-I
down-modulation and enhancement of
infectivity (By similarity).
FT SITE 20 20 Involved in reducing surface MHC-I
molecules by both impeding cell surface
retrieval of MHC-I molecules and
diverting them instead to the TGN.
FT SITE 57 58 Cleavage (by viral proteinase PR) (By
similarity).
FT SITE 69 78 SH3-binding (By similarity).
FT LIPID 2 2 N-myristoyl glycine (by host).
FT MUTAGEN 20 20 M->A: Complete loss of Nef-induced MHC-I
down-modulation, MHC-I is internalized
but not sequestered in TGN.
FT MUTAGEN 62 65 EEEB->AAAA: Complete loss of Nef-induced
MHC-I down-modulation, MHC-I is not
internalized.
FT MUTAGEN 72 72 P->A: Complete loss of Nef-induced MHC-I
down-modulation, MHC-I is not
internalized; when associated with A-75.
FT MUTAGEN 75 75 P->A: Complete loss of Nef-induced MHC-I
down-modulation, MHC-I is not
internalized; when associated with A-72.
FT CONFLICT 29 29 R -> G (in ref. 1).
SQ SEQUENCE 123 AA; 13692 MW; B5007753CD244CF CRC64;

Query Match 81.2%; Score 39; DB 1; Length 123;
Best Local Similarity 88.9%; Pred. No. 9.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
| | | | |
Db 84 AVDLSHFLK 92

RESULT 15
Q6UEVO PRELIMINARY; PRT; 131 AA.
AC Q6UEVO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Nef protein (Fragment).
GN Name=nef;
OS Human immunodeficiency virus 1.
OC Viruses; Retroïd viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Kijak G.H., Sanders-Buell E., Wolfe N.D., Mpoudi-Ngole E., Kim B.,
RA Robb M.L., Birx D.L., Burke D.S., Carr J.K., McCutchan F.E.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AY371158; AAR22204.1; -.
DR GO; GO:0005525; F:GTP binding; IEA.
DR InterPro; IPR001558; HIV Nef.
DR Pfam; PF00469; F-protein; 1.
DR ProDom; PD000031; HIV Nef; 1.
KW AIDS; Lipoprotein; Myristate.
FT NON_TER 131
SQ SEQUENCE 131 AA; 14700 MW; B5429C85C5E218F0 CRC64;

Query Match 81.2%; Score 39; DB 2; Length 131;
Best Local Similarity 88.9%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
| | | | |
Db 84 AVDLSHFLK 92

Search completed: June 29, 2005, 01:34:59
Job time : 56.2473 secs

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OM protein - protein search, using sw model

Run on: June 29, 2005, 05:18:25 ; Search time 53.8517 Seconds
(without alignments)
64.268 Million cell updates/sec

Title: US-08-170-344-79

Perfect score: 48

Sequence: 1 AVDLYHFLK 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	9	15	US-10-149-138-4197
2	48	100.0	9	15	Sequence 4197, Ap
3	48	100.0	9	16	Sequence 2184, Ap
4	48	100.0	9	17	US-10-149-138-4197
5	48	100.0	9	17	Sequence 4197, Ap
6	39	81.2	9	8	US-10-654-601-2490
7	39	81.2	9	8	Sequence 2490, Ap
8	39	81.2	9	14	US-10-751-845-120
9	39	81.2	9	14	Sequence 120, App
10	39	81.2	9	14	US-08-344-824-26
11	39	81.2	9	14	Sequence 26, Appl
12	39	81.2	9	14	US-10-128-711-2
13	39	81.2	9	14	Sequence 2, Appli
14	39	81.2	9	14	US-10-168-843A-18
15	39	81.2	9	14	Sequence 18, Appl
16	39	81.2	9	14	US-10-079-167-58
17	39	81.2	9	14	Sequence 58, Appl
18	39	81.2	9	14	US-10-360-836-62
19	39	81.2	9	14	Sequence 62, Appl
20	39	81.2	9	15	US-10-442-909-11
21	39	81.2	9	15	Sequence 11, Appl

12	39	81.2	9	15	US-10-469-256-44	Sequence 44, Appl
13	39	81.2	9	16	US-10-653-624-58	Sequence 58, Appl
14	39	81.2	9	16	US-10-833-439-58	Sequence 58, Appl
15	39	81.2	9	16	US-10-833-745-58	Sequence 58, Appl
16	39	81.2	9	16	US-10-833-745-58	Sequence 58, Appl
17	39	81.2	9	16	US-10-686-943-58	Sequence 58, Appl
18	39	81.2	12	15	US-10-469-256-42	Sequence 42, Appl
19	39	81.2	12	16	US-10-777-053-155	Sequence 155, App
20	39	81.2	12	16	US-10-777-053-581	Sequence 581, App
21	39	81.2	12	16	US-10-837-217-155	Sequence 155, App
22	39	81.2	12	16	US-10-837-217-581	Sequence 581, App
23	39	81.2	15	15	US-10-442-909-51	Sequence 51, Appl
24	39	81.2	20	15	US-10-222-463-23	Sequence 23, Appl
25	39	81.2	21	14	US-10-062-710-111	Sequence 111, App
26	39	81.2	22	14	US-10-062-710-172	Sequence 172, App
27	39	81.2	33	11	US-09-948-965E-1	Sequence 1, Appli
28	39	81.2	33	14	US-10-062-710-105	Sequence 105, App
29	39	81.2	33	15	US-10-441-788-96	Sequence 96, Appl
30	39	81.2	206	14	US-10-190-435-124	Sequence 124, App
31	39	81.2	206	15	US-10-651-836-5	Sequence 5, Appli
32	39	81.2	206	15	US-10-651-836-9	Sequence 9, Appli
33	39	81.2	206	16	US-10-333-680-6	Sequence 6, Appli
34	39	81.2	209	15	US-10-296-734-1487	Sequence 1487, Ap
35	39	81.2	215	14	US-10-203-013-9	Sequence 9, Appli
36	39	81.2	215	17	US-10-687-060-9	Sequence 9, Appli
37	39	81.2	215	17	US-10-485-048-9	Sequence 9, Appli
38	39	81.2	216	10	US-09-952-060-10	Sequence 10, Appl
39	39	81.2	216	14	US-10-149-640-2	Sequence 2, Appli
40	39	81.2	216	16	US-10-380-641-10	Sequence 10, Appl
41	39	81.2	216	17	US-10-636-730-10	Sequence 10, Appl
42	39	81.2	217	10	US-09-952-060-14	Sequence 14, Appl
43	39	81.2	217	14	US-10-149-640-6	Sequence 6, Appli
44	39	81.2	217	16	US-10-380-641-14	Sequence 14, Appl
45	39	81.2	217	17	US-10-636-730-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-10-149-138-4197
; Sequence 4197, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Bastebar
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4197
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4197

Query Match 100.0%; Score 48; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
 Db 1 AVDLYHFLK 9

RESULT 2

US-10-149-135-2184
 ; Sequence 2184, Application US/10149135
 ; Publication No. US20040053822A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fikes, John
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Sidney, John
 ; APPLICANT: Southwood, Scott
 ; APPLICANT: Chesnut, Robert
 ; APPLICANT: Celis, Esteban
 ; APPLICANT: Keogh, Elissa
 ; TITLE OF INVENTION: Inducing Cellular Immune Responses to
 ; FILE REFERENCE: 2060.0130001
 ; CURRENT FILING DATE: 2000-12-11
 ; PRIOR APPLICATION NUMBER: US/10/149,135
 ; PRIOR FILING DATE: 2000-12-11
 ; PRIOR APPLICATION NUMBER: PCT/US00/33545
 ; PRIOR FILING DATE: 2000-12-11
 ; PRIOR APPLICATION NUMBER: US 09/458,298
 ; PRIOR FILING DATE: 1999-12-10
 ; PRIOR APPLICATION NUMBER: US 09/189,702
 ; PRIOR FILING DATE: 1998-11-10
 ; PRIOR APPLICATION NUMBER: US 08/205,713
 ; PRIOR FILING DATE: 1994-03-04
 ; PRIOR APPLICATION NUMBER: US 08/159,184
 ; PRIOR FILING DATE: 1993-11-29
 ; PRIOR APPLICATION NUMBER: US 08/073,205
 ; PRIOR FILING DATE: 1993-06-04
 ; PRIOR APPLICATION NUMBER: US 08/027,146
 ; PRIOR FILING DATE: 1993-03-05
 ; NUMBER OF SEQ ID NOS: 2479
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2184
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Artificial Peptide

US-10-149-135-2184

Query Match 100.0%; Score 48; DB 15; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 AVDLYHFLK 9
 Db 1 AVDLYHFLK 9

RESULT 3

US-10-149-138-4197
 ; Sequence 4197, Application US/10149138
 ; Publication No. US20040121946A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Fikes, John
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Sidney, John
 ; APPLICANT: Southwood, Scott
 ; APPLICANT: Chesnut, Robert
 ; APPLICANT: Celis, Esteban
 ; APPLICANT: Keogh, Elissa
 ; TITLE OF INVENTION: Inducing Cellular Immune Responses to
 ; FILE REFERENCE: 2060.0140001
 ; CURRENT FILING DATE: 2002-06-10

; PRIOR APPLICATION NUMBER: PCT/US00/33591
 ; PRIOR FILING DATE: 2000-12-11
 ; PRIOR APPLICATION NUMBER: US 09/458,299
 ; PRIOR FILING DATE: 1999-12-11
 ; NUMBER OF SEQ ID NOS: 4641
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4197
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Artificial Peptide

US-10-149-138-4197

Query Match 100.0%; Score 48; DB 16; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9

Db 1 AVDLYHFLK 9

RESULT 4

US-10-654-601-2490
 ; Sequence 2490, Application US/10654601
 ; Publication No. US20050063983A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Sidney, John
 ; APPLICANT: Southwood, Scott
 ; APPLICANT: Vitiello, Maria A.
 ; APPLICANT: Livingston, Brian D.
 ; APPLICANT: Kubo, Ralph T.
 ; APPLICANT: Celis, Esteban
 ; APPLICANT: Grey, Howard M.
 ; APPLICANT: Chesnut, Robert
 ; APPLICANT: Epimmune Inc.
 ; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
 ; FILE REFERENCE: 2060.0060007
 ; CURRENT APPLICATION NUMBER: US/10/654,601
 ; CURRENT FILING DATE: 2003-09-04
 ; PRIOR APPLICATION NUMBER: US/09/239,043
 ; PRIOR FILING DATE: 1999-01-27
 ; PRIOR APPLICATION NUMBER: US 03/189,702
 ; PRIOR FILING DATE: 1998-11-10
 ; PRIOR APPLICATION NUMBER: US 08/978,291
 ; PRIOR FILING DATE: 1997-11-25
 ; PRIOR APPLICATION NUMBER: US 08/820,360
 ; PRIOR FILING DATE: 1997-03-12
 ; PRIOR APPLICATION NUMBER: US 60/013,363
 ; PRIOR FILING DATE: 1996-03-13
 ; PRIOR APPLICATION NUMBER: US 08/461,603
 ; PRIOR FILING DATE: 1995-06-05
 ; PRIOR APPLICATION NUMBER: US 08/347,610
 ; PRIOR FILING DATE: 1994-12-01
 ; PRIOR APPLICATION NUMBER: US 08/344,824
 ; PRIOR FILING DATE: 1994-11-23
 ; PRIOR APPLICATION NUMBER: US 08/278,634
 ; PRIOR FILING DATE: 1994-07-21
 ; PRIOR APPLICATION NUMBER: US 08/205,713
 ; PRIOR FILING DATE: 1994-03-04
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 2579
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2490
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Standard peptide that binds to HLA A*1101

US-10-654-601-2490

Query Match 100.0%; Score 48; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
Db 1 AVDLYHFLK 9

RESULT 5
US-10-751-845-120
; Sequence 120, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/10751,845
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 120
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-751-845-120

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Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
Db 1 AVDLYHFLK 9

RESULT 6
US-08-344-824-26
; Sequence 26, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634

; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-824-26

Query Match 81.2%; Score 39; DB 8; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
Db 1 AVDLSHFLK 9

RESULT 7
US-10-128-711-2
; Sequence 2, Application US/10128711
; Publication No. US20030099634A1
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; CHESTNUT, Robert W.
; SETTE, Alessandro D.
; CELIS, Esteban
; GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/128,711
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793

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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 9 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: unknown
;   TOPOLOGY: unknown
;   MOLECULE TYPE: peptide
;   SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-128-711-2

Query Match      81.2%; Score 39; DB 14; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
Db 1 AVDLSHFLK 9

RESULT 8
US-10-168-843A-18
; Sequence 18, Application US/10168843A
; Publication No. US20030108562A1
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; APPLICANT: International Aids Vaccine Initiative
; APPLICANT: University of Nairobi
; TITLE OF INVENTION: Improvements in or Relating to Immune Responses to HIV
; FILE REFERENCE: MJL/C1248/1/M
; CURRENT APPLICATION NUMBER: US/10/168,843A
; CURRENT FILING DATE: 2002-09-24
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-168-843A-18

Query Match      81.2%; Score 39; DB 14; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
Db 1 AVDLSHFLK 9

RESULT 9
US-10-079-167-58
; Sequence 58, Application US/10079167
; Publication No. US20030138454A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: McShane, Helen
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Reese, William
; APPLICANT: Schneider, Joerg
; TITLE OF INVENTION: Vaccination Method
; FILE REFERENCE: 2907.1000-001
; CURRENT APPLICATION NUMBER: US/10/079,167
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/454,204
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; PRIOR FILING DATE: 1997-06-09
; PRIOR APPLICATION NUMBER: PCT/GB01/04116
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: GB 00 23203.3
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 99

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: CTL Epitope of HIV-1 nef
US-10-079-167-58

Query Match      81.2%; Score 39; DB 14; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
Db 1 AVDLSHFLK 9

RESULT 10
US-10-360-836-62
; Sequence 62, Application US/10360836
; Publication No. US20030185854A1
; GENERAL INFORMATION:
; APPLICANT: Zavala, Fidel
; APPLICANT: Birkett, Ashley
; TITLE OF INVENTION: USE OF RECOMBINANT HEPATITIS B CORE
; TITLE OF INVENTION: PARTICLES TO DEVELOP VACCINES AGAINST INFECTIOUS PATHOGENS
; FILE REFERENCE: 5986/1J876
; CURRENT APPLICATION NUMBER: US/10/360,836
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/354,963
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 9
; TYPE: PRT
; ORGANISM: human immunodeficiency virus (HIV-1)
US-10-360-836-62

Query Match      81.2%; Score 39; DB 14; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
Db 1 AVDLSHFLK 9

RESULT 11
US-10-442-909-11
; Sequence 11, Application US/10442909
; Publication No. US20040001845A1
; GENERAL INFORMATION:
; APPLICANT: Altfield, Marcus
; APPLICANT: Yu, Xu
; APPLICANT: Walker, Bruce
; APPLICANT: Addo, Marylyn
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of HIV-1 Virus
; FILE REFERENCE: 24028-010
; CURRENT APPLICATION NUMBER: US/10/442,909
; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: 60/382,120
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-442-909-11
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Query Match      81.2%; Score 39; DB 15; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AVDLYHFLK 9
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Db      1 AVDSLHFLK 9

RESULT 12
US-10-469-256-44
; Sequence 44, Application US/10469256
; Publication No. US20040073008A1
; GENERAL INFORMATION:
; APPLICANT: Centro de Ingenieria Genetica y Biotecnologia
; TITLE OF INVENTION: Recombinant Poxvirus for Chimeric Proteins of the Human Immunodeficiency Virus
; FILE REFERENCE: 976-14 PCT/US
; CURRENT APPLICATION NUMBER: US/10/469,256
; CURRENT FILING DATE: 2003-08-27
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-469-256-44

Query Match      81.2%; Score 39; DB 15; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AVDLYHFLK 9
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Db      1 AVDSLHFLK 9

RESULT 13
US-10-653-624-58
; Sequence 58, Application US/10653624
; Publication No. US20040131594A1
; GENERAL INFORMATION:
; APPLICANT: McMichael, Andrew
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Schneider, Jorg
; APPLICANT: Plebanski, Magdalena
; APPLICANT: Hanke, Tomas
; APPLICANT: Smith, Geoffrey L.
; APPLICANT: Blanchard, Tom
; TITLE OF INVENTION: Methods and Reagents for Vaccination
; FILE REFERENCE: 2907.1000-000
; CURRENT APPLICATION NUMBER: US/10/653,624
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/09/454,204A
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: CTL Epitope of HIV-1 nef
US-10-653-624-58

Query Match      81.2%; Score 39; DB 16; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AVDLYHFLK 9
      ||||| |||||
Db      1 AVDSLHFLK 9

RESULT 14
US-10-833-439-58
; Sequence 58, Application US/10833439
; Publication No. US20040175365A1
; GENERAL INFORMATION:
; APPLICANT: McMichael, Andrew
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Schneider, Jorg
; APPLICANT: Plebanski, Magdalena
; APPLICANT: Hanke, Tomas
; APPLICANT: Smith, Geoffrey L.
; APPLICANT: Blanchard, Tom
; TITLE OF INVENTION: Methods and Reagents for Vaccination
; FILE REFERENCE: 2907.1000-000
; CURRENT APPLICATION NUMBER: US/10/833,439
; CURRENT FILING DATE: 2004-04-28
; PRIOR APPLICATION NUMBER: US/10/686,943
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: PCT/GB98/01681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: CTL Epitope of HIV-1 nef
US-10-833-439-58

Query Match      81.2%; Score 39; DB 16; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AVDLYHFLK 9
      ||||| |||||
Db      1 AVDSLHFLK 9

RESULT 15
US-10-833-745-58
; Sequence 58, Application US/10833745
; Publication No. US20040191272A1
; GENERAL INFORMATION:
; APPLICANT: McMichael, Andrew
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Schneider, Jorg
; APPLICANT: Plebanski, Magdalena
; APPLICANT: Hanke, Tomas
; APPLICANT: Smith, Geoffrey L.
; APPLICANT: Blanchard, Tom
; TITLE OF INVENTION: Methods and Reagents for Vaccination
; FILE REFERENCE: 2907.1000-000
; CURRENT APPLICATION NUMBER: US/10/833,745
; CURRENT FILING DATE: 2004-04-28
; PRIOR APPLICATION NUMBER: US/10/686,943
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: US/09/454,204
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; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: CTL Epitope of HIV-1 nef
US-10-833-745-58

Query Match      81.2%; Score 39; DB 16; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AVDLYHFLK 9
      |||||
Db      1 AVDLSHFLK 9

Search completed: June 29, 2005, 05:48:18
Job time : 54.8517 secs
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:37:59 ; Search time 16.8626 Seconds
(without alignments)
39.842 Million cell updates/sec

Title: US-08-170-344-79

Perfect score: 48

Sequence: 1 AVDLYHPLK 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	9	3	US-08-159-339A-125
2	48	100.0	9	4	US-08-543-608A-46
3	48	100.0	9	4	US-09-239-043D-2490
4	39	81.2	9	3	US-08-159-339A-1153
5	39	81.2	9	4	US-08-197-484-2
6	39	81.2	9	4	US-09-454-204A-58
7	39	81.2	9	4	US-09-601-729-186
8	39	81.2	9	5	PCT-US95-02121-2
9	39	81.2	16	2	US-08-484-905-43
10	39	81.2	16	3	US-08-481-985B-43
11	39	81.2	16	3	US-08-370-476-43
12	39	81.2	16	3	US-08-992-877-23
13	39	81.2	38	1	US-08-145-708A-16
14	39	81.2	38	2	US-08-331-454-16
15	39	81.2	83	2	US-08-417-210A-96
16	39	81.2	83	3	US-08-136-159A-96
17	39	81.2	123	3	US-09-124-900-10
18	39	81.2	151	3	US-08-679-493A-74
19	39	81.2	206	3	US-08-388-353-644
20	39	81.2	206	3	US-08-488-551B-644
21	39	81.2	206	3	US-08-679-493A-75
22	39	81.2	206	4	US-09-309-572-24
23	39	81.2	206	4	US-09-718-096-24
24	39	81.2	216	4	US-09-952-060-10
25	39	81.2	217	4	US-09-952-060-14
26	39	81.2	237	4	US-09-952-060-12
27	39	81.2	237	4	US-09-952-060-16

28	39	81.2	239	3	US-08-679-493A-76
29	39	81.2	266	3	US-08-815-809-5
30	39	81.2	280	2	US-08-816-155B-43
31	39	81.2	280	3	US-09-079-587-43
32	36	75.0	224	4	US-09-206-551-53
33	36	75.0	1783	4	US-09-824-574-3
34	35	72.9	83	4	US-09-621-976-5172
35	35	72.9	174	4	US-09-134-000C-4133
36	35	72.9	634	4	US-09-385-219A-26
37	34	70.8	8	4	US-09-601-729-263
38	34	70.8	26	2	US-08-251-472-4
39	34	70.8	26	3	US-09-248-082-4
40	34	70.8	66	4	US-09-248-796A-24433
41	34	70.8	233	4	US-09-107-532A-4966
42	34	70.8	390	4	US-09-711-164-405
43	34	70.8	402	4	US-09-248-796A-17687
44	34	70.8	577	4	US-09-489-039A-12056
45	33	68.8	10	3	US-08-747-599A-58

ALIGNMENTS

RESULT 1
US-08-159-339A-125
; Sequence 125, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

Sequence 76, Appl
Sequence 5, Appl
Sequence 43, Appl
Sequence 43, Appl
Sequence 53, Appl
Sequence 3, Appl
Sequence 5172, Ap
Sequence 4133, Ap
Sequence 26, Appl
Sequence 263, App
Sequence 4, Appl
Sequence 4, Appl
Sequence 24433, A
Sequence 4966, Ap
Sequence 405, App
Sequence 17687, A
Sequence 12056, A
Sequence 58, Appl

US-08-159-339A-125

Query Match 100.0%; Score 48; DB 3; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
 |||||
 Db 1 AVDLYHFLK 9

RESULT 2

US-09-543-608A-46

; Sequence 46, Application US/09543608A

; Patent No. 6602510

; GENERAL INFORMATION:

; APPLICANT: Fikes, John D.

; APPLICANT: Sette, Alessandro

; APPLICANT: Sidney, John

; APPLICANT: Southwood, Scott

; APPLICANT: Celis, Esteban

; APPLICANT: Keogh, Elissa A.

; APPLICANT: Chesnut, Robert

; APPLICANT: Epimmune Inc.

; TITLE OF INVENTION: HLA Class I A2 Tumor Associated Antigen

; TITLE OF INVENTION: Peptides and Vaccine Compositions

; FILE REFERENCE: 018623-015710US

; CURRENT APPLICATION NUMBER: US/09/543,608A

; CURRENT FILING DATE: 2002-04-05

; NUMBER OF SEQ ID NOS: 52

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 46

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Standard Peptide 940.06

US-09-543-608A-46

Query Match 100.0%; Score 48; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
 |||||
 Db 1 AVDLYHFLK 9

RESULT 3

US-09-239-043D-2490

; Sequence 2490, Application US/09239043D

; Patent No. 6689363

; GENERAL INFORMATION:

; APPLICANT: Sette, Alessandro

; APPLICANT: Sidney, John

; APPLICANT: Southwood, Scott

; APPLICANT: Vitiello, Maria A.

; APPLICANT: Livingston, Brian D.

; APPLICANT: Celis, Esteban

; APPLICANT: Kubo, Ralph T.

; APPLICANT: Grey, Howard M.

; APPLICANT: Chesnut, Robert

; APPLICANT: Epimmune Inc.

; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus

; TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions

; FILE REFERENCE: 2060.0060007

; CURRENT APPLICATION NUMBER: US/09/239,043D

; CURRENT FILING DATE: 1999-01-27

; PRIOR APPLICATION NUMBER: US 09/189,702

; PRIOR FILING DATE: 1998-11-10

; PRIOR APPLICATION NUMBER: US 08/978,291

; PRIOR FILING DATE: 1997-11-25

; PRIOR APPLICATION NUMBER: US 08/820,360

; PRIOR FILING DATE: 1997-03-12
 ; PRIOR APPLICATION NUMBER: US 60/013,363
 ; PRIOR FILING DATE: 1996-03-13
 ; PRIOR APPLICATION NUMBER: US 08/461,603
 ; PRIOR FILING DATE: 1995-06-05
 ; PRIOR APPLICATION NUMBER: US 08/347,610
 ; PRIOR FILING DATE: 1994-12-01
 ; PRIOR APPLICATION NUMBER: US 08/344,824
 ; PRIOR FILING DATE: 1994-11-23
 ; PRIOR APPLICATION NUMBER: US 08/278,634
 ; PRIOR FILING DATE: 1994-07-21
 ; PRIOR APPLICATION NUMBER: US 08/205,713
 ; PRIOR FILING DATE: 1994-03-04
 ; PRIOR APPLICATION NUMBER: US 08/197,484
 ; PRIOR FILING DATE: 1994-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 2579
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2490
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Standard peptide that binds to HLA A*1101
 US-09-239-043D-2490

Query Match 100.0%; Score 48; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
 |||||
 Db 1 AVDLYHFLK 9

RESULT 4

US-08-159-339A-1153

; Sequence 1153, Application US/08159339A

; Patent No. 6037135

; GENERAL INFORMATION:

; APPLICANT: Kubo, Ralph T.

; APPLICANT: Grey, Howard M.

; APPLICANT: Sette, Alessandro

; APPLICANT: Celis, Esteban

; TITLE OF INVENTION: HLA Binding peptides and Their

; TITLE OF INVENTION: Uses

; NUMBER OF SEQUENCES: 1254

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/159,339A

; FILING DATE: 29-NOV-1993

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/926,666

; FILING DATE: 07-AUG-1992

; APPLICATION NUMBER: US 08/027,746

; FILING DATE: 05-MAR-1993

; APPLICATION NUMBER: US 08/103,396

; FILING DATE: 06-AUG-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Weber, Ellen Lauver

; REGISTRATION NUMBER: 32,762

REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:

INFORMATION FOR SEQ ID NO: 1153:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-1153

Query Match 81.2%; Score 39; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
Db 1 AVDLSHFLK 9

RESULT 5

US-08-197-484-2
Sequence 2, Application US/08197484
Patent No. 6419931

GENERAL INFORMATION:

APPLICANT: VITIELLO, Maria A.
APPLICANT: CHESTNUT, Robert W.
APPLICANT: SETTE, Alessandro D.
APPLICANT: CELIS, Esteban
APPLICANT: GRAY, Howard

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: CTL IMMUNITY

NUMBER OF SEQUENCES: 153

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/197,484

FILING DATE: 16-FEB-1994

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/935,811

FILING DATE: 26-AUG-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/874,491

FILING DATE: 27-APR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/827,682

FILING DATE: 29-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/749,568

FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: Parmelee, Steven W.

REGISTRATION NUMBER: 31,990

REFERENCE/DOCKET NUMBER: 14137-26-4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 467-9600

TELEFAX: (206) 623-6793

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-197-484-2

Query Match 81.2%; Score 39; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
Db 1 AVDLSHFLK 9

RESULT 6

US-09-454-204A-58
Sequence 58, Application US/09454204A
Patent No. 6663871

GENERAL INFORMATION:

APPLICANT: McMichael, Andrew
APPLICANT: Hill, Adrian V.S.

APPLICANT: Gilbert, Sarah C.

APPLICANT: Schneider, Jorg

APPLICANT: Piebanski, Magdalena

APPLICANT: Hanke, Tomas

APPLICANT: Smith, Geoffrey L.

APPLICANT: Blanchard, Tom

TITLE OF INVENTION: Methods and Reagents for Vaccination

TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response

FILE REFERENCE: 2907.1000-000

CURRENT APPLICATION NUMBER: US/09/454,204A

CURRENT FILING DATE: 1999-12-09

PRIOR APPLICATION NUMBER: PCT/GB98/01681

PRIOR FILING DATE: 1998-06-09

PRIOR APPLICATION NUMBER: GB 97 11957.2

PRIOR FILING DATE: 1997-06-09

NUMBER OF SEQ ID NOS: 78

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 58

LENGTH: 9

TYPE: PRT

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: CTL Epitope of HIV-1 nef

US-09-454-204A-58

Query Match 81.2%; Score 39; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
Db 1 AVDLSHFLK 9

RESULT 7

US-09-601-729-186

Sequence 186, Application US/09601729

Patent No. 6683052

GENERAL INFORMATION:

APPLICANT: THIAM, KADER

APPLICANT: AURIAULT, CLAUDE

APPLICANT: GRAS-MASSE, HELENE

APPLICANT: LOING, ESTELLE

APPLICANT: VERWAERDE, CLAUDIE

APPLICANT: GUILLET, JEAN GERARD

TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES

TITLE OF INVENTION: THEREOF IN PHARMACEUTICAL COMPOSITIONS

FILE REFERENCE: USB-97-AU-IN

CURRENT APPLICATION NUMBER: US/09/601,729

CURRENT FILING DATE: 2000-11-20

;; PRIOR APPLICATION NUMBER: PCT/FR99/00259
;; PRIOR FILING DATE: 1999-02-05
;; PRIOR APPLICATION NUMBER: 98 01439
;; PRIOR FILING DATE: 1998-02-06
;; NUMBER OF SEQ ID NOS: 281
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 186
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: peptide
US-09-601-729-186

Query Match 81.2%; Score 39; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
|||||
Db 1 AVDLSHFLK 9

RESULT 8
PCT-US95-02121-2
;; Sequence 2, Application PC/TUS9502121
;; GENERAL INFORMATION:
;; APPLICANT:
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
;; TITLE OF INVENTION: CTL IMMUNITY
;; NUMBER OF SEQUENCES: 153
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US95/02121
;; FILING DATE: 16-FEB-1995
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/197,484
;; FILING DATE: 16-FEB-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/935,811
;; FILING DATE: 26-AUG-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/874,491
;; FILING DATE: 27-APR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/827,682
;; FILING DATE: 29-JAN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/749,568
;; FILING DATE: 26-AUG-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Parmelee, Steven W.
;; REGISTRATION NUMBER: 31,990
;; REFERENCE/DOCKET NUMBER: 14137-26-4PC
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206) 467-9600
;; TELEFAX: (415) 543-5043
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: unknown
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
PCT-US95-02121-2

Query Match 81.2%; Score 39; DB 5; Length 9;

Best Local Similarity 88.9%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 AVDLYHFLK 9
|||||
Db 1 AVDLSHFLK 9

RESULT 9
US-08-484-905-43
;; Sequence 43, Application US/08484905
;; Patent No. 5976551
;; GENERAL INFORMATION:
;; APPLICANT: Mottez, Estelle
;; APPLICANT: Abastado, Jean-Pierre
;; APPLICANT: Kourilsky, Philippe
;; TITLE OF INVENTION: An Altered Major Histocompatibility
;; TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
;; TITLE OF INVENTION: Determinant
;; NUMBER OF SEQUENCES: 127
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
;; STREET: 1300 I Street, N.W., Suite 700
;; CITY: Washington
;; STATE: D.C.
;; ZIP: 20005-3315
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy Disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS-/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/484,905
;; FILING DATE: 07-JUNE-1995
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/801,818
;; FILING DATE: 05-DEC-1991
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/792,473
;; FILING DATE: 15-NOV-1991
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Potter, Jane E. R.
;; REGISTRATION NUMBER: 33,332
;; REFERENCE/DOCKET NUMBER: 03495.0106-03000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-408-4000
;; TELEFAX: 202-408-4400
;; INFORMATION FOR SEQ ID NO: 43:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-484-905-43

Query Match 81.2%; Score 39; DB 2; Length 16;
Best Local Similarity 88.9%; Pred. No. 0.41;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
|||||
Db 6 AVDLSHFLK 14

RESULT 10
US-08-481-985B-43
;; Sequence 43, Application US/08481985B
;; Patent No. 6011146
;; GENERAL INFORMATION:

APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
TITLE OF INVENTION: Altered Major Histocompatibility Complex
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481.985B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0106-04000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-481-985B-43

Query Match 81.2%; Score 39; DB 3; Length 16;
Best Local Similarity 88.9%; Pred. No. 0.41;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
Db 6 AVDLSHFLK 14

RESULT 11
US-08-370-476-43
Sequence 43, Application US/08370476
Patent No. 6153408
GENERAL INFORMATION:
APPLICANT: Mottez, Estelle
APPLICANT: Abastado, Jean-Pierre
APPLICANT: Kourilsky, Philippe
APPLICANT: Lone, Yu-Chun
APPLICANT: Ojcius, David
APPLICANT: Casrouge, Armanda
TITLE OF INVENTION: Altered Major Histocompatibility Complex
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington

STATE: D.C.
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,476
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,575
FILING DATE: 07-SEP-1993
APPLICATION NUMBER: US 08/072,787
FILING DATE: 06-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/801,818
FILING DATE: 05-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/792,473
FILING DATE: 15-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05243.0001-01000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-370-476-43

Query Match 81.2%; Score 39; DB 3; Length 16;
Best Local Similarity 88.9%; Pred. No. 0.41;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
Db 6 AVDLSHFLK 14

RESULT 12
US-08-992-877-23
Sequence 23, Application US/08992877
Patent No. 6340461
GENERAL INFORMATION:
APPLICANT: Terman, David S
TITLE OF INVENTION: SUPERANTIGEN BASED METHODS AND COMPOSITIONS FOR
FILE REFERENCE: superantigen
CURRENT APPLICATION NUMBER: US/08/992,877
CURRENT FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/044,074
PRIOR FILING DATE: 1997-04-17
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: antigen
OTHER INFORMATION: sequences
US-08-992-877-23

Query Match 81.2%; Score 39; DB 3; Length 16;
Best Local Similarity 88.9%; Pred. No. 0.41;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
Db 6 AVDLSHFLK 14

RESULT 13
US-08-145-708A-16
; Sequence 16, Application US/08145708A
; Patent No. 5519114
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Torres, Barbara A.
; APPLICANT: Yamamoto, Janet K.
; TITLE OF INVENTION: Retroviral Superantigens, Superantigen
; TITLE OF INVENTION: Peptides, and Methods of Use
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/145,708A
; FILING DATE: 29-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF135
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; APPLICATION NUMBER: US/08/145,708A
; FILING DATE: 29-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF135
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-145-708A-16

Query Match 81.2%; Score 39; DB 1; Length 38;
Best Local Similarity 88.9%; Pred. No. 0.99;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
Db 23 AVDLSHFLK 31

RESULT 14
US-08-331-454-16
; Sequence 16, Application US/08331454
; Patent No. 5968514
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Torres, Barbara A.
; APPLICANT: Yamamoto, Janet K.
; TITLE OF INVENTION: Retroviral Superantigens, Superantigen
; TITLE OF INVENTION: Peptides, and Methods of Use
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville

; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,454
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/145,708
; FILING DATE: 29-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF135
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; APPLICATION NUMBER: US-08-331-454-16

Query Match 81.2%; Score 39; DB 2; Length 38;
Best Local Similarity 88.9%; Pred. No. 0.99;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVDLYHFLK 9
Db 23 AVDLSHFLK 31

RESULT 15
US-08-417-210A-96
; Sequence 96, Application US/08417210A
; Patent No. 5863542
; GENERAL INFORMATION:
; APPLICANT: PAOLETTI, ENZO
; APPLICANT: TARTAGLIA, JAMES
; APPLICANT: COX, WILLIAM I.
; TITLE OF INVENTION: IMMUNODEFICIENCY RECOMBINANT POXVIRUS
; NUMBER OF SEQUENCES: 148
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
; STREET: 530 FIFTH AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,210A
; FILING DATE: 05-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KOWALSKI, THOMAS J.
; REGISTRATION NUMBER: 32,147
; REFERENCE/DOCKET NUMBER: 454310-2690
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-840-3333

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; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 83 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: amino acid
US-08-417-210A-96

Query Match      81.2%; Score 39; DB 2; Length 83;
Best Local Similarity 88.9%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy      1 AVDLYHFLK 9
        |||||
Db      20 AVDLSHFLK 28
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Search completed: June 29, 2005, 01:44:32
Job time : 17.9126 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:32:21 ; Search time 12.5275 Seconds
(without alignments)
76.805 Million cell updates/sec

Title: US-08-170-344-78
Perfect score: 52
Sequence: 1 KVPYALINK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	73.1	1038	1 JC5757	DNA-directed DNA p
2	38	73.1	1038	2 T18222	DNA polymerase del
3	38	73.1	1097	1 RNBYL3	DNA-directed DNA p
4	37	71.2	658	2 S38890	dnak-type molecula
5	36	69.2	672	2 T43716	dnak-type molecula
6	36	69.2	672	2 T43723	dnak-type molecula
7	36	69.2	1791	2 T02909	hypothetical prote
8	35	67.3	85	2 T09500	dnak-type molecula
9	35	67.3	338	2 T06603	hypothetical prote
10	35	67.3	521	2 B82127	sulfate permease f
11	35	67.3	616	2 H84474	probable Athila re
12	35	67.3	663	2 T04078	dnak-type molecula
13	35	67.3	663	2 T04080	dnak-type molecula
14	35	67.3	694	2 S41868	DNA-directed RNA p
15	35	67.3	842	2 G90576	heat shock atp-dep
16	35	67.3	931	2 AF3276	ATP-dependent clp
17	35	67.3	1378	2 A81393	DNA-directed RNA p
18	35	67.3	1439	2 T02087	gag/pol polyprotei
19	34	65.4	370	2 AC0173	probable iron-sulf
20	34	65.4	455	2 T06357	dnak-type molecula
21	34	65.4	503	2 S64787	pre-mRNA splicing
22	34	65.4	663	2 T03581	dnak-type molecula
23	34	65.4	664	2 T06598	dnak-type molecula
24	34	65.4	666	2 T06358	dnak-type molecula
25	34	65.4	667	2 S21879	dnak-type molecula
26	34	65.4	668	2 S21880	dnak-type molecula
27	34	65.4	668	2 S71171	dnak-type molecula
28	34	65.4	668	2 T46574	dnak-type molecula
29	34	65.4	755	2 T15791	hypothetical prote

30	34	65.4	1501	2 C84512	probable retroelem
31	33.5	64.4	1081	2 T20698	hypothetical prote
32	33	63.5	152	2 F89792	hypothetical prote
33	33	63.5	165	2 S43898	mcrD protein - Met
34	33	63.5	171	2 D90372	hypothetical prote
35	33	63.5	212	2 E90409	ribonuclease HII (
36	33	63.5	315	2 F91250	probable major hea
37	33	63.5	375	1 A48257	alcohol dehydrogen
38	33	63.5	375	1 I60970	alcohol dehydrogen
39	33	63.5	375	1 I60973	alcohol dehydrogen
40	33	63.5	422	2 C89784	hypothetical prote
41	33	63.5	485	2 S37050	H+-exporting ATPas
42	33	63.5	505	2 S76478	hypothetical prote
43	33	63.5	632	2 C71327	probable phosphogl
44	33	63.5	1021	2 S26985	probable DNA-direc
45	33	63.5	1084	1 S19661	DNA-directed DNA p

ALIGNMENTS

RESULT 1

JC5757
DNA-directed DNA polymerase (EC 2.7.7.7) III - yeast (Candida albicans)
N;Alternate names: DNA polymerase III
C;Species: Candida albicans
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 27-Oct-2003
C;Accession: JC5757; S60677
R;Nolan, T.; Rosamond, J.
Gene 183, 159-165, 1996
A;Title: Isolation and molecular characterisation of the POL3 gene from Candida albica
A;Reference number: JC5757; MUID:97149294; PMID:8996102
A;Accession: JC5757
A;Molecule type: DNA
A;Residues: 1-1038 <NOL>
A;Cross-references: EMBL:X88804
A;Note: submitted to the EMBL Data Library, June 1995
C;Comment: This enzyme plays a role in DNA replication.
C;Genetics:
A;Gene: pol3
C;Superfamily: DNA polymerase
C;Keywords: nucleotidyltransferase; zinc finger
F;942-961/Region: zinc finger CCCC motif
F;992-1010/Region: zinc finger CCCC motif

Query Match 73.1%; Score 38; DB 1; Length 1038;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 FPYALINK 10
||| ||||
DB 734 FPYLLINK 741

RESULT 2

T18222
DNA polymerase delta chain - yeast (Candida albicans)
C;Species: Candida albicans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18222
R;Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, November 1998
A;Reference number: Z18831
A;Accession: T18222
A;Status: preliminary; translated from GR/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1038 <BAR>
A;Cross-references: UNIPROT:P46588; EMBL:AL033396; PIDN:CAA21949.1
C;Genetics:
A;Note: CA35A5.06c
C;Superfamily: DNA polymerase

Query Match 73.1%; Score 38; DB 2; Length 1038;

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Best Local Similarity 87.5%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FPYALINK 10
   ||| |||
Db 734 FPYLLINK 741

RESULT 3
RNBVL3
A;Description: DNA-directed DNA polymerase (EC 2.7.7.7) III large chain - yeast (Saccharomyces cerevisiae)
N;Alternate names: DNA-directed DNA polymerase delta large chain; protein D2166; protein
C;Species: Saccharomyces cerevisiae
C;Date: 30-Jun-1991 #sequence_revision 23-Aug-1996 #text_change 09-Jul-2004
C;Accession: S67644; S19638; S05743; S67417; S72105; S19058
R;Ballesta, J.P.G.; Remacha, M.; Soler-Mira, A.; Jimenez, A.; Garcia-Cantalejo, J.M.; Bo
submitted to the Protein Sequence Database, July 1996
A;Reference number: S67629
A;Accession: S67644
A;Molecule type: DNA
A;Residues: 1-1097 <BAL>
A;Cross-references: UNIPROT:P15436; EMBL:Z74150; NID:G1431141; PIDN:CAA98669.1; PID:G143
A;Experimental source: strain S288C
R;Morrison, A.; Sugino, A.
Nucleic Acids Res. 20, 375, 1992
A;Title: Nucleotide sequence of the POL3 gene encoding DNA polymerase III (delta) of Sac
A;Reference number: S19638; MUID:92158636; PMID:1741270
A;Accession: S19638
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-77,'EL',80-1097 <MOR>
A;Cross-references: EMBL:X61920; NID:G4190; PIDN:CAA43922.1; PID:G4191
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
R;Boulet, A.; Simon, M.; Faye, G.; Bauer, G.A.; Burgers, P.M.J.
EMBO J. 8, 1849-1854, 1989
A;Title: Structure and function of the Saccharomyces cerevisiae CDC2 gene encoding the 1
A;Reference number: S05743; MUID:89356661; PMID:2670563
A;Accession: S05743
A;Molecule type: DNA
A;Residues: 1-188,'R',190-203,'D',205-346,'YL',349,'LRNHS',355,'VMCYSD',364-646,'HY',650
A;Cross-references: EMBL:X15477; NID:G3479; PIDN:CAA33504.1; PID:G3480
R;Bozkovic, J.; Saiz, J.E.; Soler-Mira, A.; Garcia-Cantalejo, J.; Revuelta, J.L.; Jimine
submitted to the EMBL Data Library, February 1996
A;Reference number: S67406
A;Accession: S67417
A;Molecule type: DNA
A;Residues: 1-1097 <BOS>
A;Cross-references: EMBL:X95644; NID:G1199535; PIDN:CAA64911.1; PID:G1199547
R;Saiz, J.E.; Buitrago, M.J.; Garcia, R.; Revuelta, J.L.; del Rey, F.
Yeast 12, 1077-1084, 1996
A;Title: The sequence of a 20.3 kb DNA fragment from the left arm of Saccharomyces cerev
A;Reference number: S72094; MUID:97051597; PMID:8896274
A;Accession: S72105
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1097 <SAI>
A;Cross-references: EMBL:X95644; NID:G1199535; PIDN:CAA64911.1; PID:G1199547
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
C;Genetics:
A;Gene: SGP;CDC2; POL3; MIPS:YDL102w; SGD:S0002260
A;Cross-references: MIPS:YDL102w; SGD:S0002260
A;Map position: 4L
C;Superfamily: DNA polymerase
C;Keywords: DNA binding; DNA replication; heterodimer; nucleotidyltransferase; zinc fing
F;1009-1027/Region: zinc finger CCCC motif
F;1056-1074/Region: zinc finger CCCC motif

Query Match 73.1%; Score 38; DB 1; Length 1097;
Best Local Similarity 87.5%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FPYALINK 10
   ||| |||

```

```

Db 806 FPYLLINK 813

RESULT 4
S38890
A;Description: molecular chaperone GRP78/BiP - Phytophthora cinnamomi
N;Alternate names: heat shock protein BiP
C;Species: Phytophthora cinnamomi
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S38890; S38889
R;Lehnen, L.P.; Wilkinson, J.M.; Hardham, A.R.
submitted to the EMBL Data Library, November 1993
A;Description: A Phytophthora cinnamomi gene encodes a protein similar to rat glucose r
A;Reference number: S38890
A;Accession: S38890
A;Molecule type: DNA
A;Residues: 1-658 <LEH>
A;Cross-references: UNIPROT:Q12752; EMBL:X75673; NID:G429117; PIDN:CAA53369.1; PID:G429
R;Lehnen, L.P.; Duniec, J.; Hardham, A.R.
submitted to the EMBL Data Library, November 1993
A;Reference number: S38889
A;Accession: S38889
A;Molecule type: mRNA
A;Residues: 158-658 <LE2>
A;Cross-references: EMBL:X75672; NID:G429115; PIDN:CAA53368.1; PID:G429116
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 71.2%; Score 37; DB 2; Length 658;
Best Local Similarity 60.8%; Pred. No. 25;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KVFPYALINK 10
   ||| |||
Db 113 KLJFYLLVKNK 122

RESULT 5
T43716
A;Description: molecular chaperone BiP [imported] - Aspergillus awamori
C;Species: Aspergillus awamori
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 11-May-2000
C;Accession: T43716
R;Hijarrubia, M.J.; Casqueiro, J.; Gutierrez, S.; Fernandez, F.J.; Martin, J.F.
Curr. Genet. 32, 139-146, 1997
A;Title: Characterization of the biP gene of Aspergillus awamori encoding a protein wit
A;Reference number: Z22645; MUID:97439746; PMID:9294262
A;Accession: T43716
A;Status: preliminary; translated from GB/EMBL/DDDBJ
A;Molecule type: DNA
A;Residues: 1-672 <HIJ>
A;Cross-references: EMBL:Y12504; PIDN:CAA73106.1
A;Experimental source: ATCC 22342
C;Genetics:
A;Gene: biP
A;Introns: 51/1; 116/2; 485/1
C;Superfamily: heat shock protein 70

Query Match 69.2%; Score 36; DB 2; Length 672;
Best Local Similarity 60.0%; Pred. No. 41;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KVFPYALINK 10
   ||| |||
Db 133 KHFPYKVNK 142

RESULT 6
T43723
A;Description: molecular chaperone biPA [imported] - Aspergillus awamori
C;Species: Aspergillus awamori

```

Query Match	67.3%; Score 35; DB 2; Length 85;
Best Local Similarity	50.0%; Pred. No. 7.3;
Matches	5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY	1 KVFPPYALINK 10 : : 21 KLUPYKIVNK 30
Db	
RESULT 9	
T06603	
hypothetical protein F16J13.30 - Arabidopsis thaliana	
C:Species: Arabidopsis thaliana (mouse-ear cress)	
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004	
C:Accession: T06603	
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft	
submitted to the Protein Sequence Database, April 1999	
A:Reference number: Z15789	
A:Accession: T06603	
A:Molecule type: DNA	
A:Residues: 1-338 <BEV>	
A:CROSS-references: UNIPROT:Q9S261; EMBL:AL049638; GSPDB:GN00062; ATSP:F16J13.30	
A:Experimental source: cultivar Columbia; BAC clone F16J13	
C:Genetics:	
A:Gene: ATSP:F16J13.30	
A:Map position: 4	
A:Introns: 56/1; 93/3; 126/1; 159/3; 178/3; 229/2; 246/3; 283/3; 316/2	
Query Match	67.3%; Score 35; DB 2; Length 338;
Best Local Similarity	60.0%; Pred. No. 31;
Matches	6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY	1 KVFPPYALINK 10 : : 66 KIILPYCSINK 75
Db	
RESULT 10	
B82127	
sulfate permease family protein VC2031 [imported] - Vibrio cholerae (strain N16961 sero	
C:Species: Vibrio cholerae	
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004	
C:Accession: B82127	
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J	
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,	
l. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.	
Nature 406, 477-483, 2000	
A>Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.	
A:Reference number: AB2035; MUID:20406833; PMID:10952301	
A:Accession: B82127	
A>Status: preliminary	
A:Molecule type: DNA	
A:Residues: 1-521 <HEI>	
A:CROSS-references: UNIPROT:Q9KQG7; GB:AE004277; GB:AE003852; NID:g9656571; PIDN:NAF951	
A:Experimental source: serogroup O1; strain N16961; biotype El Tor	
C:Genetics:	
A:Gene: VC2031	
A:Map position: 1	
C:Superfamily: integral membrane protein HP0228	
Query Match	67.3%; Score 35; DB 2; Length 521;
Best Local Similarity	85.7%; Pred. No. 50;
Matches	6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	2 VFPPYALI 8 : 242 IFPPYALI 248
Db	
RESULT 11	
H84474	
probable Athila retroelement ORF1 protein [imported] - Arabidopsis thaliana	
C:Species: Arabidopsis thaliana (mouse-ear cress)	

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C;Accession: H84474
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.; Eusse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: H84474
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-616 <STO>
 A;Cross-references: UNIPROT:Q9ZQ03; GB:A5002093; NID:g4388724; PIDN:AAD19762.1; GSPDB:GN
 C;Genetics:
 A;Gene: At2g06110
 A;Map position: 2

Query Match 67.3%; Score 35; DB 2; Length 616;
 Best Local Similarity 50.0%; Pred. No. 59;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFPPYALINK 10
 |:|:|:|:
 Db 172 KLFPPYSLVGE 181

RESULT 12

T04078
 dnak-type molecular chaperone cBiPe2 - maize
 N;Alternate names: luminal binding protein cBiPe2
 C;Species: Zea mays (maize)
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C;Accession: T04078
 R;Wrobel, R.L.; O'Brian, G.R.; Boston, R.S. Gene 204, 105-113, 1997
 A;Title: Comparative analysis of BiP gene expression in maize endosperm.
 A;Reference number: Z15191; MUID:98094260; PMID:9434171
 A;Accession: T04078
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-663 <WRO>
 A;Cross-references: UNIPROT:P24067; EMBL:U58208; NID:gi575127; PIDN:AAC49899.1; PID:gi575127
 C;Function:
 A;Description: involved in protein folding and assembling/disassembling of protein complex
 C;Superfamily: heat shock protein 70
 C;Keywords: ATP; molecular chaperone

Query Match 67.3%; Score 35; DB 2; Length 663;
 Best Local Similarity 60.0%; Pred. No. 64;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KVFPPYALINK 10
 |:|:|:|:
 Db 117 KLVPPYKIINK 126

RESULT 13

T04080
 dnak-type molecular chaperone cBiPe3 - maize
 N;Alternate names: luminal binding protein cBiPe3
 C;Species: Zea mays (maize)
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C;Accession: T04080
 R;Wrobel, R.L.; O'Brian, G.R.; Boston, R.S. Gene 204, 105-113, 1997
 A;Title: Comparative analysis of BiP gene expression in maize endosperm.
 A;Reference number: Z15191; MUID:98094260; PMID:9434171
 A;Accession: T04080
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-663 <WRO>
 A;Cross-references: UNIPROT:Q24581; EMBL:U58209; NID:gi575129; PIDN:AAC49900.1; PID:gi575129
 C;Function:

A;Description: involved in protein folding and assembling/disassembling of protein complex
 C;Superfamily: heat shock protein 70
 C;Keywords: ATP; molecular chaperone

Query Match 67.3%; Score 35; DB 2; Length 663;
 Best Local Similarity 60.0%; Pred. No. 64;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KVFPPYALINK 10
 |:|:|:|:
 Db 117 KLVPPYKIINK 126

RESULT 14

S41868
 DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - *Campylobacter jejuni* (fragment)
 C;Species: *Campylobacter jejuni*
 C;Date: 06-Jan-1995 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
 C;Accession: S41868
 R;Bustamante, V.; Sanchez-Lopez, F.; Bobadilla, M.; Puente, J.L.; Calva, E. submitted to the EMBL Data Library, January 1994
 A;Reference number: S41868
 A;Accession: S41868
 A;Molecule type: DNA
 A;Residues: 1-694 <BUS>
 A;Cross-references: UNIPROT:Q46124; EMBL:X77304; NID:g452609; PIDN:CAA54509.1; PID:g452609
 C;Genetics:
 A;Gene: rpoB
 C;Superfamily: DNA-directed RNA polymerase beta chain
 C;Keywords: nucleotidyltransferase; transcription

Query Match 67.3%; Score 35; DB 2; Length 694;
 Best Local Similarity 77.8%; Pred. No. 67;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KVFPPYALIN 9
 |:|:|:|:
 Db 164 KVMPPYDLIN 172

RESULT 15

G90576
 heat shock atp-dependent proteinase [imported] - *Mycoplasma pulmonis* (strain UAB CTIP)
 C;Species: *Mycoplasma pulmonis*
 C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
 C;Accession: G90576
 R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I. Nucleic Acids Res. 29, 2145-2153, 2001
 A;Title: The complete genome sequence of the murine respiratory pathogen *Mycoplasma pulmonis*
 A;Reference number: A99512; MUID:21267165; PMID:11353084
 A;Accession: G90576
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-842 <KUR>
 A;Cross-references: UNIPROT:Q98049; GB:AL445566; PID:gi14089933; PIDN:CAC13692.1; GSPDB:G90576
 A;Experimental source: strain UAB CTIP
 C;Genetics:
 A;Gene: MYPUP_5190
 C;Superfamily: ATP-dependent Lon protease

Query Match 67.3%; Score 35; DB 2; Length 842;
 Best Local Similarity 66.7%; Pred. No. 82;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VFPYALINK 10
 |:|:|:|:
 Db 189 IFPKALINK 197

Search completed: June 29, 2005, 01:38:54
 Job time : 13.5275 secs

GenCore version 5.1.6
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OM protein -- protein search, using sw model

Run on: June 28, 2005, 23:28:22 ; Search time 60.2747 Seconds
(without alignments)
84.958 Million cell updates/sec

Title: US-08-170-344-78
Perfect score: 52
Sequence: 1 KVFYPYALINK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	80.8	519	2	Q6CKE3 Kluyveromyces
2	42	80.8	661	2	Q77164 entamoeba h
3	38	73.1	268	2	Q6NXA8 brachydanio
4	38	73.1	1038	1	DPOD CANAL
5	38	73.1	1054	2	Q6BH09 candida alb
6	38	73.1	1072	2	Q6CH16 debaryomyce
7	38	73.1	1081	1	Q6CH16 yarrowia li
8	38	73.1	1092	2	Q755K6 ashbya goss
9	38	73.1	1096	2	Q6FK27 candida gla
10	38	73.1	1097	1	DPOD YEAST
11	38	73.1	1101	2	Q6CPW9 kluyveromyc
12	38	73.1	1104	2	Q8X0N7 neurospora
13	38	73.1	1109	2	Q642R8 xenopus lae
14	37	71.2	314	2	Q9BIR1 leptomonas
15	37	71.2	339	2	Q8JS09 phthorinaea
16	37	71.2	445	2	Q6AFH3 leifeonia x
17	37	71.2	608	2	Q6UXX2 homo sapien
18	37	71.2	658	2	Q7DM14 phytophthor
19	36	69.2	346	2	Q8VP05 bordetella
20	36	69.2	496	2	Q7SX93 brachydanio
21	36	69.2	499	2	Q7YYD2 cryptospori
22	36	69.2	666	2	Q8KW18 ruegeria sp
23	36	69.2	672	1	GR78 ASPAW
24	36	69.2	672	1	GR78 ASPAW
25	36	69.2	672	1	GR78 ASPNG
26	36	69.2	1012	2	Q74MD1 nanoarchaeu
27	36	69.2	1308	2	Q9Q06 soil-borne
28	36	69.2	1308	2	Q9Q08 soil-borne
29	36	69.2	1791	2	Q9SUD1 arabadopsis
30	36	69.2	1816	2	Q9JAD2 soil-borne
31	36	69.2	1816	2	Q9JAD3 soil-borne

32	35	67.3	231	2	Q6TB15 hirtella bi
33	35	67.3	231	2	Q6TBL0 atuna racem
34	35	67.3	307	2	Q8KLX9 pseudomonas
35	35	67.3	313	2	Q8GYC7 arabidopsis
36	35	67.3	323	2	Q7V116 prochloroco
37	35	67.3	338	2	Q9S261 arabidopsis
38	35	67.3	372	2	Q7M751 mus musculu
39	35	67.3	380	2	Q7RTX2 homo sapien
40	35	67.3	521	2	Q9KQ77 vibrio chol
41	35	67.3	616	2	Q9ZQ03 arabidopsis
42	35	67.3	638	1	DNAK BUCAP
43	35	67.3	654	2	Q9EN03 buchnera ap
44	35	67.3	662	2	Q24967 ansacta moo
45	35	67.3	663	1	BIP2 MAIZE

ALIGNMENTS

RESULT 1
Q6CKE3 PRELIMINARY; PRT; 519 AA.
AC Q6CKE3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Similarity.
GN ORFNames=KLLA0F11341g;
OS Kluyveromyces lactis NRRL Y-1140.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=284590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-1140;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Bayne E., Bleykasten C.,
RA Boissame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Pellenz J.M., Nikolski M., Oxtas S., Olier-Kalogeropoulos O.,
RA Swennens D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpetti C., Gaillardin C., Weissenbach J.,
RT "Genome evolution in yeasts."
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-1140;
RA Genoscope;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: CR382126; CAG98304.1; -
SQ SEQUENCE 519 AA; 58955 MW; 1A196B9E6F89E3AF CRC64;

Query Match 80.8%; Score 42; DB 2; Length 519;
Best Local Similarity 70.0%; Pred. No. 14;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVFYPYALINK 10
|||: :||
Db ... 212 KVFYPYALINK 221

RESULT 2
Q77164 PRELIMINARY; PRT; 661 AA.
ID O77164
AC O77164;

```

DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 70 kDa heat shock protein Hsp70-Bip.
GN Name=Bip;
OS Entamoeba histolytica.
OC Eukaryota, Entamoebidae; Entamoeba.
OX NCBI_TaxID=5759;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HM-1:IMSS;
RA Samuelson J., Field J.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AF082519; AAC64065.1; -.
DR HSSP; P04475; 1Q5L.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR000886; ER_target_S.
DR InterPro; IPR001023; Hsp70.
DR InterPro; IPR00169; Pept_cys_acsite.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00014; ER_TARGET; UNKNOWN_1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 661 AA; 73546 MW; 8FC1384158DFD922 CRC64;

Query Match 80.8%; Score 42; DB 2; Length 661;
Best Local Similarity 70.0%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KVPFYALINK 10
|:|:|:|:|
Db 113 KLFPYKIINK 122

RESULT 3
Q6NXA8 PRELIMINARY; PRT; 268 AA.
AC Q6NXA8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein zgc:77058.
GN ORFNames=zgc:77058;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg K.H., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC067167; AAH67167.1; -.
DR ZFIN; ZDB-GENE-040426-2507; zgc:77058.
KW Hypothetical protein.
SQ SEQUENCE 268 AA; 27711 MW; EA452A6C908EF8DC6 CRC64;

Query Match 73.1%; Score 38; DB 2; Length 268;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FPYALINK 10
|:|:|:|:|
Db 185 FPYSIINK 192

RESULT 4
ID DP0D CANAL STANDARD; PRT; 1038 AA.
AC P46588; Q9URM0;
DT 01-NOV-1995 (Rel. 32, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 03-JUL-2004 (Rel. 44, Last annotation update)
DE DNA polymerase delta catalytic subunit (EC 2.7.7.7) (DNA polymerase
III).
GN Names=POL3; ORFNames=Ca35A5.06c;
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CA124;
RA Ball T., Rosamond J.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1161;
RA Oliver K., Harris D., Barrell B.G., Rajandream M.A.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: This polymerase possesses two enzymatic activities: DNA
synthesis (polymerase) and an exonucleolytic activity that
degrades single stranded DNA in the 3' to 5' direction.
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
+ {DNA}[N].
CC -1- SUBUNIT: Heterodimer with subunits of 125 kDa and 50 kDa. The 125
kDa subunit contains the polymerase active site and most likely
the active site for the 3'-5' exonuclease activity.
CC -1- SUBCELLULAR LOCATION: Nucleus.
CC -1- MISCELLANEOUS: In eukaryotes there are five DNA polymerases:
alpha, beta, gamma, delta, and epsilon which are responsible for
different reactions of DNA synthesis.
CC -1- SIMILARITY: Belongs to the DNA polymerase type-B family.
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CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
DR EMBL; X88804; CAA61282.1; -.
DR EMBL; AL033396; CAA21949.1; -.

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DR PIR; T18222; T18222.
DR HSBP; Q56366; 1QHT.
DR InterPro; IPR006172; DNA_pol_B.
DR InterPro; IPR006133; DNA_pol_B_exo.
DR InterPro; IPR006134; DNA_pol_B_region.
DR InterPro; IPR004578; Pol2.
DR Pfam; PF00136; DNA_pol_B.
DR PRINTS; PR00106; DNAPOLE.
DR SMART; SM00486; POLBc; 1.
DR TIGRfam; TIGR00592; pol2.
DR PROSITE; PS00116; DNA_POLYMERASE_B; 1.
KW DNA replication; DNA-binding; DNA-directed DNA polymerase;
KW Exonuclease; Hydrolase; Nuclear protein; Transferase; Zinc-finger.
FT ZN_FING 942 961 C4-type (Potential).
FT ZN_FING 992 1010 C4-type (Potential).
FT CONFLICT 172 172 H -> P (in Ref. 1).
FT CONFLICT 772 772 R -> Q (in Ref. 1).
SQ SEQUENCE 1038 AA; 118874 MW; CD43A51985AD299F CRC64;

Query Match 73.1%; Score 38; DB 1; Length 1038;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FPYALINK 10
Db 734 FPYLLINK 741

RESULT 5
Q6BH09 PRELIMINARY; PRT; 1054 AA.
AC Q6BH09;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to sp|P46588 Candida albicans DNA polymerase delta catalytic
DE subunit.
GN ORFNames=DEHA0G23650q;
OS Debaryomyces hansenii CBS767.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycet.
OX NCBI_TaxID=284592;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisarame A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RN Nature 430:35-44(2004).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG Genoscope;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + {DNA} (N).
CC -1- SIMILARITY: Belongs to the DNA polymerase type-B family.
DR EMBL; CR382139; CAG91022.1; -.
DR GO; GO:0005634; C:nucleus; IEA.

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DR GO; GO:0008408; F:3'-5' exonuclease activity; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.
DR GO; GO:0006260; F:DNA replication; IEA.
DR InterPro; IPR006172; DNA_pol_B.
DR InterPro; IPR006133; DNA_pol_B_exo.
DR InterPro; IPR004578; Pol2.
DR InterPro; IPR005829; Sug transporter.
DR Pfam; PF00136; DNA_pol_B; 1.
DR PRINTS; PR00106; DNAPOLE.
DR SMART; SM00486; POLBc; 1.
DR TIGRfam; TIGR00592; pol2.
DR PROSITE; PS00116; DNA_POLYMERASE_B; 1.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; UNKNOWN 1.
KW DNA replication; DNA-binding; DNA-directed DNA polymerase;
KW Transferase.
SQ SEQUENCE 1054 AA; 120974 MW; 12A1BB47D60B6E84 CRC64;

Query Match 73.1%; Score 38; DB 2; Length 1054;
Best Local Similarity 87.5%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FPYALINK 10
Db 752 FPYLLINK 759

RESULT 6
Q6CHI6 PRELIMINARY; PRT; 1072 AA.
AC Q6CHI6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to sp|P46588 Candida albicans DNA polymerase delta catalytic
DE subunit.
GN ORFNames=YALI0A08426g;
OS Yarrowia lipolytica CLIB99.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=284591;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisarame A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RN Nature 430:35-44(2004).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG Genoscope;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + {DNA} (N).
CC -1- SIMILARITY: Belongs to the DNA polymerase type-B family.
DR EMBL; CR382127; CAG83802.1; -.

```


KW DNA replication; DNA-binding; DNA-directed DNA polymerase;
 SQ TRANSFERASE.

SEQUENCE 1092 AA; 123389 MW; 2C97077B54B7D6DD CRC64;

Query Match 73.1%; Score 38; DB 2; Length 1092;
 Best Local Similarity 87.5%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FPYALINK 10
 ||| ||||
 Db 801 FPYLLINK 808

RESULT 9

Q6FKZ7 PRELIMINARY; PRT; 1096 AA.

AC Q6FKZ7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Candida glabrata strain CBS138 chromosome I complete sequence.
 GN ORFNames=CAGL0L07348g;
 OS Candida glabrata CBS138.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 ON NCBI_TaxID=284593;
 RN SEQUENCE FROM N.A.
 RC STRAIN=CBS138;
 RG Genolevures;
 RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
 RA Goffard N., Frangul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
 RA Boisarame A., Boyer J., Cattolico L., Confaniolieri F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantraux F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicaut J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
 RA Pellenz S., Potter S., Richard G.F., Straub M.L., Suleau A.,
 RA Sweeney D., Tekia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Boucher C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
 RA Winkler P., Souciet J.L.;
 RT "Genome evolution in yeasts.";
 RL Nature 430:35-44(2004).
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
 CC + {DNA} (N).
 CC -1- SIMILARITY: Belongs to the DNA polymerase type-B family.
 DR EMBL; CR380958; CAG62067.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0008408; F:3'-5' exonuclease activity; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
 DR GO; GO:000166; F:nucleotide binding; IEA.
 DR GO; GO:0006260; P:DNA replication; IEA.
 DR InterPro; IPR006133; DNA_pol_B.
 DR InterPro; IPR006172; DNA_pol_B_exo.
 DR InterPro; IPR006134; DNA_pol_B_region.
 DR InterPro; IPR004578; Pol2.
 DR Pfam; PF00136; DNA_pol_B; 1.
 DR Pfam; PF03104; DNA_pol_B_exo; 1.
 DR PRINTS; PR01106; DNAPOLE.
 DR SMART; SM00486; POLBc; 1.
 DR TIGRFAMs; TIGR00592; pol2; 1.
 DR PROSITE; PS00116; DNA_POLYMERASE_B; 1.
 KW DNA replication; DNA-binding; DNA-directed DNA polymerase;
 SQ TRANSFERASE.

SEQUENCE 1096 AA; 124390 MW; 92DD001D5PBEA97 ARC64;

Query Match 73.1%; Score 38; DB 2; Length 1096;
 Best Local Similarity 87.5%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FPYALINK 10
 ||| ||||
 Db 805 FPYLLINK 812

RESULT 10

DPOD YEAST
 ID -DPOD YEAST STANDARD; PRT; 1097 AA.

AC P15436;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE DNA polymerase delta catalytic subunit (EC 2.7.7.7) (DNA polymerase III).
 GN Name=POL3; Synonyms=CDC2, TEX1; OrderedLocusNames=YDL102W;
 GN ORFNames=D2166;
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 ON NCBI_TaxID=4932;
 RN SEQUENCE FROM N.A.
 RC STRAIN=YAB2;
 RX MEDLINE=89356661; PubMed=2670563;
 RA Boulet A., Simon M., Faye G., Bauer G.A., Burgers M.J.;
 RT "Structure and function of the Saccharomyces cerevisiae CDC2 gene encoding the large subunit of DNA polymerase III.";
 RL EMBO J. 8:1849-1854(1989).
 RN [2]
 RP SEQUENCE FROM N.A., AND REVISIONS.
 RX MEDLINE=92158636; PubMed=1741270;
 RA Morrison A., Sugino A.;
 RT "Nucleotide sequence of the POL3 gene encoding DNA polymerase III (delta) of Saccharomyces cerevisiae.";
 RN Nucleic Acids Res. 20:375-375(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288c / FY1679;
 RX MEDLINE=97051597; PubMed=8896274;
 DOI=10.1002/STICI1097-0061(199609)12:10B<1077::AID-YEAB>3.3.CO;2-Q;
 RA Salz J.E., Sutcliffe M.J., Garcia R., Revuelta J.L., del Rey F.;
 RT "The sequence of a 20.3 kb DNA fragment from the left arm of Saccharomyces cerevisiae chromosome IV contains the KIN28, PHO2, POL3 and DUN1 genes, and six new open reading frames.";
 RL Yeast 12:1077-1084(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97313263; PubMed=9169867;
 RA Jacq C., Alt-Moerbe J., Andre B., Arnold W., Bahr A., Ballesta J.P.G.,
 RA Bagues M., Baron L., Becker A., Bateau N., Bloecker H., Blugeon C.,
 RA Boskovic J., Brandt P., Brueckner M., Buitrago M.J., Coster F.,
 RA Delaveau T., del Rey F., Dujon B., Eide L.G., Garcia-Cantalejo J.M.,
 RA Goffeau A., Gomez-Peris A., Granotier C., Hanemann V., Hanein T.,
 RA Hoheisel J.D., Jaeger W., Jimenez A., Joniaux J.-L., Kraemer C.,
 RA Kuester H., Laamanen P., Legros Y., Louis E.J., Moeller-Rieker S.,
 RA Monnet A., Moro M., Mueller-Auer S., Nussbaumer B., Paricio N.,
 RA Paulin L., Perea J., Perez-Alonso M., Perez-Ortin J.E., Pohl T.M.,
 RA Prydz H., Purnelle B., Rasmussen S.W., Remacha M., Revuelta J.L.,
 RA Rieger M., Salom D., Salz J.E., Saren A.-M., Schaefer M.,
 RA Scharfe M., Schmidt E.R., Schneider C., Scholler P., Schwarz S.,
 RA Urrestazu L.A., Verhaselt P., Vissers S., Voet M., Volckaert G.,
 RA Wagner G., Wambutt R., Wedler H., Woelfl S., Harris D.E.,
 RA Bowman S., Brown D., Churcher C.M., Connor R., Dedman K., Gentles S.,
 RA Hamlin N., Hunt S., Jones L., McDonald S., Murphy L., Niblett D.,
 RA Odell C., Oliver K., Rajandream M.A., Richards C., Shore L.,
 RA Walsh S.V., Barrill B.G., Dietrich F.S., Mulligan J.T., Allen E.,
 RA Araujo R., Aviles E., Bero A., Carpenter J., Chen E., Chery J.M.,
 RA Chung E., Duncan M., Hunicke-Smith S., Hyman R.W., Komp C.,
 RA Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A.,
 RA Oefner P., Oh C., Petel F.X., Roberts D., Schramm S., Schroeder M.,
 RA Shogren T., Shroff N., Winant A., Yelton M.A., Botstein D.,
 RA Davis R.W., Johnston M., Andrews S., Brinkman R., Cooper J., Ding H.,

RA Du Z., Favello A., Fulton L., Gattung S., Greco T., Hallsworth K.,
RA Hawkins J., Hillier L.W., Jier M., Johnson D., Johnston L.,
RA Kirsten J., Kubacka T., Langston Y., Latreille P., Le T., Mardis E.,
RA Menezes S., Miller N., Nhan M., Pauley A., Peluso D., Rifkin L.,
RA Riles L., Taich A., Trevaaskis E., Vagnati D., Wilcox L., Wohlman P.,
RA Vaudin M., Wilson R., Waterston R., Albermann K., Hani J., Heumann K.,
RA Kleine K., Mewes H.-W., Zollner A., Zaccaria P.,
RA "the nucleotide sequence of Saccharomyces cerevisiae chromosome IV.",
RL Nature 387:75-78 (1997).
RN [5]
RN EXONUCLEASE ACTIVITY.
RX MEDLINE=91293091; PubMed=1648480;
RX Simon M., Giot L., Paye G.;
RA "The 3' to 5' exonuclease activity located in the DNA polymerase delta
RT subunit of Saccharomyces cerevisiae is required for accurate
RT replication.";
RL EMBO J. 10:2165-2170 (1991).
CC -1- FUNCTION: This polymerase possesses two enzymatic activities: DNA
CC synthesis (polymerase) and an exonucleolytic activity that
CC degrades single stranded DNA in the 3' to 5' direction.
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + [DNA] (N).
CC -1- SUBUNIT: Heterodimer with subunits of 125 kDa and 55 kDa. The 125
CC kDa subunit contains the polymerase active site and most likely
CC the active site for the 3'-5' exonuclease activity.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- MISCELLANEOUS: In eukaryotes there are five DNA polymerases:
CC alpha, beta, gamma, delta, and epsilon which are responsible for
CC different reactions of DNA synthesis.
CC -1- SIMILARITY: Belongs to the DNA polymerase type-B family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X15477; CAA33504.1; ALT_SEQ.
CC EMBL; X61920; CAA43922.1; -.
CC EMBL; X95644; CAA64911.1; -.
CC EMBL; Z74150; CAA98669.1; -.
CC PIR; S67644; RNEYL3.
CC HSSP; Q56366; 1QHT.
CC GERMOnline; 140344; -.
CC SGD; S000002260; CDC2.
CC GO; GO:0006298; P:mismatch repair; NAS.
CC InterPro; IPR006172; DNA_pol_B.
CC InterPro; IPR006133; DNA_pol_B_exo.
CC InterPro; IPR006134; DNA_pol_B_region.
CC InterPro; IPR004578; Pol2.
CC Pfam; PF001136; DNA_pol_B; 1.
CC Pfam; PF031104; DNA_pol_B_exo; 1.
CC PRINTS; PR00106; DNAPOLB.
CC SMART; SM00486; POLB; 1.
CC TIGRFAMs; TIGR00592; pol2; 1.
CC PROSITE; PS00116; DNA-Binding; DNA-directed DNA polymerase;
CC DNA replication; DNA-Binding; Nuclear protein; Transferase; Zinc-finger.
CC Exonuclease; Hydrolase; Nuclear protein; Transferase; Zinc-finger.
FT ZN_FING 1009 1027 C4-type (Potential).
FT ZN_FING 1056 1074 C4-type (Potential).
FT CONFLICT 78 79 DV -> EL (in Ref. 1 and 2).
SQ SEQUENCE 1097 AA; 124590 MW; 16E4588BB4168DA CRC64;

Query Match 73.1%; Score 38; DB 1; Length 1097;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FPYALINK 10
| | | | |
Db 806 FPYLLINK 813

RESULT 11
ID Q6CPW9 PRELIMINARY; PRT; 1101 AA.
AC Q6CPW9;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Kluyveromyces lactic strain NRRL Y-1140 chromosome E of strain NRRL Y-
DE 1140 of Kluyveromyces lactis.
GN ORFNames=KLIA0R01606g;
OS Kluyveromyces lactis NRRL Y-1140.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=284590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-1140;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neveglisse C., Talia E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barney S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boixame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre J., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hannequin C., Jaumiaux N., Joyet P., Kachouri R.,
RA Karrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolaki M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Sellenne D., Tekata F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weisenbach J.,
RA Wincker P., Souciet J.L.;
RL "Genome evolution in yeasts.";
RL Nature 430:35-44 (2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-1140;
RG Genoscope;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + [DNA] (N).
CC -1- SIMILARITY: Belongs to the DNA polymerase type-B family.
CC EMBL; CR382125; CAG99107.1; -.
CC GO; GO:0005634; C:nucleus; IEA.
CC GO; GO:0008408; F:3'-5' exonuclease activity; IEA.
CC GO; GO:0003677; F:DNA binding; IEA.
CC GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
CC GO; GO:0000166; F:nucleotide binding; IEA.
CC GO; GO:0006260; P:DNA replication; IEA.
CC InterPro; IPR006172; DNA_pol_B.
CC InterPro; IPR006133; DNA_pol_B_exo.
CC InterPro; IPR004578; Pol2.
CC Pfam; PF001136; DNA_pol_B; 1.
CC Pfam; PF031104; DNA_pol_B_exo; 1.
CC PRINTS; PR00106; DNAPOLB.
CC SMART; SM00486; POLB; 1.
CC TIGRFAMs; TIGR00592; pol2; 1.
CC PROSITE; PS00116; DNA POLYMERASE B; 1.
CC DNA replication; DNA-Binding; DNA-directed DNA polymerase;
CC DNA replication; DNA-Binding; DNA-directed DNA polymerase;
CC Transference.
SQ SEQUENCE 1101 AA; 124365 MW; B45D1DD9837C8203 CRC64;

Query Match 73.1%; Score 38; DB 2; Length 1101;
Best Local Similarity 87.5%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FPYALINK 10
| | | | |
Db 804 FPYLLINK 811

RESULT 12

Q8XON7 Q8XON7 PRELIMINARY; PRT; 1104 AA.
 AC Q8XON7;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Probable DNA-directed DNA polymerase III.
 GN Name=H10H4.020;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 [1]
 SEQUENCE FROM N.A.
 RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA German Neurospora genome project;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
 CC + [DNA] (N).
 CC -1- SIMILARITY: Belongs to the DNA polymerase type-B family.
 DR EMBL; AL670010; CAD21389.1; -.
 DR HSSP; Q56366; 1QHT.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0008408; F:3'-5' exonuclease activity; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006260; P:DNA replication; IEA.
 DR Pfam; PF00136; DNA_pol_B; 1.
 DR Pfam; PF03104; DNA_pol_B_exo; 1.
 DR PRINTS; PR00106; DNAPOLB.
 DR SMART; SMO0486; POLBc; 1.
 DR TIGRFAMs; TIGR00592; pol2; 1.
 DR PROSITE; PS00116; DNA_POLYMERASE_B; 1.
 KW DNA replication; DNA-binding; DNA-directed DNA polymerase;
 KW Transferase.
 SQ SEQUENCE 1104 AA; 125507 MW; 3BSALA0BFD26042F CRC64;

Query Match 73.1%; Score 38; DB 2; Length 1104;
 Best Local Similarity 87.5%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FPYALINK 10

Db 796 FPYLLINK 803

RESULT 13

Q642R8 Q642R8 PRELIMINARY; PRT; 1109 AA.
 AC Q642R8;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE MGC83185 protein.
 GN Name=MGC83185;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8355;
 [1]
 SEQUENCE FROM N.A.
 RA Tissue=Embryo;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;

"Genetic and genomic tools for Xenopus research: The NIH Xenopus
 initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RX PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RA "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RA Klein S., Gerhard D.S.;

RA Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC081093; AAH81093.1; -.

SQ SEQUENCE 1109 AA; 125448 MW; AD6570EAD4CEFOB9 CRC64;

Query Match 73.1%; Score 38; DB 2; Length 1109;

Best Local Similarity 87.5%; Pred. No. 1.8e+02;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FPYALINK 10

Db 804 FPYLLINK 811

RESULT 14

Q9BIR1 Q9BIR1 PRELIMINARY; PRT; 314 AA.
 AC Q9BIR1;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE DNA polymerase delta catalytic chain (EC 2.7.7.7) (Fragment).
 GN Name=dnap;
 OS Leptomonas collosoma.
 OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leptomonas.
 OX NCBI_TaxID=5686;
 [1]
 SEQUENCE FROM N.A.
 RA Yurchenko V.;

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF351198; AAK30251.1; -.

DR HSSP; Q56366; 1QHT.
 DR GO; GO:0008408; F:3'-5' exonuclease activity; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
 DR GO; GO:0000166; F:nucleotide binding; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006260; P:DNA replication; IEA.
 DR InterPro; IPR006172; DNA_pol_B.
 DR InterPro; IPR006134; DNA_pol_B_region.
 DR Pfam; PF00136; DNA_pol_B; 1.
 DR PRINTS; PR00106; DNAPOLB.
 DR PROSITE; PS00116; DNA_POLYMERASE_B; 1.

KW Nucleotidyltransferase; Transferase.
FT NON_TER 1
FT NON_TER 314 314
SQ SEQUENCE 314 AA; 35243 MW; 749789D8F04F668F CRC64;

Query Match 71.2%; Score 37; DB 2; Length 314;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 FPPYALINK 10
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| | | | |
Db 136 FPPYSLMNK 143

RESULT 15
Q8JS09 PRELIMINARY; PRT; 339 AA.
AC Q8JS09;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein PhopGV050.
GN Name=PhopGV050;
OS Phthorimaea operculella granulovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
OX NCBI_TaxID=192584;
RN [1]
RP SEQUENCE FROM N.A.
RA Croizier L., Taha A., Croizier G., Lopez Ferber M.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF499596; AAM70248.1; -.
DR InterPro; IPR007748; DUF673.
DR Pfam; PF05054; DUF673; 1.
KW Hypothetical protein.
SQ SEQUENCE 339 AA; 39233 MW; DFC32093BB1006B3 CRC64;

Query Match 71.2%; Score 37; DB 2; Length 339;
Best Local Similarity 55.6%; Pred. No. 88;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VFPYALINK 10
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: | | | | : |
Db 13 IFPYAMVQK 21

Search completed: June 29, 2005, 01:34:57
Job time : 63.2747 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 29, 2005, 05:18:25 ; Search time 59.8352 Seconds
(without alignments)
64.268 Million cell updates/sec

Title: US-08-170-344-78

Perfect score: 52

Sequence: 1 KVPFYALINK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	10	8	US-08-344-824-12
2	52	100.0	10	14	US-10-116-118-29
3	52	100.0	10	15	US-10-149-138-4196
4	52	100.0	10	15	US-10-149-138-4198
5	52	100.0	10	15	US-10-149-138-4200
6	52	100.0	10	15	US-10-149-138-4355
7	52	100.0	10	15	US-10-149-138-4356
8	52	100.0	10	15	US-10-149-138-4358
9	52	100.0	10	15	US-10-149-138-4359
10	52	100.0	10	15	US-10-149-135-2183
11	52	100.0	10	15	US-10-149-135-2185

Sequence 2187, Ap	10	15	US-10-149-135-2187
Sequence 2295, Ap	10	15	US-10-149-135-2295
Sequence 2296, Ap	10	15	US-10-149-135-2296
Sequence 2298, Ap	10	15	US-10-149-135-2298
Sequence 2299, Ap	10	15	US-10-149-135-2299
Sequence 4196, Ap	10	16	US-10-149-138-4196
Sequence 4198, Ap	10	16	US-10-149-138-4198
Sequence 4200, Ap	10	16	US-10-149-138-4200
Sequence 4355, Ap	10	16	US-10-149-138-4355
Sequence 4356, Ap	10	16	US-10-149-138-4356
Sequence 4358, Ap	10	16	US-10-149-138-4358
Sequence 4359, Ap	10	16	US-10-149-138-4359
Sequence 2489, Ap	10	17	US-10-654-601-2489
Sequence 2576, Ap	10	17	US-10-654-601-2576
Sequence 119, App	10	17	US-10-751-845-119
Sequence 45, Appl	10	14	US-10-116-118-45
Sequence 43, Appl	10	14	US-10-116-118-43
Sequence 44, Appl	10	14	US-10-116-118-44
Sequence 8, Appl	734	14	US-10-270-875-8
Sequence 9, Appl	734	14	US-10-270-875-9
Sequence 8, Appl	734	14	US-10-270-878-8
Sequence 9, Appl	734	14	US-10-270-878-9
Sequence 8, Appl	734	14	US-10-270-786-8
Sequence 9, Appl	734	14	US-10-270-786-9
Sequence 8, Appl	734	14	US-10-270-710-8
Sequence 9, Appl	734	14	US-10-270-710-9
Sequence 8, Appl	734	14	US-10-270-859-8
Sequence 9, Appl	734	14	US-10-270-859-9
Sequence 8, Appl	734	14	US-10-270-846-8
Sequence 9, Appl	734	14	US-10-270-846-9
Sequence 45, Appl	734	14	US-10-684-141-45
Sequence 45, Appl	1081	17	US-10-810-486-45
Sequence 3369, Ap	38	73.1	1096
Sequence 1577, Ap	38	73.1	1097

ALIGNMENTS

RESULT 1
US-08-344-824-12
; Sequence 12, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:


```

; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4200
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4200

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Query Match          100.0%; Score 52; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 KVFPYALINK 10
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Db      1 KVFPYALINK 10

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RESULT 6
US-10-149-138-4355
; Sequence 4355, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4355
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4355

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Query Match          100.0%; Score 52; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 KVFPYALINK 10
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Db      1 KVFPYALINK 10

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RESULT 7
US-10-149-138-4356
; Sequence 4356, Application US/10149138

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; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4356
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4356

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Query Match          100.0%; Score 52; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 KVFPYALINK 10
      |||||
Db      1 KVFPYALINK 10

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```

RESULT 8
US-10-149-138-4358
; Sequence 4358, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4358
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4358

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Query Match          100.0%; Score 52; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 KVFPYALINK 10

```

```
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Db      1 KVPFYLALINK 10

RESULT 9
US-10-149-138-4359
; Sequence 4359, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Eteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4359
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4359

Query Match      100.0%; Score 52; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVPFYLALINK 10
Db      1 KVPFYLALINK 10

RESULT 10
US-10-149-135-2183
; Sequence 2183, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Eteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: PCT/US00/33545
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US/10/149,135
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2183
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-2183

Query Match      100.0%; Score 52; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVPFYLALINK 10
Db      1 KVPFYLALINK 10

RESULT 11
US-10-149-135-2185
; Sequence 2185, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Eteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2185
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-2185

Query Match      100.0%; Score 52; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVPFYLALINK 10
Db      1 KVPFYLALINK 10

RESULT 12
US-10-149-135-2187
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; Sequence 2187, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2187
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-2187

Query Match      100.0%; Score 52; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFPPYALINK 10
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Db      1 KVFPPYALINK 10

RESULT 13
US-10-149-135-2295
; Sequence 2295, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2187
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-2187

Query Match      100.0%; Score 52; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFPPYALINK 10
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Db      1 KVFPPYALINK 10

RESULT 14
US-10-149-135-2296
; Sequence 2296, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2296
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-2296

Query Match      100.0%; Score 52; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFPPYALINK 10
      |||||
Db      1 KVFPPYALINK 10
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; Sequence 2187, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2295
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-2295

Query Match      100.0%; Score 52; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFPPYALINK 10
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Db      1 KVFPPYALINK 10

RESULT 14
US-10-149-135-2296
; Sequence 2296, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2296
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-2296

Query Match      100.0%; Score 52; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVFPPYALINK 10
      |||||
Db      1 KVFPPYALINK 10
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RESULT 15
US-10-149-135-2298
; Sequence 2298, Application US/10149135
; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Eteban
; APPLICANT: Keogh, Elises
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: MAGE2/3 Using Peptide and Nucleic Acid Compositions
; CURRENT APPLICATION NUMBER: US/10/149,135
; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2298
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-2298

Query Match 100.0%; Score 52; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVPFPYALINK 10
| | | | | | | |
Db 1 KVPFPYALINK 10

Search completed: June 29, 2005, 05:48:17
Job time : 59.8352 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:37:59 ; Search time 18.7363 Seconds
(without alignments)
39.842 Million cell updates/sec

Title: US-08-170-344-78
Perfect score: 52
Sequence: 1 KVPFYALINK 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	10	3	US-08-159-339A-124
2	52	100.0	10	4	US-09-543-608A-45
3	52	100.0	10	4	US-09-239-043D-2489
4	52	100.0	10	4	US-09-239-043D-2576
5	38	73.1	734	4	US-09-585-858-8
6	38	73.1	734	4	US-09-585-858-9
7	38	73.1	734	4	US-10-270-878-8
8	38	73.1	734	4	US-10-270-878-9
9	35	67.3	306	4	US-09-328-352-8079
10	35	67.3	655	4	US-09-632-538C-36
11	35	67.3	749	4	US-09-489-039A-12279
12	34	65.4	458	4	US-09-270-767-43904
13	34	65.4	593	4	US-09-836-503B-2
14	34	65.4	593	4	US-09-836-410A-1
15	34	65.4	700	4	US-09-836-503B-5
16	34	65.4	710	4	US-09-836-503B-4
17	34	65.4	723	4	US-09-836-503B-3
18	34	65.4	759	4	US-09-328-352-7650
19	34	65.4	870	4	US-09-270-767-60178
20	34	65.4	885	1	US-08-484-105-14
21	34	65.4	885	1	US-08-484-106-14
22	34	65.4	896	4	US-09-270-767-44723
23	34	65.4	1433	4	US-09-543-681A-7342
24	33	63.5	116	4	US-09-640-211A-1121
25	33	63.5	131	4	US-09-248-796A-15066
26	33	63.5	150	4	US-09-270-767-39283
27	33	63.5	150	4	US-09-270-767-54500

28	33	63.5	572	4	US-09-248-796A-15736
29	33	63.5	735	4	US-09-585-858-10
30	33	63.5	735	4	US-10-270-878-10
31	33	63.5	738	4	US-09-585-858-6
32	33	63.5	738	4	US-09-585-858-7
33	33	63.5	738	4	US-10-270-878-6
34	33	63.5	738	4	US-10-270-878-7
35	33	63.5	846	4	US-09-270-767-42096
36	33	63.5	1107	1	US-08-366-577-2
37	33	63.5	1107	5	PCT-US96-00005-2
38	32	61.5	75	4	US-09-134-000C-3474
39	32	61.5	215	4	US-09-248-796A-27992
40	32	61.5	216	4	US-09-270-767-44783
41	32	61.5	252	4	US-09-328-352-7325
42	32	61.5	359	3	US-09-134-001C-5618
43	32	61.5	371	4	US-09-710-279-628
44	32	61.5	424	4	US-09-543-681A-7210
45	32	61.5	425	4	US-09-710-279-2604

ALIGNMENTS

RESULT 1
US-08-159-339A-124
; Sequence 124, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq For Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 124:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

Sequence 15736, A
Sequence 10, Appl
Sequence 10, Appl
Sequence 6, Appl
Sequence 7, Appl
Sequence 6, Appl
Sequence 7, Appl
Sequence 7, Appl
Sequence 42096, A
Sequence 2, Appl
Sequence 2, Appl
Sequence 3474, Ap
Sequence 27992, A
Sequence 44783, A
Sequence 7325, Ap
Sequence 5618, Ap
Sequence 628, App
Sequence 7210, Ap
Sequence 2604, Ap

US-08-159-339A-124

Query Match 100.0%; Score 52; DB 3; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00041;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFPYALINK 10
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 Db 1 KVFPYALINK 10

RESULT 2

US-09-543-608A-45

; Sequence 45, Application US/09543608A
 ; Patent No. 6602510

; GENERAL INFORMATION:

; APPLICANT: Fikes, John D.
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Sidney, John
 ; APPLICANT: Southwood, Scott
 ; APPLICANT: Celis, Esteban
 ; APPLICANT: Keogh, Elissa A.
 ; APPLICANT: Chesnut, Robert
 ; APPLICANT: Epimmune Inc.

; TITLE OF INVENTION: HLA Class I A2 Tumor Associated Antigen
 ; TITLE OF INVENTION: Peptides and Vaccine Compositions

; FILE REFERENCE: 018623-015710US

; CURRENT APPLICATION NUMBER: US/09/543,608A

; CURRENT FILING DATE: 2002-04-05

; NUMBER OF SEQ ID NOS: 52

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 45

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Standard Peptide 941.12

US-09-543-608A-45

Query Match 100.0%; Score 52; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00041;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFPYALINK 10
 |||||
 Db 1 KVFPYALINK 10

RESULT 3

US-09-239-043D-2489

; Sequence 2489, Application US/09239043D

; Patent No. 6689363

; GENERAL INFORMATION:

; APPLICANT: Sette, Alessandro
 ; APPLICANT: Sidney, John
 ; APPLICANT: Southwood, Scott
 ; APPLICANT: Vitiello, Maria A.
 ; APPLICANT: Livingston, Brian D.
 ; APPLICANT: Celis, Esteban
 ; APPLICANT: Kubo, Ralph T.
 ; APPLICANT: Grey, Howard M.
 ; APPLICANT: Chesnut, Robert
 ; APPLICANT: Epimmune Inc.

; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus

; TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions

; FILE REFERENCE: 2060.0060007

; CURRENT APPLICATION NUMBER: US/09/239,043D

; CURRENT FILING DATE: 1999-01-27

; PRIOR APPLICATION NUMBER: US 09/189,702

; PRIOR FILING DATE: 1998-11-10

; PRIOR APPLICATION NUMBER: US 08/978,291

; PRIOR FILING DATE: 1997-11-25

; PRIOR APPLICATION NUMBER: US 08/820,360

; PRIOR FILING DATE: 1997-03-12
 ; PRIOR APPLICATION NUMBER: US 60/013,363
 ; PRIOR FILING DATE: 1996-03-13
 ; PRIOR APPLICATION NUMBER: US 08/461,603
 ; PRIOR FILING DATE: 1995-06-05
 ; PRIOR APPLICATION NUMBER: US 08/347,610
 ; PRIOR FILING DATE: 1994-12-01
 ; PRIOR APPLICATION NUMBER: US 08/344,824
 ; PRIOR FILING DATE: 1994-11-23
 ; PRIOR APPLICATION NUMBER: US 08/278,634
 ; PRIOR FILING DATE: 1994-07-21
 ; PRIOR APPLICATION NUMBER: US 08/205,713
 ; PRIOR FILING DATE: 1994-03-04
 ; PRIOR APPLICATION NUMBER: US 08/197,484
 ; PRIOR FILING DATE: 1994-02-16
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 2579
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2489
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Standard peptide that binds to HLA A*0301, A*6801
 US-09-239-043D-2489

Query Match 100.0%; Score 52; DB 4; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.00041;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFPYALINK 10

|||||

Db 1 KVFPYALINK 10

RESULT 4

US-09-239-043D-2576

; Sequence 2576, Application US/09239043D

; Patent No. 6689363

; GENERAL INFORMATION:

; APPLICANT: Sette, Alessandro
 ; APPLICANT: Sidney, John
 ; APPLICANT: Southwood, Scott
 ; APPLICANT: Vitiello, Maria A.
 ; APPLICANT: Livingston, Brian D.
 ; APPLICANT: Celis, Esteban
 ; APPLICANT: Kubo, Ralph T.
 ; APPLICANT: Grey, Howard M.
 ; APPLICANT: Chesnut, Robert
 ; APPLICANT: Epimmune Inc.

; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus

; TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions

; FILE REFERENCE: 2060.0060007

; CURRENT APPLICATION NUMBER: US/09/239,043D

; CURRENT FILING DATE: 1999-01-27

; PRIOR APPLICATION NUMBER: US 09/189,702

; PRIOR FILING DATE: 1998-11-10

; PRIOR APPLICATION NUMBER: US 08/978,291

; PRIOR FILING DATE: 1997-11-25

; PRIOR APPLICATION NUMBER: US 08/820,360

; PRIOR FILING DATE: 1997-03-12

; PRIOR APPLICATION NUMBER: US 60/013,363

; PRIOR FILING DATE: 1996-03-13

; PRIOR APPLICATION NUMBER: US 08/461,603

; PRIOR FILING DATE: 1995-06-05

; PRIOR APPLICATION NUMBER: US 08/347,610

; PRIOR FILING DATE: 1994-12-01

; PRIOR APPLICATION NUMBER: US 08/344,824

; PRIOR FILING DATE: 1994-11-23

; PRIOR APPLICATION NUMBER: US 08/278,634

; PRIOR FILING DATE: 1994-07-21

; PRIOR APPLICATION NUMBER: US 08/205,713

; PRIOR FILING DATE: 1994-03-04

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; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2576
; LENGTH: 10
; TYPE: PRT
; ORGANISM: A3CON1 peptide
US-09-239-043D-2576

Query Match      100.0%; Score 52; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KVPFYLALINK 10
Db      1 KVPFYLALINK 10
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RESULT 5
US-09-585-858-8
; Sequence 8, Application US/09585858
; Patent No. 6492161
; GENERAL INFORMATION:
; APPLICANT: Sigrður Hjorleifsdóttir
; APPLICANT: Guðmundur O. Hreggvidsson
; APPLICANT: Olafur H. Fridjonsson
; APPLICANT: Arnthor Aevarsson
; APPLICANT: Jakob K. Kristjansson
; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
; FILE REFERENCE: 2739.1001-001
; CURRENT APPLICATION NUMBER: US/09/585,858
; CURRENT FILING DATE: 2000-12-18
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Candida albicans (Yeast)
US-09-585-858-8

Query Match      73.1%; Score 38; DB 4; Length 734;
Best Local Similarity 87.5%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 FPYALINK 10
Db      561 FPYLLINK 568
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RESULT 6
US-09-585-858-9
; Sequence 9, Application US/09585858
; Patent No. 6492161
; GENERAL INFORMATION:
; APPLICANT: Sigrður Hjorleifsdóttir
; APPLICANT: Guðmundur O. Hreggvidsson
; APPLICANT: Olafur H. Fridjonsson
; APPLICANT: Arnthor Aevarsson
; APPLICANT: Jakob K. Kristjansson
; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
; FILE REFERENCE: 2739.1001-001
; CURRENT APPLICATION NUMBER: US/09/585,858
; CURRENT FILING DATE: 2000-12-18
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 9
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-585-858-9

Query Match      73.1%; Score 38; DB 4; Length 734;
Best Local Similarity 87.5%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 FPYALINK 10
Db      564 FPYLLINK 571
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RESULT 7
US-10-270-878-8
; Sequence 8, Application US/10270878
; Patent No. 6818425
; GENERAL INFORMATION:
; APPLICANT: Sigrður Hjorleifsdóttir
; APPLICANT: Guðmundur O. Hreggvidsson
; APPLICANT: Olafur H. Fridjonsson
; APPLICANT: Arnthor Aevarsson
; APPLICANT: Jakob K. Kristjansson
; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
; FILE REFERENCE: 2739.1001-001
; CURRENT APPLICATION NUMBER: US/10/270,878
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/585,858
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Candida albicans (Yeast)
US-10-270-878-8

Query Match      73.1%; Score 38; DB 4; Length 734;
Best Local Similarity 87.5%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      3 FPYALINK 10
Db      561 FPYLLINK 568
      |||||
RESULT 8
US-10-270-878-9
; Sequence 9, Application US/10270878
; Patent No. 6818425
; GENERAL INFORMATION:
; APPLICANT: Sigrður Hjorleifsdóttir
; APPLICANT: Guðmundur O. Hreggvidsson
; APPLICANT: Olafur H. Fridjonsson
; APPLICANT: Arnthor Aevarsson
; APPLICANT: Jakob K. Kristjansson
; TITLE OF INVENTION: Bacteriophage RM378 of a Thermophilic
; FILE REFERENCE: 2739.1001-001
; CURRENT APPLICATION NUMBER: US/10/270,878
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/585,858
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 734
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-270-878-9
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; FILE REFERENCE: 73.1%; Score 38; DB 4; Length 734;
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12279
; LENGTH: 749
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-489-039A-12279

Query Match      67.3%; Score 35; DB 4; Length 749;
Best Local Similarity 82.5%; Pred. No. 1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      3 FPYALINK 10
Db      564 FPYLLINK 571

RESULT 9
US-09-328-352-8079
; Sequence 8079, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 8079
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
; US-09-328-352-8079

Query Match      67.3%; Score 35; DB 4; Length 306;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 KVPFYPALIN 9
Db      111 KIPFVLPN 119

RESULT 10
US-09-632-538C-36
; Sequence 36, Application US/09632538C
; Patent No. 6440674
; GENERAL INFORMATION:
; APPLICANT: Misra, Santosh et al.
; TITLE OF INVENTION: PLANT PROMOTER DERIVED FROM LUMINAL BINDING PROTEIN GENE AND METH
; FILE REFERENCE: 54359
; CURRENT APPLICATION NUMBER: US/09/632,538C
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 36
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Pseudotsuga menziesii
; US-09-632-538C-36

Query Match      67.3%; Score 35; DB 4; Length 655;
Best Local Similarity 50.0%; Pred. No. 88;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy      1 KVPFYPALINK 10
Db      110 KLLPYKIVNK 119

RESULT 11
US-09-489-039A-12279
; Sequence 12279, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 10872/518
; CURRENT APPLICATION NUMBER: US/09/836,503B
; CURRENT FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 60/197,977
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-836-503B-2

Query Match      65.4%; Score 34; DB 4; Length 593;
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; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12279
; LENGTH: 749
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-489-039A-12279

Query Match      67.3%; Score 35; DB 4; Length 749;
Best Local Similarity 82.5%; Pred. No. 1e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      3 FPYALINK 10
Db      447 FPYAVLNR 454

RESULT 12
US-09-270-767-43904
; Sequence 43904, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43904
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
; US-09-270-767-43904

Query Match      65.4%; Score 34; DB 4; Length 458;
Best Local Similarity 75.0%; Pred. No. 95;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      3 FPYALINK 10
Db      132 FPYVLLNK 139

RESULT 13
US-09-836-503B-2
; Sequence 2, Application US/09836503B
; Patent No. 6696415
; GENERAL INFORMATION:
; APPLICANT: Children's Hospital Research Foundation
; APPLICANT: Gendron, Robert L.
; APPLICANT: Paradis, Helene
; TITLE OF INVENTION: Treatment of Ocular Neovascularization and Related Diseases
; FILE REFERENCE: 10872/518
; CURRENT APPLICATION NUMBER: US/09/836,503B
; CURRENT FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 60/197,977
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-836-503B-2

Query Match      65.4%; Score 34; DB 4; Length 593;
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Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFPYAL 7
Db 557 KLFYAL 563

RESULT 14
US-09-836-410A-1
; Sequence 1, Application US/09836410A
; Patent No. 6812340
; GENERAL INFORMATION:
; APPLICANT: Children's Hospital Research Foundation
; APPLICANT: Gendron, Robert L.
; APPLICANT: Paradis, Helene
; TITLE OF INVENTION: Inhibition of Bone Tumor Formation Using Antisense cDNA Therapy
; FILE REFERENCE: 10872/518
; CURRENT APPLICATION NUMBER: US/09/836,410A
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: US 60/197,977
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 593
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-836-410A-1

Query Match 65.4%; Score 34; DB 4; Length 593;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFPYAL 7
Db 557 KLFYAL 563

RESULT 15
US-09-836-503B-5
; Sequence 5, Application US/09836503B
; Patent No. 6696415
; GENERAL INFORMATION:
; APPLICANT: Children's Hospital Research Foundation
; APPLICANT: Gendron, Robert L.
; APPLICANT: Paradis, Helene
; TITLE OF INVENTION: Treatment of Ocular Neovascularization and Related Diseases
; FILE REFERENCE: 10872/518
; CURRENT APPLICATION NUMBER: US/09/836,503B
; CURRENT FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: US 60/197,977
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 700
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-836-503B-5

Query Match 65.4%; Score 34; DB 4; Length 700;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVFPYAL 7
Db 664 KLFYAL 670

Search completed: June 29, 2005, 01:44:31
Job time : 18.7863 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:32:21 ; Search time 12.5275 Seconds
(without alignments)
76.805 Million cell updates/sec

Title: US-08-170-344-77
Perfect score: 55
Sequence: 1 FLPSDYFPSV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	51	92.7	181	2 S53178	core antigen - hep
2	51	92.7	183	1 NKVLA2	core antigen - hep
3	51	92.7	183	1 NKVLCP	core antigen - hep
4	51	92.7	183	2 S53181	core antigen - hep
5	51	92.7	183	2 S53260	core antigen - hep
6	51	92.7	183	2 S53214	core antigen - hep
7	51	92.7	183	2 S53175	core antigen - hep
8	51	92.7	183	2 S53267	core antigen - hep
9	51	92.7	183	2 S53155	core antigen - hep
10	51	92.7	183	2 S53152	core antigen - hep
11	51	92.7	183	2 S53221	core antigen - hep
12	51	92.7	183	2 S53232	core antigen - hep
13	51	92.7	183	2 S43490	core antigen - hep
14	51	92.7	183	2 S53129	core antigen - hep
15	51	92.7	183	2 S53286	core antigen - hep
16	51	92.7	183	2 S53189	core antigen - hep
17	51	92.7	183	2 S53169	core antigen - hep
18	51	92.7	183	2 S53137	core antigen - hep
19	51	92.7	183	2 S53184	core antigen - hep
20	51	92.7	183	2 S53143	core antigen - hep
21	51	92.7	183	2 S53270	core antigen - hep
22	51	92.7	185	2 S53288	core antigen - hep
23	51	92.7	195	1 NKVLH3	core antigen - hep
24	51	92.7	211	1 NKVLA1	e antigen precurs
25	51	92.7	212	1 NKVLAH	e antigen precurs
26	51	92.7	212	1 NKVLBH	e antigen precurs
27	51	92.7	212	1 NKVLJ1	e antigen precurs
28	51	92.7	212	1 NKVLJ2	e antigen precurs
29	51	92.7	212	2 S53238	e antigen precurs

30	51	92.7	212	2 S53227	e antigen precurs
31	51	92.7	212	2 S67504	e antigen precurs
32	51	92.7	212	2 S53281	e antigen precurs
33	51	92.7	212	2 S53240	e antigen precurs
34	51	92.7	212	2 S53272	e antigen precurs
35	51	92.7	212	2 S53229	e antigen precurs
36	51	92.7	212	2 S53202	e antigen precurs
37	51	92.7	212	2 S53163	e antigen precurs
38	51	92.7	212	2 S53216	e antigen precurs
39	51	92.7	212	2 S53257	e antigen precurs
40	51	92.7	212	2 S53255	e antigen precurs
41	51	92.7	212	2 S20746	e antigen precurs
42	51	92.7	212	2 S20750	e antigen precurs
43	51	92.7	212	2 S53236	e antigen precurs
44	51	92.7	212	2 S32204	e antigen precurs
45	51	92.7	212	2 S53204	e antigen precurs

ALIGNMENTS

RESULT 1
S53178
core antigen - hepatitis B virus (isolate patient Addis'89)
N;Alternate names: HBC antigen
N;Contains: core antigen
C;Species: hepatitis B virus, HBV
A;Variety: isolate patient Addis'89
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S53178
R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A;Reference number: S53112
A;Accession: S53178
A;Molecule type: DNA
A;Residues: 1-181 <LAI>
A;Cross-references: UNIPROT:Q67995; EMBL:X85278; NID:g736069; PIDN:CAA59S80.1; PID:g736
A;Experimental source: isolate patient Addis'89
A;Note: due to a stop codon between the alternative initiators the e antigen precursor
C;Genetics:
A;Gene: C
C;Superfamily: hepatitis B virus core antigen
C;Keywords: core protein

Query Match 92.7%; Score 51; DB 2; Length 181;
Best Local Similarity 90.0%; Pred. No. 0.062;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLPSDYFPSV 10
|||||:||||
DB 18 FLPSDFFPSV 27

RESULT 2
NKVLA2
core antigen - hepatitis B virus (subtype adyw)
C;Species: hepatitis B virus, HBV
A;Variety: subtype adyw
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: B93217; A03711
R;Pasek, M.; Goto, T.; Gilbert, W.; Zink, B.; Schaller, H.; Mackay, P.; Leadbetter, G.;
Nature 282, 575-579, 1979
A;Title: Hepatitis B virus genes and their expression in E. coli.
A;Reference number: A93217; MUID:81012115; PMID:399329
A;Accession: B93217
A;Molecule type: DNA
A;Residues: 1-183 <PAS>
A;Cross-references: UNIPROT:P03147; GB:J02202; NID:g329637; PIDN:AAA45486.1; PID:g32963
A;Experimental source: subtype adyw
A;Note: due to a stop codon between the alternative initiators the e antigen precursor
C;Genetics:
A;Gene: C
C;Superfamily: hepatitis B virus core antigen

C;Keywords: core protein
F;1-183/Product: core antigen #status predicted <MAT>

Query Match 92.7%; Score 51; DB 1; Length 183;
Best Local Similarity 90.0%; Pred. No. 0.063;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYFPPSV 10
Db 18 FLPSDFPPSV 27
|||||:||||

RESULT 3

NKVUCP
core antigen - hepatitis B virus (strain LSH, chimpanzee)
N;Alternate names: Hbc antigen
C;Species: hepatitis B virus, HBV
A;Variety: strain LSH, chimpanzee
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C;Accession: A28885
R;Vaudin, M.; Woistenholme, A.J.; Tsiquaye, K.N.; Zuckerman, A.J.; Harrison, T.J.
J. Gen. Virol. 69, 1383-1389, 1988
A;Title: The complete nucleotide sequence of the genome of a hepatitis B virus isolated
A;Reference number: A92796; MUID:88258473; PMID:2838576
A;Accession: A28885
A;Molecule type: DNA
A;Residues: 1-183 <LAI>
A;Cross-references: UNIPROT:P12901; EMBL:D00220; NID:g221505; PIDN:BAA00157.1; PID:g2215
A;Experimental source: strain LSH, chimpanzee
A;Note: due to a stop codon between the alternative initiators the e antigen precursor
C;Genetics:
A;Gene: C
C;Superfamily: hepatitis B virus core antigen
C;Keywords: core protein

Query Match 92.7%; Score 51; DB 1; Length 183;
Best Local Similarity 90.0%; Pred. No. 0.063;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYFPPSV 10
Db 18 FLPSDFPPSV 27
|||||:||||

RESULT 4

S53181
core antigen - hepatitis B virus
N;Alternate names: Hbc antigen
C;Species: hepatitis B virus, HBV
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S53181; S53291
R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A;Reference number: S53112
A;Accession: S53181
A;Molecule type: DNA
A;Residues: 1-183 <LAI>
A;Cross-references: UNIPROT:Q67997; EMBL:X85279; NID:g736073; PIDN:CAA59583.1; PID:g7360
A;Experimental source: isolate patient Bitti'89
A;Note: due to a stop codon between the alternative initiators the e antigen precursor
C;Accession: S53291

A;Molecule type: DNA
A;Residues: 1-20,'T',22-37,'L',39,'D',41-57,'E',59-76,'Q',78-83,'L',85-86,'N',88-146,'S'
A;Cross-references: EMBL:X85263; NID:g736232; PIDN:CAA59538.1; PID:g736235
A;Experimental source: isolate patient Amoroso'89
A;Note: due to a stop codon between the alternative initiators the e antigen precursor
C;Genetics:
A;Gene: C
C;Superfamily: hepatitis B virus core antigen
C;Keywords: core protein

Query Match 92.7%; Score 51; DB 2; Length 183;

Best Local Similarity 90.0%; Pred. No. 0.063;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYFPPSV 10
Db 18 FLPSDFPPSV 27
|||||:||||

RESULT 5

S53260
core antigen - hepatitis B virus (isolate patient Mannoni-3'94)
N;Alternate names: Hbc antigen
C;Species: hepatitis B virus, HBV
A;Variety: isolate patient Mannoni-3'94
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S53260
R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A;Reference number: S53112
A;Accession: S53260
A;Molecule type: DNA
A;Residues: 1-183 <LAI>
A;Cross-references: UNIPROT:Q68060; EMBL:X85311; NID:g736187; PIDN:CAA59655.1; PID:g736
A;Experimental source: isolate patient Mannoni-3'94
A;Note: due to a stop codon between the alternative initiators the e antigen precursor
C;Genetics:
A;Gene: C
C;Superfamily: hepatitis B virus core antigen
C;Keywords: core protein

Query Match 92.7%; Score 51; DB 2; Length 183;
Best Local Similarity 90.0%; Pred. No. 0.063;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYFPPSV 10
Db 18 FLPSDFPPSV 27
|||||:||||

RESULT 6

S53214
core antigen - hepatitis B virus (isolate patient Castag-2'86)
N;Alternate names: Hbc antigen
C;Species: hepatitis B virus, HBV
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S53214
R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A;Reference number: S53112
A;Accession: S53214
A;Molecule type: DNA
A;Residues: 1-183 <LAI>
A;Cross-references: UNIPROT:Q68023; EMBL:X85292; NID:g736120; PIDN:CAA59614.1; PID:g736
A;Experimental source: isolate patient Castag-2'86
A;Note: due to a stop codon between the alternative initiators the e antigen precursor
C;Genetics:
A;Gene: C
C;Superfamily: hepatitis B virus core antigen
C;Keywords: core protein

Query Match 92.7%; Score 51; DB 2; Length 183;
Best Local Similarity 90.0%; Pred. No. 0.063;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYFPPSV 10
Db 18 FLPSDFPPSV 27
|||||:||||

RESULT 7

S53175
core antigen - hepatitis B virus (isolate patient Boi'90)
N;Alternate names: Hbc antigen
N;Contains: core antigen
C;Species: hepatitis B virus, HBV
A;Variety: isolate patient Boi'90
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S53175
R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A;Reference number: S53112
A;Accession: S53175
A;Molecule type: DNA
A;Residues: 1-183 <LAI>
A;Cross-references: UNIPROT:Q67993; EMBL:X85277; NID:g736065; PIDN:CAAS59577.1; PID:g736065
A;Experimental source: isolate patient Boi'90
A;Note: due to a stop codon between the alternative initiators the e antigen precursor
C;Genetics:
A;Gene: C
C;Superfamily: hepatitis B virus core antigen
C;Keywords: core protein

Query Match 92.7%; Score 51; DB 2; Length 183;
Best Local Similarity 90.0%; Pred. No. 0.063;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYPPSV 10
|||||:||||
Db 18 FLPSDFPPSV 27

RESULT 8
S53267
core antigen - hepatitis B virus (isolate patient Lucianoc'92)
N;Alternate names: Hbc antigen
N;Contains: core antigen
C;Species: hepatitis B virus, HBV
A;Variety: isolate patient Lucianoc'92
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S53267
R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A;Reference number: S53112
A;Accession: S53267
A;Molecule type: DNA
A;Residues: 1-183 <LAI>
A;Cross-references: UNIPROT:Q68064; EMBL:X85260; NID:g736197; PIDN:CAAS59530.1; PID:g73620
A;Experimental source: isolate patient Lucianoc'92
A;Note: due to a stop codon between the alternative initiators the e antigen precursor
C;Genetics:
A;Gene: C
C;Superfamily: hepatitis B virus core antigen
C;Keywords: core protein

Query Match 92.7%; Score 51; DB 2; Length 183;
Best Local Similarity 90.0%; Pred. No. 0.063;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYPPSV 10
|||||:||||
Db 18 FLPSDFPPSV 27

RESULT 9
S53155
core antigen - hepatitis B virus (isolate patient Usai'89)
N;Alternate names: Hbc antigen
N;Contains: core antigen
C;Species: hepatitis B virus, HBV
A;Variety: isolate patient Usai'89
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S53155
R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.

submitted to the EMBL Data Library, March 1995
A;Reference number: S53112
A;Accession: S53155
A;Molecule type: DNA
A;Residues: 1-183 <LAI>
A;Cross-references: UNIPROT:Q67976; EMBL:X85270; NID:g736037; PIDN:CAAS59559.1; PID:g736037
A;Experimental source: isolate patient Usai'89
A;Note: due to a stop codon between the alternative initiators the e antigen precursor
C;Genetics:
A;Gene: C
C;Superfamily: hepatitis B virus core antigen
C;Keywords: core protein

Query Match 92.7%; Score 51; DB 2; Length 183;
Best Local Similarity 90.0%; Pred. No. 0.063;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYPPSV 10
|||||:||||
Db 18 FLPSDFPPSV 27

RESULT 10
S53152
core antigen - hepatitis B virus (isolate patient Tufariello'89)
N;Alternate names: Hbc antigen
N;Contains: core antigen
C;Species: hepatitis B virus, HBV
A;Variety: isolate patient Tufariello'89
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S53152
R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A;Reference number: S53112
A;Accession: S53152
A;Molecule type: DNA
A;Residues: 1-183 <LAI>
A;Cross-references: UNIPROT:Q67973; EMBL:X85269; NID:g736033; PIDN:CAAS59556.1; PID:g736033
A;Experimental source: isolate patient Tufariello'89
A;Note: due to a stop codon between the alternative initiators the e antigen precursor
C;Genetics:
A;Gene: C
C;Superfamily: hepatitis B virus core antigen
C;Keywords: core protein

Query Match 92.7%; Score 51; DB 2; Length 183;
Best Local Similarity 90.0%; Pred. No. 0.063;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYPPSV 10
|||||:||||
Db 18 FLPSDFPPSV 27

RESULT 11
S53221
core antigen - hepatitis B virus (isolate patient Giulianioc'92)
N;Alternate names: Hbc antigen
N;Contains: core antigen
C;Species: hepatitis B virus, HBV
A;Variety: isolate patient Giulianioc'92
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S53221
R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A;Reference number: S53112
A;Accession: S53221
A;Molecule type: DNA
A;Residues: 1-183 <LAI>
A;Cross-references: UNIPROT:Q68027; EMBL:X85258; NID:g736127; PIDN:CAAS59525.1; PID:g736127
A;Experimental source: isolate patient Giulianioc'92
A;Note: due to a stop codon between the alternative initiators the e antigen precursor
C;Genetics:

A;Gene: C
C;Superfamily: hepatitis B virus core antigen
C;Keywords: core protein

Query Match 92.7%; Score 51; DB 2; Length 183;
Best Local Similarity 90.0%; Pred. No. 0.063;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLPSDYPPSV 10
|||||:||||
Db 18 FLPSDFPPSV 27

RESULT 12

S53232
core antigen - hepatitis B virus (isolate patient Dettori-2'87)
N;Alternate names: HBC antigen
N;Contains: core antigen
C;Species: hepatitis B virus, HBV
A;Variety: isolate patient Dettori-2'87
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S53232
R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A;Reference number: S53112
A;Accession: S53232
A;Molecule type: DNA
A;Residues: 1-183 <LAI>
A;Cross-references: UNIPROT:Q68037; EMBL:X85299; NID:g736146; PIDN:CAA59629.1; PID:g736146
A;Experimental source: isolate patient Dettori-2'87
A;Note: due to a stop codon between the alternative initiators the e antigen precursor
C;Genetics:
A;Gene: C
C;Superfamily: hepatitis B virus core antigen
C;Keywords: core protein

Query Match 92.7%; Score 51; DB 2; Length 183;
Best Local Similarity 90.0%; Pred. No. 0.063;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLPSDYPPSV 10
|||||:||||
Db 18 FLPSDFPPSV 27

RESULT 13

S43490
core antigen - hepatitis B virus (subtype adr)
N;Alternate names: HBC antigen
N;Contains: core antigen
C;Species: hepatitis B virus, HBV
A;Variety: subtype adr
C;Date: 07-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S43490
R;Loncarevic, I.F.; Zentgraf, H.; Schroeder, C.H.
Nucleic Acids Res. 18, 4940, 1990
A;Title: Sequence of a replication competent hepatitis B virus genome with a prex open h
A;Reference number: S12598; MUID:90370503; PMID:2395664
A;Accession: S43490
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-183 <LON>
A;Cross-references: UNIPROT:Q67951; EMBL:X52939; NID:g457780; PIDN:CAA37112.1; PID:g457780
A;Experimental source: subtype adr
A;Note: due to a stop codon between the alternative initiators the e antigen precursor
C;Genetics:
A;Gene: C
C;Superfamily: hepatitis B virus core antigen
C;Keywords: core protein

Query Match 92.7%; Score 51; DB 2; Length 183;
Best Local Similarity 90.0%; Pred. No. 0.063;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLPSDYPPSV 10
|||||:||||
Db 18 FLPSDFPPSV 27

RESULT 14

S53129
core antigen - hepatitis B virus
N;Alternate names: HBC antigen
N;Contains: core antigen
C;Species: hepatitis B virus, HBV
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S53129
R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A;Reference number: S53112
A;Accession: S53129
A;Molecule type: DNA
A;Residues: 1-183 <LAI>
A;Cross-references: UNIPROT:Q67946; EMBL:X85254; NID:g736003; PIDN:CAA59512.1; PID:g736003
C;Genetics:
A;Gene: C
C;Superfamily: hepatitis B virus core antigen
C;Keywords: core protein

Query Match 92.7%; Score 51; DB 2; Length 183;
Best Local Similarity 90.0%; Pred. No. 0.063;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLPSDYPPSV 10
|||||:||||
Db 18 FLPSDFPPSV 27

RESULT 15

S53286
core antigen - hepatitis B virus (isolate patient Salvatorec'92)
N;Alternate names: HBC antigen
N;Contains: core antigen
C;Species: hepatitis B virus, HBV
A;Variety: isolate patient Salvatorec'92
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S53286
R;Lai, M.E.; Mazzoleni, A.P.; Porru, A.; Balestrieri, A.
submitted to the EMBL Data Library, March 1995
A;Reference number: S53112
A;Accession: S53286
A;Molecule type: DNA
A;Residues: 1-183 <LAI>
A;Cross-references: UNIPROT:Q68079; EMBL:X85261; NID:g736224; PIDN:CAA59533.1; PID:g736224
A;Experimental source: isolate patient Salvatorec'92
A;Note: due to a stop codon between the alternative initiators the e antigen precursor
C;Genetics:
A;Gene: C
C;Superfamily: hepatitis B virus core antigen
C;Keywords: core protein

Query Match 92.7%; Score 51; DB 2; Length 183;
Best Local Similarity 90.0%; Pred. No. 0.063;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLPSDYPPSV 10
|||||:||||
Db 18 FLPSDFPPSV 27

Search completed: June 29, 2005, 01:38:53
Job time : 12.5275 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:28:22 ; Search time 60.2747 Seconds
(without alignments)
84.958 Million cell updates/sec

Title: US-08-170-344-77
Perfect score: 55
Sequence: 1 FLPSDYPPSV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	98.2	212	2 Q769J2	Q769J2 hepatitis b
2	51	92.7	42	2 Q9E0V1	Q9E0V1 hepatitis b
3	51	92.7	56	2 Q9WP60	Q9WP60 hepatitis b
4	51	92.7	64	2 Q9QR82	Q9QR82 hepatitis b
5	51	92.7	65	2 Q6UB18	Q6UB18 hepatitis b
6	51	92.7	65	2 Q9J3T4	Q9J3T4 hepatitis b
7	51	92.7	65	2 Q9J3T5	Q9J3T5 hepatitis b
8	51	92.7	65	2 Q9J3T6	Q9J3T6 hepatitis b
9	51	92.7	65	2 Q9J3T7	Q9J3T7 hepatitis b
10	51	92.7	66	2 Q91A47	Q91A47 hepatitis b
11	51	92.7	66	2 Q91A48	Q91A48 hepatitis b
12	51	92.7	66	2 Q91A49	Q91A49 hepatitis b
13	51	92.7	66	2 Q91A50	Q91A50 hepatitis b
14	51	92.7	66	2 Q91A51	Q91A51 hepatitis b
15	51	92.7	66	2 Q91A52	Q91A52 hepatitis b
16	51	92.7	66	2 Q91A53	Q91A53 hepatitis b
17	51	92.7	66	2 Q91A54	Q91A54 hepatitis b
18	51	92.7	66	2 Q91A56	Q91A56 hepatitis b
19	51	92.7	66	2 Q91A58	Q91A58 hepatitis b
20	51	92.7	66	2 Q91A60	Q91A60 hepatitis b
21	51	92.7	66	2 Q91A68	Q91A68 hepatitis b
22	51	92.7	66	2 Q91A70	Q91A70 hepatitis b
23	51	92.7	66	2 Q91A72	Q91A72 hepatitis b
24	51	92.7	66	2 Q91A74	Q91A74 hepatitis b
25	51	92.7	66	2 Q91A76	Q91A76 hepatitis b
26	51	92.7	66	2 Q91A82	Q91A82 hepatitis b
27	51	92.7	66	2 Q91A84	Q91A84 hepatitis b
28	51	92.7	66	2 Q91A86	Q91A86 hepatitis b
29	51	92.7	66	2 Q91S27	Q91S27 hepatitis b
30	51	92.7	71	2 Q616R2	Q616R2 hepatitis b
31	51	92.7	71	2 Q616R6	Q616R6 hepatitis b

32	51	92.7	71	2 Q616R8	Q616R8 hepatitis b
33	51	92.7	71	2 Q616S0	Q616S0 hepatitis b
34	51	92.7	71	2 Q616S4	Q616S4 hepatitis b
35	51	92.7	71	2 Q616S6	Q616S6 hepatitis b
36	51	92.7	71	2 Q616S8	Q616S8 hepatitis b
37	51	92.7	71	2 Q616T0	Q616T0 hepatitis b
38	51	92.7	71	2 Q616T2	Q616T2 hepatitis b
39	51	92.7	71	2 Q616T4	Q616T4 hepatitis b
40	51	92.7	71	2 Q616T6	Q616T6 hepatitis b
41	51	92.7	71	2 Q616T8	Q616T8 hepatitis b
42	51	92.7	71	2 Q616U0	Q616U0 hepatitis b
43	51	92.7	71	2 Q616U2	Q616U2 hepatitis b
44	51	92.7	71	2 Q616U4	Q616U4 hepatitis b
45	51	92.7	71	2 Q616U6	Q616U6 hepatitis b

ALIGNMENTS

RESULT 1
Q769J2 PRELIMINARY; PRT; 212 AA.
AC Q769J2; 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Core protein.
DE Namespre-C/C;
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Tran H.T., Ushijima H., Quang V.X., Win K.M., Luengrojanakul P., Kikuchi K., Sata T., Abe K.;
RA "Genotype C of hepatitis B virus can be classified into at least two subgroups";
RL J. Gen. Virol. 85:283-292 (2004).
DR EMBL; AB112408; BAD05052.1; -;
DR InterPro; IPR002006; Hepatitis core.
DR Pfam; PF00906; Hepatitis_core; 1;
SQ SEQUENCE 212 AA; 24445 MW; E34413B32E80P75 CRC64;
Query Match 98.2%; Score 54; DB 2; Length 212;
Best Local Similarity 90.0%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYPPSV 10
|||
Db 47 FLPSDYPPSI 56

RESULT 2
Q9E0V1 PRELIMINARY; PRT; 42 AA.
AC Q9E0V1; 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Core protein.
DE Namespre-C/C;
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Tagger A., Binelli G., Donato F., Ribero M.L.;
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289942; AAG25224.1; -;
DR InterPro; IPR002006; Hepatitis_core.
DR Pfam; PF00906; Hepatitis_core; 1;
SQ SEQUENCE 42 AA; 4753 MW; 93672F3BACDE3194 CRC64;

Query Match 92.7%; Score 51; DB 2; Length 42;
 Best Local Similarity 90.0%; Pred. No. 0.061; Mismatches 0; Gaps 0;
 Matches 9; Conservative 1; Indels 0; Gaps 0;

Qy 1 FLPSDYPPSV 10
 Db 18 FLPSDFFPSV 27
 |||||:||||

RESULT 3
 Q9WP60 ID Q9WP60 PRELIMINARY; PRT; 56 AA.
 AC Q9WP60;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Pre-C/C protein.
 GN Name=pre-C/C;
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20037832; PubMed=10573161;
 RA Priekchat P., Weisel H., Will H., Gunther S.;
 RT "Hepatitis B virus genomes from long-term immunosuppressed virus
 RT carriers are modified by specific mutations in several regions.";
 RL J. Gen. Virol. 80:2685-2691(1999).
 DR EMBL; AF143306; AAD37953.1; -;
 DR InterPro; IPR02006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core_1.
 SQ SEQUENCE 56 AA; 6313 MW; 2F5B075F0F39CC7B CRC64;

Query Match 92.7%; Score 51; DB 2; Length 56;
 Best Local Similarity 90.0%; Pred. No. 0.084; Mismatches 1; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Indels 0; Gaps 0;

Qy 1 FLPSDYPPSV 10
 Db 47 FLPSDFFPSV 56
 |||||:||||

RESULT 4
 Q9QRR2 ID Q9QRR2 PRELIMINARY; PRT; 64 AA.
 AC Q9QRR2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Core mutant protein.
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Serum;
 RA Saxena A., Acharya S.K., Nayak B., Panda S.K.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF115421; AAD49186.1; -;
 DR InterPro; IPR02006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core_1.
 SQ SEQUENCE 64 AA; 7196 MW; 12AB9C46EB302D80 CRC64;

Query Match 92.7%; Score 51; DB 2; Length 64;
 Best Local Similarity 90.0%; Pred. No. 0.097; Mismatches 1; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYPPSV 10
 Db 18 FLPSDFFPSV 27
 |||||:||||

RESULT 5

Q6UB18 ID Q6UB18 PRELIMINARY; PRT; 65 AA.
 AC Q6UB18;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Core protein (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hallett R.L., Teo C.G.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY374227; AAQ83759.1; -;
 DR InterPro; IPR02006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core_1.
 FT NON_TER 1 1
 FT NON_TER 65 65
 SQ SEQUENCE 65 AA; 7186 MW; 6F334F0ADA7831CE CRC64;

Query Match 92.7%; Score 51; DB 2; Length 65;
 Best Local Similarity 90.0%; Pred. No. 0.098; Mismatches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYPPSV 10
 Db 9 FLPSDFFPSV 18
 |||||:||||

RESULT 6
 Q9J3T4 ID Q9J3T4 PRELIMINARY; PRT; 65 AA.
 AC Q9J3T4;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Core protein (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20187639; PubMed=10720502;
 RA Ngui S.L., Watkins R.P., Hepconstall J., Teo C.G.;
 RT "Selective transmission of hepatitis B virus after percutaneous
 RT exposure.";
 RL J. Infect. Dis. 181:838-843(2000).
 DR EMBL; AF204958; AAF67531.1; -;
 DR InterPro; IPR02006; Hepatitis_core.
 DR Pfam; PF00906; Hepatitis_core_1.
 FT NON_TER 1 1
 FT NON_TER 65 65
 SQ SEQUENCE 65 AA; 7129 MW; 63034F0ADA7831CE CRC64;

Query Match 92.7%; Score 51; DB 2; Length 65;
 Best Local Similarity 90.0%; Pred. No. 0.098; Mismatches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYPPSV 10
 Db 9 FLPSDFFPSV 18
 |||||:||||

RESULT 7
 Q9J3T5 ID Q9J3T5 PRELIMINARY; PRT; 65 AA.
 AC Q9J3T5;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Core protein (Fragment).
 OS Hepatitis B virus.

OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20187639; PubMed=10720502;
 RA Ngui S.L., Watkins R.P., Heptonstall J., Teo C.G.;
 RT "Selective transmission of hepatitis B virus after percutaneous
 exposure.";
 RL J. Infect. Dis. 181:838-843 (2000).
 DR EMBL; AF204957; AAF67530.1; -;
 DR InterPro; IPR002006; Hepatitis core.
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON_TER 1
 FT NON_TER 65
 SQ SEQUENCE 65 AA; 7152 MW; 7BA6A9BFA7831CE CRC64;
 Query Match 92.7%; Score 51; DB 2; Length 65;
 Best Local Similarity 90.0%; Pred. No. 0.098;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYPPSV 10
 |||||:||||
 Db 9 FLPSDFFPSV 18

RESULT 8

O9J3T6 PRELIMINARY; PRT; 65 AA.
 AC O9J3T6
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Core protein (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20187639; PubMed=10720502;
 RA Ngui S.L., Watkins R.P., Heptonstall J., Teo C.G.;
 RT "Selective transmission of hepatitis B virus after percutaneous
 exposure.";
 RL J. Infect. Dis. 181:838-843 (2000).
 DR EMBL; AF204956; AAF67529.1; -;
 DR InterPro; IPR002006; Hepatitis core.
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON_TER 1
 FT NON_TER 65
 SQ SEQUENCE 65 AA; 7157 MW; 79B34EA1C0C831CE CRC64;

Query Match 92.7%; Score 51; DB 2; Length 65;
 Best Local Similarity 90.0%; Pred. No. 0.098;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYPPSV 10
 |||||:||||
 Db 9 FLPSDFFPSV 18

RESULT 9

O9J3T7 PRELIMINARY; PRT; 65 AA.
 AC O9J3T7
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Core protein (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20187639; PubMed=10720502;

RA Ngui S.L., Watkins R.P., Heptonstall J., Teo C.G.;
 RT "Selective transmission of hepatitis B virus after percutaneous
 exposure.";
 RL J. Infect. Dis. 181:838-843 (2000).
 DR EMBL; AF204955; AAF67528.1; -;
 DR InterPro; IPR002006; Hepatitis core.
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON_TER 1
 FT NON_TER 65
 SQ SEQUENCE 65 AA; 7129 MW; 62B34PB4C0C831CA CRC64;

Query Match 92.7%; Score 51; DB 2; Length 65;
 Best Local Similarity 90.0%; Pred. No. 0.098;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYPPSV 10
 |||||:||||
 Db 9 FLPSDFFPSV 18

RESULT 10

O91A47 PRELIMINARY; PRT; 66 AA.
 ID O91A47
 AC O91A47
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Precore/core protein (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=11472634; DOI=10.1186/1471-2180-1-10;
 RA Castro L.D., Niel C., Gomes S.A.;
 RT "Low frequency of mutations in the core promoter and precore regions
 of hepatitis B virus in anti-HBe positive Brazilian carriers.";
 RL BMC Microbiol. 1:10-10 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA De Castro L., Niel C., Gomes S.A.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF390015; AAL16423.1; -;
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON_TER 66
 FT NON_TER 66
 SQ SEQUENCE 66 AA; 7356 MW; 89A1375595C16E96 CRC64;

Query Match 92.7%; Score 51; DB 2; Length 66;
 Best Local Similarity 90.0%; Pred. No. 0.1;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYPPSV 10
 |||||:||||
 Db 47 FLPSDFFPSV 56

RESULT 11

O91A48 PRELIMINARY; PRT; 66 AA.
 ID O91A48
 AC O91A48
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Precore/core protein (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=11472634; DOI=10.1186/1471-2180-1-10;
 RA Castro L.D., Niel C., Gomes S.A.;
 RT "Low frequency of mutations in the core promoter and precore regions
 of hepatitis B virus in anti-HBe positive Brazilian carriers.";

RL BMC Microbiol. 1:10-10(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA De Castro L., Niel C., Gomes S.A.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF390013; AAL16421.1; -
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON TER 66
 SQ SEQUENCE 66 AA; 7370 MW; 8EA6375595C43E96 CRC64;
 Query Match 92.7%; Score 51; DB 2; Length 66;
 Best Local Similarity 90.0%; Pred. No. 0.1;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FLPSDYPPSV 10
 Db 47 FLPSDFFPSV 56
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RESULT 12
 Q91A49 PRELIMINARY; PRT; 66 AA.
 AC Q91A49
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Precore/core protein (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=11472634; DOI=10.1186/1471-2180-1-10;
 RA Castro L.D., Niel C., Gomes S.A.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF390012; AAL16420.1; -
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON TER 66
 SQ SEQUENCE 66 AA; 7370 MW; 8EA6375595C43E96 CRC64;
 Query Match 92.7%; Score 51; DB 2; Length 66;
 Best Local Similarity 90.0%; Pred. No. 0.1;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FLPSDYPPSV 10
 Db 47 FLPSDFFPSV 56
 |||||:||||

RESULT 13
 Q91A50 PRELIMINARY; PRT; 66 AA.
 AC Q91A50
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Precore/core protein (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=11472634; DOI=10.1186/1471-2180-1-10;
 RA Castro L.D., Niel C., Gomes S.A.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF390013; AAL16421.1; -
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON TER 66
 SQ SEQUENCE 66 AA; 7370 MW; 8EA6375595C43E96 CRC64;
 Query Match 92.7%; Score 51; DB 2; Length 66;
 Best Local Similarity 90.0%; Pred. No. 0.1;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FLPSDYPPSV 10
 Db 47 FLPSDFFPSV 56
 |||||:||||

RESULT 14
 Q91A51 PRELIMINARY; PRT; 66 AA.
 AC Q91A51
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Precore/core protein (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=11472634; DOI=10.1186/1471-2180-1-10;
 RA Castro L.D., Niel C., Gomes S.A.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF390010; AAL16418.1; -
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON TER 66
 SQ SEQUENCE 66 AA; 7492 MW; 95BA4PF652C1C4D3 CRC64;
 Query Match 92.7%; Score 51; DB 2; Length 66;
 Best Local Similarity 90.0%; Pred. No. 0.1;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FLPSDYPPSV 10
 Db 47 FLPSDFFPSV 56
 |||||:||||

RESULT 15
 Q91A52 PRELIMINARY; PRT; 66 AA.
 AC Q91A52
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Precore/core protein (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=11472634; DOI=10.1186/1471-2180-1-10;
 RA Castro L.D., Niel C., Gomes S.A.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF390011; AAL16419.1; -
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON TER 66
 SQ SEQUENCE 66 AA; 7418 MW; 8EBA5AE352C43E96 CRC64;
 Query Match 92.7%; Score 51; DB 2; Length 66;
 Best Local Similarity 90.0%; Pred. No. 0.1;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FLPSDYPPSV 10
 Db 47 FLPSDFFPSV 56
 |||||:||||

RESULT 16
 Q91A53 PRELIMINARY; PRT; 66 AA.
 AC Q91A53
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Precore/core protein (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=11472634; DOI=10.1186/1471-2180-1-10;
 RA Castro L.D., Niel C., Gomes S.A.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF390011; AAL16419.1; -
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON TER 66
 SQ SEQUENCE 66 AA; 7418 MW; 8EBA5AE352C43E96 CRC64;
 Query Match 92.7%; Score 51; DB 2; Length 66;
 Best Local Similarity 90.0%; Pred. No. 0.1;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FLPSDYPPSV 10
 Db 47 FLPSDFFPSV 56
 |||||:||||

RESULT 17
 Q91A54 PRELIMINARY; PRT; 66 AA.
 AC Q91A54
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Precore/core protein (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=11472634; DOI=10.1186/1471-2180-1-10;
 RA Castro L.D., Niel C., Gomes S.A.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF390012; AAL16420.1; -
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON TER 66
 SQ SEQUENCE 66 AA; 7492 MW; 95BA4PF652C1C4D3 CRC64;
 Query Match 92.7%; Score 51; DB 2; Length 66;
 Best Local Similarity 90.0%; Pred. No. 0.1;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FLPSDYPPSV 10
 Db 47 FLPSDFFPSV 56
 |||||:||||

RESULT 18
 Q91A55 PRELIMINARY; PRT; 66 AA.
 AC Q91A55
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Precore/core protein (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=11472634; DOI=10.1186/1471-2180-1-10;
 RA Castro L.D., Niel C., Gomes S.A.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF390013; AAL16421.1; -
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON TER 66
 SQ SEQUENCE 66 AA; 7418 MW; 8EBA5AE352C43E96 CRC64;
 Query Match 92.7%; Score 51; DB 2; Length 66;
 Best Local Similarity 90.0%; Pred. No. 0.1;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FLPSDYPPSV 10
 Db 47 FLPSDFFPSV 56
 |||||:||||

RESULT 19
 Q91A56 PRELIMINARY; PRT; 66 AA.
 AC Q91A56
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Precore/core protein (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=11472634; DOI=10.1186/1471-2180-1-10;
 RA Castro L.D., Niel C., Gomes S.A.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF390014; AAL16422.1; -
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON TER 66
 SQ SEQUENCE 66 AA; 7418 MW; 8EBA5AE352C43E96 CRC64;
 Query Match 92.7%; Score 51; DB 2; Length 66;
 Best Local Similarity 90.0%; Pred. No. 0.1;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FLPSDYPPSV 10
 Db 47 FLPSDFFPSV 56
 |||||:||||

RESULT 20
 Q91A57 PRELIMINARY; PRT; 66 AA.
 AC Q91A57
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Precore/core protein (Fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=11472634; DOI=10.1186/1471-2180-1-10;
 RA Castro L.D., Niel C., Gomes S.A.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF390015; AAL16423.1; -
 DR Pfam; PF00906; Hepatitis_core; 1.
 FT NON TER 66
 SQ SEQUENCE 66 AA; 7418 MW; 8EBA5AE352C43E96 CRC64;
 Query Match 92.7%; Score 51; DB 2; Length 66;
 Best Local Similarity 90.0%; Pred. No. 0.1;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FLPSDYPPSV 10
 Db 47 FLPSDFFPSV 56
 |||||:||||

RP SEQUENCE FROM N.A.
RA De Castro L., Niel C., Gomes S.A.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF390009; AAL16417.1; -;
DR Pfam; PF00906; Hepatitis_core; 1.
FT NON_TER 66
SQ SEQUENCE 66 AA; 7370 MW; 8EA6375595C43E96 CRC64;

Query Match 92.7%; Score 51; DB 2; Length 66;
Best Local Similarity 90.0%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYFFSV 10
| | | | |
Db 47 FLPSDYFFSV 56

Search completed: June 29, 2005, 01:34:54
Job time : 60.2747 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 05:18:25 ; Search time 59.8352 Seconds
(without alignments)
64.268 Million cell updates/sec

Title: US-08-170-344-77

Perfect score: 55

Sequence: 1 FLPSDYPPSV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	10	8	US-08-344-824-11
2	55	100.0	10	10	US-09-898-860-126
3	55	100.0	10	11	US-09-935-476-4
4	55	100.0	10	14	US-10-094-699-108
5	55	100.0	10	14	US-10-359-431-25
6	55	100.0	10	15	US-10-371-525-226
7	55	100.0	10	15	US-10-026-066-86
8	55	100.0	10	15	US-10-371-069-226
9	55	100.0	10	15	US-10-371-645-226
10	55	100.0	10	15	US-10-117-937-24
11	55	100.0	10	15	US-10-371-260-226

12	55	100.0	10	15	US-10-448-521-45	Sequence 45, Appl
13	55	100.0	10	15	US-10-149-138-4189	Sequence 4189, Ap
14	55	100.0	10	15	US-10-149-138-4190	Sequence 4190, Ap
15	55	100.0	10	15	US-10-149-138-4191	Sequence 4191, Ap
16	55	100.0	10	15	US-10-149-138-4192	Sequence 4192, Ap
17	55	100.0	10	15	US-10-149-138-4193	Sequence 4193, Ap
18	55	100.0	10	15	US-10-149-138-4194	Sequence 4194, Ap
19	55	100.0	10	15	US-10-149-138-4350	Sequence 4350, Ap
20	55	100.0	10	15	US-10-149-138-4351	Sequence 4351, Ap
21	55	100.0	10	15	US-10-149-138-4352	Sequence 4352, Ap
22	55	100.0	10	15	US-10-149-138-4353	Sequence 4353, Ap
23	55	100.0	10	15	US-10-149-138-4354	Sequence 4354, Ap
24	55	100.0	10	15	US-10-149-135-2176	Sequence 2176, Ap
25	55	100.0	10	15	US-10-149-135-2177	Sequence 2177, Ap
26	55	100.0	10	15	US-10-149-135-2178	Sequence 2178, Ap
27	55	100.0	10	15	US-10-149-135-2179	Sequence 2179, Ap
28	55	100.0	10	15	US-10-149-135-2180	Sequence 2180, Ap
29	55	100.0	10	15	US-10-149-135-2181	Sequence 2181, Ap
30	55	100.0	10	15	US-10-149-135-2290	Sequence 2290, Ap
31	55	100.0	10	15	US-10-149-135-2291	Sequence 2291, Ap
32	55	100.0	10	15	US-10-149-135-2292	Sequence 2292, Ap
33	55	100.0	10	15	US-10-149-135-2293	Sequence 2293, Ap
34	55	100.0	10	15	US-10-149-135-2294	Sequence 2294, Ap
35	55	100.0	10	15	US-10-619-454-1	Sequence 1, Appl1
36	55	100.0	10	16	US-10-149-138-4189	Sequence 4189, Ap
37	55	100.0	10	16	US-10-149-138-4190	Sequence 4190, Ap
38	55	100.0	10	16	US-10-149-138-4191	Sequence 4191, Ap
39	55	100.0	10	16	US-10-149-138-4192	Sequence 4192, Ap
40	55	100.0	10	16	US-10-149-138-4193	Sequence 4193, Ap
41	55	100.0	10	16	US-10-149-138-4194	Sequence 4194, Ap
42	55	100.0	10	16	US-10-149-138-4350	Sequence 4350, Ap
43	55	100.0	10	16	US-10-149-138-4351	Sequence 4351, Ap
44	55	100.0	10	16	US-10-149-138-4352	Sequence 4352, Ap
45	55	100.0	10	16	US-10-149-138-4353	Sequence 4353, Ap

ALIGNMENTS

RESULT 1
US-08-344-824-11
; Sequence 11, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:

```
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-344-824-11

Query Match 100.0%; Score 55; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYPPSV 10
Db 1 FLPSDYPPSV 10

RESULT 2
US-09-898-860-126
; Sequence 126, Application US/09898860
; Publication No. US20030144482A1
; GENERAL INFORMATION:
; APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
; STEVEN A.
; TITLE OF INVENTION: MELANOMA ANTIGENS AND
; THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
; METHODS
; NUMBER OF SEQUENCES: 126
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/898,860
; FILING DATE: 03-Jul-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/267,439
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/417,174
; FILING DATE: 05-APR-1995
; APPLICATION NUMBER: US/08/231,565
; FILING DATE: 22-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: CAROL M. GRUPPI
; REGISTRATION NUMBER: 37,341
; REFERENCE/DOCKET NUMBER: 2026-4124US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 126:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 126:
US-09-898-860-126

Query Match 100.0%; Score 55; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYPPSV 10
Db 1 FLPSDYPPSV 10

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYPPSV 10
Db 1 FLPSDYPPSV 10

RESULT 3
US-09-935-476-4
; Sequence 4, Application US/09935476
; Publication No. US20040096445A1
; GENERAL INFORMATION:
; APPLICANT: EpImmune, Inc.
; APPLICANT: Sidney, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Grey, Howard
; APPLICANT: Southwood, Scott
; TITLE OF INVENTION: SUBUNIT VACCINES WITH A2 SUPERMOTIFS
; FILE REFERENCE: 39963-20029.20
; CURRENT APPLICATION NUMBER: US/09/935,476
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 09/346,105
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: US 60/264,969
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Analog of the HBV core 18027 epitope
US-09-935-476-4

Query Match 100.0%; Score 55; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYPPSV 10
Db 1 FLPSDYPPSV 10

RESULT 4
US-10-094-699-108
; Sequence 108, Application US/10094699
; Publication No. US20030046714A1
; GENERAL INFORMATION:
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: CTIMM.015A
; CURRENT APPLICATION NUMBER: US/10/094,699
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/274,063
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-094-699-108

Query Match 100.0%; Score 55; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYPPSV 10
Db 1 FLPSDYPPSV 10
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```

; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: Immune Response and Methods of Using the Same.
; CURRENT APPLICATION NUMBER: US/10/371,525
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/311,784
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 226
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBC 18-27 analog (peptide 941.01)
US-10-371-525-226

Query Match      100.0%; Score 55; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FLPSDYFPSV 10
Db      1 FLPSDYFPSV 10

RESULT 7
US-10-026-066-86
; Sequence 86, Application US/10026066
; Publication No. US20030215425A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN
; FILE REFERENCE: CTLIMM.21C1P1C
; CURRENT APPLICATION NUMBER: US/10/026,066
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 09/561,074
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/560,465
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,572
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 09/561,571
; PRIOR APPLICATION NUMBER: PCT/US01/13806
; PRIOR FILING DATE: 2001-04-27
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-026-066-86

Query Match      100.0%; Score 55; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FLPSDYFPSV 10
Db      1 FLPSDYFPSV 10

RESULT 8
US-10-371-069-226
; Sequence 226, Application US/10371069
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; APPLICANT: Chisari, Francis V.
; TITLE OF INVENTION: Peptides for Inducing Cytotoxic T
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/359,431
; FILING DATE: 05-Feb-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,540
; FILING DATE: 26-AUG-1991
; APPLICATION NUMBER: US 07/935,898
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 08/100,870
; FILING DATE: 02-AUG-1993
; APPLICATION NUMBER: WO PCT/US94/08685
; FILING DATE: 01-AUG-1994
; APPLICATION NUMBER: US 08/591,502
; FILING DATE: 20-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Lockyer, Jean M.
; REGISTRATION NUMBER: 44,879
; REFERENCE/DOCKET NUMBER: 014740-000231US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-10-359-431-225

Query Match      100.0%; Score 55; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FLPSDYFPSV 10
Db      1 FLPSDYFPSV 10

RESULT 6
US-10-371-525-226
; Sequence 226, Application US/10371525
; Publication No. US20030203869A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
```

```

; Publication No. US20030216342A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 226
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBC 18-27 analog (peptide 941.01)
US-10-371-069-226

Query Match          100.0%; Score 55; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FLPSDYPPSV 10
Db      1 FLPSDYPPSV 10

RESULT 9
US-10-371-645-226
; Sequence 226, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 226
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBC 18-27 analog (peptide 941.01)
US-10-371-645-226

Query Match          100.0%; Score 55; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FLPSDYPPSV 10
Db      1 FLPSDYPPSV 10

US-10-117-937-24
; Sequence 24, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-24

Query Match          100.0%; Score 55; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FLPSDYPPSV 10
Db      1 FLPSDYPPSV 10

RESULT 11
US-10-371-260-226
; Sequence 226, Application US/10371260
; Publication No. US20030220285A1
; GENERAL INFORMATION:
; APPLICANT: EPIMMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.13
; CURRENT APPLICATION NUMBER: US/10/371,260
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 226
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBC 18-27 analog (peptide 941.01)
US-10-371-260-226

Query Match          100.0%; Score 55; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FLPSDYPPSV 10
Db      1 FLPSDYPPSV 10
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US-10-371-260-226

Query Match 100.0%; Score 55; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLPSDYPPSV 10
Db 1 FLPSDYPPSV 10
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RESULT 12

US-10-448-521-45
; Sequence 45, Application US/10448521
; Publication No. US20040018205A1
; GENERAL INFORMATION:
; APPLICANT: FIRAT, HUSEYIN
; APPLICANT: LANGLADE-DEMOYAN, PIERRE
; APPLICANT: VILMER, ETIENNE
; APPLICANT: LEMONNIER, FRANCOIS
; APPLICANT: ROHRLEICH, PIERRE
; APPLICANT: YOTNDA, PATRICIA
; TITLE OF INVENTION: MUTATED IMMUNOGENIC PEPTIDES DERIVED FROM B9M,
; TITLE OF INVENTION: POLYNUCLEOTIDES CODING FOR SAME AND THERAPEUTIC USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 02356.0082
; CURRENT APPLICATION NUMBER: US/10/448,521
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: PCT/FR01/03779
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: CA 2,325,666
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 10
; TYPE: PRT
; ORGANISM: human herpesvirus
US-10-448-521-45

Query Match 100.0%; Score 55; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLPSDYPPSV 10
Db 1 FLPSDYPPSV 10
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RESULT 13

US-10-149-138-4189
; Sequence 4189, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4189

; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4189

Query Match 100.0%; Score 55; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLPSDYPPSV 10
Db 1 FLPSDYPPSV 10
|||||

RESULT 14

US-10-149-138-4190
; Sequence 4190, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4190
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4190

Query Match 100.0%; Score 55; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FLPSDYPPSV 10
Db 1 FLPSDYPPSV 10
|||||

RESULT 15

US-10-149-138-4191
; Sequence 4191, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10/149,138
; CURRENT FILING DATE: 2002-06-10

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; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4191
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4191

Query Match      100.0%; Score 55; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FLPSDYPPSV 10
        |||||
Db      1 FLPSDYPPSV 10

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Job time : 60.8352 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:37:59 ; Search time 18.7363 Seconds
(without alignments)
39.842 Million cell updates/sec

Title: US-08-170-344-77
Perfect score: 55
Sequence: 1 FLPSDYPPSV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	10	1	US-08-195-075-12
2	55	100.0	10	1	US-08-363-691-9
3	55	100.0	10	2	US-08-417-174-126
4	55	100.0	10	3	US-08-159-339A-647
5	55	100.0	10	3	US-09-267-439-126
6	55	100.0	10	3	US-08-992-877-1
7	55	100.0	10	4	US-09-311-784A-226
8	55	100.0	10	4	US-09-073-138-126
9	55	100.0	10	4	US-09-497-232-4
10	55	100.0	10	4	US-09-543-608A-43
11	55	100.0	10	4	US-08-591-502B-25
12	55	100.0	10	4	US-08-234-784B-97
13	55	100.0	10	4	US-09-239-043D-2307
14	55	100.0	10	4	US-09-239-043D-2307
15	55	100.0	10	5	PCT-US95-01672-12
16	51	92.7	10	1	US-08-787-547-90
17	51	92.7	10	1	US-08-464-235-23
18	51	92.7	10	2	US-08-468-279-5
19	51	92.7	10	3	US-08-159-339A-644
20	51	92.7	10	3	US-08-463-486-23
21	51	92.7	10	3	US-08-464-496-23
22	51	92.7	10	3	US-08-992-877-39
23	51	92.7	10	4	US-08-197-484-4
24	51	92.7	10	4	US-08-913-612A-51
25	51	92.7	10	4	US-09-311-784A-91
26	51	92.7	10	4	US-08-591-502B-69
27	51	92.7	10	4	US-09-239-043D-2521

28	51	92.7	10	4	US-10-266-463A-51	Sequence 51, Appl
29	51	92.7	10	5	PCT-US92-07218-23	Sequence 23, Appl
30	51	92.7	10	5	PCT-US94-02195-23	Sequence 23, Appl
31	51	92.7	10	5	PCT-US95-02121-4	Sequence 4, Appli
32	51	92.7	11	4	US-09-239-043D-2302	Sequence 2302, Ap
33	51	92.7	11	4	US-09-239-043D-2303	Sequence 2303, Ap
34	51	92.7	11	4	US-09-239-043D-2433	Sequence 2433, Ap
35	51	92.7	12	4	US-09-239-043D-2304	Sequence 2304, Ap
36	51	92.7	12	4	US-09-239-043D-2408	Sequence 2408, Ap
37	51	92.7	12	4	US-09-239-043D-2485	Sequence 2485, Ap
38	51	92.7	13	3	US-08-464-496-24	Sequence 24, Appl
39	51	92.7	13	3	US-08-197-484-109	Sequence 109, App
40	51	92.7	13	5	PCT-US92-07218-24	Sequence 24, Appl
41	51	92.7	13	5	PCT-US95-02121-109	Sequence 109, App
42	51	92.7	17	2	US-08-468-279-2	Sequence 2, Appli
43	51	92.7	17	4	US-08-591-502B-67	Sequence 67, Appl
44	51	92.7	17	4	US-08-591-502B-75	Sequence 75, Appl
45	51	92.7	23	3	US-08-464-496-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-08-195-075-12
; Sequence 12, Application US/08195075
; Patent No. 5550214
; GENERAL INFORMATION:
; APPLICANT: Eberlein M.D., Timothy J.
; APPLICANT: Peoples M.D., George E.
; APPLICANT: Yoshino M.D., Ichiro
; APPLICANT: Goedegebuure Ph.D., Peter
; TITLE OF INVENTION: Isolated Antigenic Oncogene Peptide
; TITLE OF INVENTION: Fragments and Uses
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Choate, Hall & Stewart
; STREET: 53 State Street, Exchange Place
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,075
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan Esq., Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: 092662-003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-227-5020
; TELEFAX: 617-227-7566
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-195-075-12
Query Match 100.0%; Score 55; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FLPSDYPPSV 10
Db 1 FLPSDYPPSV 10

```

RESULT 2
US-08-363-691-9
; Sequence 9, Application US/08363691
; Patent No. 5770201
; GENERAL INFORMATION:
; APPLICANT: Goulmy, Els A.J.M.
; APPLICANT: Hunt, Donald H.
; APPLICANT: Engelhard, Victor H.
; TITLE OF INVENTION: HA-2 Antigenic Peptide
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ronald J. Baron, Esq.
; ADDRESSEE: Hoffmann & Baron
; STREET: 350 Jericho Turnpike
; CITY: Jericho
; STATE: New York
; COUNTRY: USA
; ZIP: 11753
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,691
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA: No. 5770201e
; ATTORNEY/AGENT INFORMATION:
; NAME: Baron, Ronald J.
; REGISTRATION NUMBER: 29,281
; REFERENCE/DOCKET NUMBER: 294-30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 822-3550
; TELEFAX: (516) 822-3582
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-363-691-9
Query Match 100.0%; Score 55; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYFPPSV 10
Db 1 FLPSDYFPPSV 10

RESULT 3
US-08-417-174-126
; Sequence 126, Application US/08417174
; Patent No. 594075
; GENERAL INFORMATION:
; APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
; APPLICANT: STEVEN A.
; TITLE OF INVENTION: MELANOMA ANTIGENS AND
; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
; METHODS
; NUMBER OF SEQUENCES: 126
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:

```

```

; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/417,174
; FILING DATE: 05-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/231,565
; FILING DATE: 22-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CAROL M. GRUPPI
; REGISTRATION NUMBER: 37,341
; REFERENCE/DOCKET NUMBER: 2026-4124U51
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 126:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
;
US-08-417-174-126
Query Match 100.0%; Score 55; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYFPPSV 10
Db 1 FLPSDYFPPSV 10

RESULT 4
US-08-159-339A-647
; Sequence 647, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:

```

NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 647:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-647

Query Match 100.0%; Score 55; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYPPSV 10
| | | | | | | | | |
Db 1 FLPSDYPPSV 10

RESULT 5
US-09-267-439-126
Sequence 126, Application US/09267439
Patent No. 6270778
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/267,439
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: amino acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-09-267-439-126

Query Match 100.0%; Score 55; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYPPSV 10
| | | | | | | | | |
Db 1 FLPSDYPPSV 10

RESULT 6
US-08-992-877-1
Sequence 1, Application US/08992877
Patent No. 6340461
GENERAL INFORMATION:
APPLICANT: Terman, David S
TITLE OF INVENTION: SUPERANTIGEN BASED METHODS AND COMPOSITIONS FOR
TREATMENT OF INFECTIOUS DISEASE
TITLE OF INVENTION: superantigen
FILE REFERENCE: US/08/992,877
CURRENT APPLICATION NUMBER: 1997-12-17
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/044,074
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 1
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: antigen
OTHER INFORMATION: sequences
US-08-992-877-1

Query Match 100.0%; Score 55; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYPPSV 10
| | | | | | | | | |
Db 1 FLPSDYPPSV 10

RESULT 7
US-09-311-784A-226
Sequence 226, Application US/09311784A
Patent No. 6534482
GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Hermanson, Gary G.
APPLICANT: Sette, Alessandro
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert W.
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Expression Vectors for Stimulating an
Immune Response and Methods of Using the Same
FILE REFERENCE: 39963-20022.01
CURRENT APPLICATION NUMBER: US/09/311,784A
CURRENT FILING DATE: 1999-05-13
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: US 60/085,751
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 226
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HBC 18-27 analog (peptide 941.01)
US-09-311-784A-226

Query Match 100.0%; Score 55; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00099;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYPPSV 10
 |||||
 Db 1 FLPSDYPPSV 10

RESULT 8

US-09-073-138-126
 ; Sequence 126, Application US/09073138
 ; Patent No. 6537560
 ; GENERAL INFORMATION:
 ; APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
 ; APPLICANT: STEVEN A.
 ; TITLE OF INVENTION: MELANOMA ANTIGENS AND
 ; TITLE OF INVENTION: THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
 ; TITLE OF INVENTION: METHODS
 ; NUMBER OF SEQUENCES: 126
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
 ; STREET: 345 PARK AVENUE
 ; CITY: NEW YORK
 ; STATE: NEW YORK
 ; COUNTRY: USA
 ; ZIP: 10154
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY DISK
 ; COMPUTER: IBM PC COMPATIBLE
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: ASCII
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/073,138
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/417,174
 ; FILING DATE: 05-APR-1995
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: CAROL M. GRUPPI
 ; REGISTRATION NUMBER: 37,341
 ; REFERENCE/DOCKET NUMBER: 2026-4124US1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 758-4800
 ; TELEFAX: (212) 751-6849
 ; TELEX: 421792
 ; INFORMATION FOR SEQ ID NO: 126:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10
 ; TYPE: amino acid
 ; STRANDEDNESS: Unknown
 ; TOPOLOGY: Unknown
 ; MOLECULE TYPE: Peptide
 ; US-09-073-138-126

Query Match 100.0%; Score 55; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00099;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYPPSV 10
 |||||
 Db 1 FLPSDYPPSV 10

RESULT 9

US-09-497-232-4
 ; Sequence 4, Application US/09497232
 ; Patent No. 660012
 ; GENERAL INFORMATION:
 ; APPLICANT: AGRAWAL, Babita
 ; KRANTZ, Mark J.
 ; REDDISH, Mark J.
 ; LONGENECKER, B. Michael
 ; TITLE OF INVENTION: METHOD FOR GENERATING ACTIVATED T-CELLS

; AND ANTIGEN-PULSED ANTIGEN-PRESENTING CELLS
 ;
 ; NUMBER OF SEQUENCES: 34
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FOLEY & LARDNER
 ; STREET: 3000 K Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/497,232
 ; FILING DATE: 03-Feb-2000
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/074,410
 ; FILING DATE: 08-MAY-1998
 ; APPLICATION NUMBER: US 60/045,949
 ; FILING DATE: 08-MAY-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Saxe, Bernhard D.
 ; REGISTRATION NUMBER: 28,665
 ; REFERENCE/DOCKET NUMBER: 042881/0114
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 672-5300
 ; TELEFAX: (202) 672-5399
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: <Unknown>
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 ; US-09-497-232-4

Query Match 100.0%; Score 55; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00099;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYPPSV 10
 |||||
 Db 1 FLPSDYPPSV 10

RESULT 10

US-09-543-608A-43
 ; Sequence 43, Application US/09543608A
 ; Patent No. 6602510
 ; GENERAL INFORMATION:
 ; APPLICANT: Fikes, John D.
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Sidney, John
 ; APPLICANT: Southwood, Scott
 ; APPLICANT: Celis, Esteban
 ; APPLICANT: Keogh, Elissa A.
 ; APPLICANT: Chesnut, Robert
 ; APPLICANT: Epimmune Inc.
 ; TITLE OF INVENTION: HLA Class I A2 Tumor Associated Antigen
 ; TITLE OF INVENTION: Peptides and Vaccine Compositions
 ; FILE REFERENCE: 018623-015710US
 ; CURRENT APPLICATION NUMBER: US/09/543,608A
 ; CURRENT FILING DATE: 2002-04-05
 ; NUMBER OF SEQ ID NOS: 52
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 43
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Standard Peptide 941.01
US-09-543-608A-43

Query Match      100.0%; Score 55; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FLPSDYPPSV 10
Db      1 FLPSDYPPSV 10

RESULT 11
US-08-591-502B-25
; Sequence 25, Application US/08591502B
; Patent No. 6607727
; GENERAL INFORMATION:
; APPLICANT: Chisari, Francis V.
; TITLE OF INVENTION: Peptides for Inducing Cytotoxic T
; Lymphocyte Responses to Hepatitis B Virus
; NUMBER OF SEQUENCES: 99
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/591.502B
; FILING DATE: 20-May-1996
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,540
; FILING DATE: 26-AUG-1991
; APPLICATION NUMBER: US 07/935,898
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 08/100,870
; FILING DATE: 02-AUG-1993
; APPLICATION NUMBER: WO PCT/US94/08685
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 014740-000230US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:

US-08-591-502B-25

Query Match      100.0%; Score 55; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FLPSDYPPSV 10
Db      1 FLPSDYPPSV 10

RESULT 12
US-08-234-784B-97
; Sequence 97, Application US/08234784B
; Patent No. 6660276
; GENERAL INFORMATION:
; APPLICANT: Slingluff, Craig L, Jr.
; APPLICANT: Engelhard, Victor H.
; APPLICANT: Hunt, Donald F.
; APPLICANT: Shabanowitz, Jeffrey
; APPLICANT: Cox, Andrea L.
; TITLE OF INVENTION: PEPTIDES RECOGNIZED BY MELANOMA-SPECIFIC
; CYTOTOXIC LYMPHOCYTES, AND USES
; NUMBER OF SEQUENCES: 97
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch
; COMPUTER: IBM compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/234,784B
; FILING DATE: 29-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/197,399
; FILING DATE: 16-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: SLINGLUFF=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 97:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-234-784B-97

Query Match      100.0%; Score 55; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 FLPSDYPPSV 10
Db      1 FLPSDYPPSV 10

RESULT 13
US-09-239-043D-2307
; Sequence 2307, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Basteen
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
```

```
; TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2307
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV analog peptide
; US-09-239-043D-2307

Query Match          100.0%; Score 55; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYFPPSV 10
   |||||
Db 1 FLPSDYFPPSV 10

RESULT 14
US-09-239-043D-2487
; Sequence 2487, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esceban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard W.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
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; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2487
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Standard peptide that binds to HLA A*0201, HLA
; US-09-239-043D-2487

Query Match          100.0%; Score 55; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYFPPSV 10
   |||||
Db 1 FLPSDYFPPSV 10

RESULT 15
PCT-US95-01672-12
; Sequence 12, Application PC/TUS9501672
; GENERAL INFORMATION:
; APPLICANT: Eberlein M.D., Timothy J.
; APPLICANT: Peoples M.D., George E.
; APPLICANT: Yoshino M.D., Ichiro
; APPLICANT: Goedegebuure Ph.D., Peter
; TITLE OF INVENTION: Isolated Antigenic Oncogene Peptide
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Choate, Hall & Stewart
; STREET: 53 State Street, Exchange Place
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/01672
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kaplan Esq., Warren A.
; REGISTRATION NUMBER: 34,199
; REFERENCE/DOCKET NUMBER: 092662-003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617:227-5020
; TELEFAX: 617:227-7566
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US95-01672-12
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Query Match 100.0%; Score 55; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00099;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FLPSDYPPSV 10
| | | | | | | |
Db 1 FLPSDYPPSV 10

Search completed: June 29, 2005, 01:44:31
Job time : 19.7863 secs

This Page Blank (uspto)

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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:32:21 ; Search time 11.2747 Seconds
(without alignments)
76.805 Million cell updates/sec

Title: US-08-170-344-76

Perfect score: 47

Sequence: 1 YLEPAIAKY 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79.*

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	80.9	326	JQ0855	hypothetical 36.8K
2	38	80.9	345	2	probable capsid po
3	38	80.9	348	2	probable capsid po
4	37	78.7	352	2	H ₂ -transporting AT
5	37	78.7	377	2	hypothetical prote
6	35	74.5	1502	2	hypothetical prote
7	34	72.3	108	2	tributyltin chlori
8	34	72.3	132	2	O-antigen transpor
9	34	72.3	564	2	hypothetical prote
10	34	72.3	1169	2	hypothetical prote
11	33	70.2	286	2	hypothetical prote
12	33	70.2	339	2	hypothetical prote
13	33	70.2	484	2	2-nitropropane dio
14	33	70.2	484	2	amidase (EC 3.5.-
15	33	70.2	548	2	t-complex-type mol
16	33	70.2	1168	2	hypothetical prote
17	32	68.1	2054	2	hypothetical prote
18	32	68.1	156	2	hypothetical prote
19	32	68.1	204	2	hypothetical prote
20	32	68.1	310	2	probable proline d
21	32	68.1	440	2	hypothetical prote
22	32	68.1	584	2	probable membrane
23	32	68.1	679	2	hypothetical prote
24	32	68.1	872	2	endopeptidase Clp
25	31	66.0	1286	1	hypothetical prote
26	31	66.0	126	2	hypothetical prote
27	31	66.0	175	2	hypothetical prote
28	31	66.0	178	2	pantothenate metab
29	31	66.0	213	2	hypothetical prote
30	31	66.0	230	2	transcription acti

30	31	66.0	230	2	B97951	hypothetical prote
31	31	66.0	243	2	S16723	coenzyme F420 hydr
32	31	66.0	244	1	GSBPP4	head size determin
33	31	66.0	244	2	F42465	head size determin
34	31	66.0	265	2	S73587	M3068 homolog D02_
35	31	66.0	277	2	AF1312	ketopantoate hydro
36	31	66.0	309	2	AC0489	probable membrane
37	31	66.0	318	1	KIRHUR1	ribose-phosphate d
38	31	66.0	318	1	KIRTR1	ribose-phosphate d
39	31	66.0	320	2	S46824	ribose-phosphate d
40	31	66.0	321	2	S60393	ribose-phosphate d
41	31	66.0	323	2	T04826	hypothetical prote
42	31	66.0	334	2	T20728	hypothetical prote
43	31	66.0	347	2	B95949	probable fructose-
44	31	66.0	350	2	AB2226	hypothetical prote
45	31	66.0	368	2	TL3815	NADH2 dehydrogenas

ALIGNMENTS

RESULT 1

JQ0855
hypothetical 36.8K protein - Escherichia coli retron Ec67
N;Alternate names: gpQ protein homolog
C;Species: Escherichia coli retron Ec67
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: JQ0855
R;Hsu, M.Y.; Inouye, M.; Inouye, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 9454-9458, 1990
A;Title: Retron for the 67-base multicopy single-stranded DNA from Escherichia coli: a
A;Reference number: JQ0851; MUID:91067724; PMID:1701261
A;Accession: JQ0855
A;Molecule type: DNA
A;Residues: 1-326 <HSU>
A;Cross-references: UNIPROT:P21314; GB:M55249; NID:gl45143; PIDN:AAA23404.1; PID:gl45151
A;Experimental source: E. coli strain Cl-1
C;Genetics:
A;Note: insertion site is equivalent to 19 min of E. coli K12 genetic map

Query Match 80.9%; Score 38; DB 2; Length 326;
Best Local Similarity 87.5%; Pred. No. 3.4;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LEPAIAKY 9
|||:||||
Db 126 LEPAIAKY 133

RESULT 2

AI0926
probable capsid portal protein [imported] - Salmonella enterica subsp. enterica serovar typhi
C;Species: Salmonella enterica subsp. enterica serovar typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AI0926
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar typhi
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AI0926
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-345 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD09435.1; PID:gl6504552; GSPDB:GN00176
C;Genetics:
A;Gene: STY3674

Query Match 80.9%; Score 38; DB 2; Length 345;
Best Local Similarity 87.5%; Pred. No. 3.6;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LEPAIAKY 9
 ||||:||||
 Db 126 LEPAIAKY 133

RESULT 3
 A11037
 probable capsid portal protein [imported] - Salmonella enterica subsp. enterica serovar
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A:Note: this species has also been called Salmonella typhi
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C:Accession: A11037
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Conington, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
 A:Reference number: AB0502; MUID:21534947; PMID:11677608
 A:Accession: A11037
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-348 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD06750.1; PID:g16505401; GSPDB:GN00176
 C:Genetics:
 A:Gene: STV4628

Query Match 80.9%; Score 38; DB 2; Length 348;
 Best Local Similarity 87.5%; Pred. No. 3.7; Mismatches 1; Indels 0; Gaps 0;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LEPAIAKY 9
 ||||:||||
 Db 129 LEPAIAKY 136

RESULT 4
 C84364
 H+-transporting ATP synthase subunit C [imported] - Halobacterium sp. NRC-1
 C:Species: Halobacterium sp. NRC-1
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: C84364
 R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
 ; Leithausen, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabc
 Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
 A:Title: Genome sequence of Halobacterium species NRC-1.
 A:Reference number: A84160; MUID:20504483; PMID:11016950
 A:Accession: C84364
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-352 <STO>
 A:Cross-references: UNIPROT:Q9HNE1; GB:A8004437; NID:g10581556; PIDN:AAG20279.1; GSPDB:G
 C:Genetics:
 A:Gene: atpC
 C:Superfamily: H+ transporting ATP synthase C subunit

Query Match 78.7%; Score 37; DB 2; Length 352;
 Best Local Similarity 77.8%; Pred. No. 6.1; Mismatches 0; Indels 2; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

Qy 1 YLEPAIAKY 9
 ||||:||||
 Db 160 YLEPAIADY 168

RESULT 5
 T16763
 hypothetical protein R151.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: T16763
 R;Fulton, L.
 submitted to the EMBL Data Library, February 1994
 A:Description: The sequence of C. elegans cosmid R151.
 A:Reference number: S44639
 A:Accession: T16763
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-377 <FUL>
 A:Cross-references: UNIPROT:Q21994; EMBL:U00036; NID:g458996; PID:g459000; PIDN:AAA5065.
 A:Experimental source: strain Bristol N2
 C:Genetics:
 A:Gene: CESP:R151.2
 A:Introns: 11/1; 63/3; 235/2; 293/2; 346/3
 C:Superfamily: ribose-phosphate pyrophosphokinase catalytic chain

Query Match 78.7%; Score 37; DB 2; Length 377;
 Best Local Similarity 77.8%; Pred. No. 6.6; Mismatches 2; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YLEPAIAKY 9
 ||||:||||
 Db 204 YLEPAIAKY 212

RESULT 6
 T41008
 hypothetical protein SPC1494.07 - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T41008
 R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.
 submitted to the EMBL Data Library, June 1998
 A:Reference number: Z21963
 A:Accession: T41008
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1502 <WOO>
 A:Cross-references: UNIPROT:O60081; EMBL:AL023776; PIDN:CAA19305.1; GSPDB:GN00067; SPDB:
 A:Experimental source: strain 972h-; cosmid c1494
 C:Genetics:
 A:Gene: SPDB:SPCC1494.07
 A:Map position: 2

Query Match 74.5%; Score 35; DB 2; Length 1502;
 Best Local Similarity 100.0%; Pred. No. 83; Mismatches 0; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YLEPAIA 7
 ||||:||||
 Db 850 YLEPAIA 856

RESULT 7
 JN0895
 tributyltin chloride resistant protein - Alteromonas sp. (strain M-1)
 C:Species: Alteromonas sp.
 C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 17-Mar-1999
 C:Accession: JN0895
 R;Fukagawa, T.; Suzuki, S.
 Biochem. Biophys. Res. Commun. 194, 733-740, 1993
 A:Title: Cloning of gene responsible for tributyltin chloride (TBTCl) resistance in TBT
 A:Reference number: JN0895; MUID:93343930; PMID:8343157
 A:Accession: JN0895
 A:Molecule type: DNA
 A:Residues: 1-108 <FUK>
 A:Keywords: membrane protein
 C:KeyWords: Region: hydrophilic

Query Match 72.3%; Score 34; DB 2; Length 108;
 Best Local Similarity 87.5%; Pred. No. 7.2; Mismatches 1; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      2 LEPAIAKY 9
      |||||
Db      68 LTPAIAKY 75

RESULT 8
B69063
O-antigen transporter homolog - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: B69063
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: B69063
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-132 <MTH>
A:Cross-references: UNIPROT:O27516; GB:AE000598; GB:AE000666; NID:g2622579; PIDN:AAB8594
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH1472

      Query Match      72.3%; Score 34; DB 2; Length 132;
      Best Local Similarity 87.5%; Pred. No. 9;
      Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 LEPAIAKY 9
      |||||
Db      64 LPPAIAKY 71

RESULT 9
T18776
hypothetical protein B0513.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18776
R:Matthews, L.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19020
A:Accession: T18776
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-564 <WIL>
A:Cross-references: UNIPROT:O45228; EMBL:Z82256; PIDN:CAB05117.1; GSPDB:GN00022; CESP:BO
A:Experimental source: clone B0513
C:Genetics:
A:Gene: CESP:B0513.5
A:Map position: 4
A:Introns: 125/3; 160/2; 245/3; 359/2; 427/3; 494/3

      Query Match      72.3%; Score 34; DB 2; Length 564;
      Best Local Similarity 75.0%; Pred. No. 45;
      Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YLEPAIAK 8
      |||||
Db      344 YLQPAISK 351

RESULT 10
C84547
hypothetical protein At2g17030 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: C84547
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
```

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euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: C84547
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1169 <STO>
A:Cross-references: UNIPROT:Q7XJL8; GB:AE002093; NID:g5598360; PIDN:AAF18598.1; GSPDB:G
C:Genetics:
A:Gene: At2g17030
A:Map position: 2

      Query Match      72.3%; Score 34; DB 2; Length 1169;
      Best Local Similarity 66.7%; Pred. No. 1e+02;
      Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 YLEPAIAKY 9
      |||||
Db      157 YLEKAVVKY 165

RESULT 11
F89796
hypothetical protein SA0305 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: F89796
R:Kuroda, M.; Ohka, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu
ma, A.; Mizutani-Uii, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: F89796
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-286 <KUR>
A:Cross-references: UNIPROT:Q99WRO; GB:BA000018; PID:g13700231; PIDN:BA041529.1; GSPDB:
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA0305

      Query Match      70.2%; Score 33; DB 2; Length 286;
      Best Local Similarity 55.6%; Pred. No. 35;
      Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 YLEPAIAKY 9
      |||||
Db      252 YIEPKVAHY 260

RESULT 12
AC3567
2-nitropropane dioxygenase (EC 1.13.11.32) [imported] - Brucella melitensis (strain 16t
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AC3567
R:DeiVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,
; Mazur, M.; Goitsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella meliten
A:Reference number: AD3252; PMID:11756688
A:Accession: AC3567
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-339 <KUR>
A:Cross-references: UNIPROT:Q8YCR8; GB:AE008918; PIDN:AAL53702.1; PID:g17984624; GSPDB:
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEII0460
A:Map position: 11
C:Keywords: oxidoreductase
```

Query Match 70.2%; Score 33; DB 2; Length 339;
 Best Local Similarity 75.0%; Pred. No. 42;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YLEPAIAK 8
 ||:||||
 Db 262 YLKPSIAK 269

RESULT 13

T00158
 amidase (EC 3.5.-.-) - Staphylococcus aureus phase phi PVL
 N;Alternate names: peptidoglycan hydrolase
 C;Species: Staphylococcus aureus phase phi PVL
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C;Accession: T00158
 R;Kaneko, J.; Kimura, T.; Kawakami, Y.; Tomita, T.; Kamio, Y.
 Biosci. Biotechnol. Biochem. 61, 1960-1962, 1997
 A;Title: Pantan-Valentine leukocidin genes in a phage-like particle isolated from mitomy
 A;Reference number: Z14119; MUID:98067870; PMID:9404084
 A;Accession: T00158
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-484 <KAN>
 A;Cross-references: UNIPROT:O80064; EMBL:AB009866; NID:d1204727; PIDN:BAA31898.1; PID:dl
 C;Keywords: hydrolase

Query Match 70.2%; Score 33; DB 2; Length 484;
 Best Local Similarity 66.7%; Pred. No. 63;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YLEPAIAKY 9
 |:||||
 Db 208 YITENIAKY 216

RESULT 14

T43895
 t-complex-type molecular chaperone Tcp1 homolog [imported] - slime mold (Dictyostelium d
 C;Species: Dictyostelium discoideum
 C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
 C;Accession: T43895
 R;Iijima, M.; Shimizu, H.; Tanaka, Y.; Urushihara, H.
 Gene 213, 101-106, 1998
 A;Title: A Dictyostelium discoideum homologue to Tcp-1 is essential for growth and devel
 A;Reference number: Z22716; MUID:98296258; PMID:9630545
 A;Accession: T43895
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-548 <IIJ>
 A;Cross-references: UNIPROT:O76126; EMBL:AB008158; NID:g3395663; PIDN:BAA32082.1; PID:g3
 C;Genetics:
 A;Gene: Tcp-1
 C;Superfamily: molecular chaperone t-complex-type

Query Match 70.2%; Score 33; DB 2; Length 548;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LEPAIAK 8
 ||||||
 Db 504 LEPAIAK 510

RESULT 15

S76195
 hypothetical protein sll1527 - Synechocystis sp. (strain PCC 6803)
 C;Species: Synechocystis sp.
 A;Variety: PCC 6803
 C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C;Accession: S76195
 R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O. K.; Okumura, S.; Shimpou, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud
 DNA Res. 3, 109-136, 1996
 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
 s.
 A;Reference number: S74322; MUID:97061201; PMID:8905231
 A;Accession: S76195
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1168 <KAN>
 A;Cross-references: UNIPROT:P74359; EMBL:D90914; GB:AB001339; NID:g1653477; PIDN:BAA184
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C;Superfamily: Synechocystis hypothetical protein sll1527

Query Match 70.2%; Score 33; DB 2; Length 1168;
 Best Local Similarity 55.6%; Pred. No. 1.7e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YLEPAIAKY 9
 ||:||||
 Db 343 YLXPGLAKF 351

Search completed: June 29, 2005, 01:38:53
 Job time : 12.2747 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:28:22 ; Search time 54.2473 Seconds
(without alignments)
84.958 Million cell updates/sec

Title: US-08-170-344-76
Perfect score: 47
Sequence: 1 YLEPATAKY 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	80.9	207	2 Q8LN52	Q8LN52 oryza sativ
2	38	80.9	326	1 YR75_ECOLI	P21314 escherichia
3	38	80.9	337	2 Q62MU7	Q62MU7 burkholderi
4	38	80.9	345	2 Q8Z359	Q8Z359 salmonella
5	38	80.9	345	2 Q8FJ15	Q8FJ15 escherichia
6	38	80.9	348	2 Q8Z186	Q8Z186 salmonella
7	38	80.9	351	2 Q62GG0	Q62GG0 burkholderi
8	38	80.9	351	2 Q63L88	Q63L88 burkholderi
9	38	80.9	351	2 Q63Y14	Q63Y14 burkholderi
10	38	80.9	370	2 Q63Y58	Q63Y58 burkholderi
11	38	80.9	468	2 Q8W5J7	Q8W5J7 oryza sativ
12	38	80.9	468	2 Q7XD63	Q7XD63 oryza sativ
13	38	80.9	505	2 Q75G62	Q75G62 oryza sativ
14	38	80.9	534	2 Q87KR7	Q87KR7 vibrio para
15	37	78.7	261	2 Q6VY34	Q6VY34 turkey astr
16	37	78.7	318	2 Q95Q86	Q95Q86 caenorhabdi
17	37	78.7	319	2 Q9BI73	Q9BI73 caenorhabdi
18	37	78.7	352	1 VATC_HALN1	Q9HNE1 halobacteri
19	37	78.7	377	2 Q21994	Q21994 caenorhabdi
20	37	78.7	446	2 Q6AHR3	Q6AHR3 caenorhabdi
21	37	78.7	724	2 Q9Q3G5	Q9Q3G5 turkey astr
22	36	76.6	175	1 C16A_LOCM1	P83952 locusta mig
23	36	76.6	175	1 C16B_LOCM1	P83994 locusta mig
24	36	76.6	595	2 Q6ZH94	Q6ZH94 oryza sativ
25	36	76.6	1375	2 Q7S242	Q7S242 neurospora
26	36	76.6	1384	2 Q872G8	Q872G8 neurospora
27	36	76.6	2567	2 Q7SC21	Q7SC21 neurospora
28	35	74.5	257	2 Q7NJ59	Q7NJ59 gloeobacter
29	35	74.5	346	2 Q8ZMS9	Q8ZMS9 salmonella
30	35	74.5	1133	2 Q6MKG4	Q6MKG4 bdellovibri
31	35	74.5	1502	2 Q60081	Q60081 schizosacch

RESULT 1

Q8LN52 PRELIMINARY; PRT; 207 AA.
AC Q8LN52; 207 AA.
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative aristolochene synthase, 3'-partial (Fragment).
GN Name=P0031G09.1;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoideae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M., Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S., Fadrosch D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL [2]
RN SEQUENCE FROM N.A.
RP Buell R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC092211; AA05003.1; -;
DR HSSP; Q40577; IHX9.
DR Gramene; Q8LN52; -;
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR008930; Terp_cyc_toroid.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene synth; 1.
FT NON TER 207
SQ SEQUENCE 207 AA; 23247 MW; AE217F61461679A9 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 207;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YLEPATAKY 9

Db 199 YLEPGLARY 207

RESULT 2

YR75_ECOLI STANDARD; PRT; 326 AA.
ID YR75_ECOLI
AC P21314;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)

32 34 72.3 132 2 027516
33 34 72.3 138 2 07PGQ1
34 34 72.3 194 2 08EJ18
35 34 72.3 207 1 TBTA_ALTSM
36 34 72.3 320 2 0751A4
37 34 72.3 387 2 0931W9
38 34 72.3 395 2 084CX1
39 34 72.3 485 1 SYE_SYNEL
40 34 72.3 564 1 PROD_CABEL
41 34 72.3 657 2 Q8STE3
42 34 72.3 761 2 Q8DI88
43 34 72.3 769 2 Q8TKI7
44 34 72.3 963 2 Q6HAC7
45 34 72.3 1038 2 Q7QD58

ALIGNMENTS

027516 methanobact
Q7pgq1 anopheles g
08ej18 shewanella
P32820 alteromonas
Q751a4 ashbya goss
Q931w9 streptomyce
Q84cx1 uncultured
Q8dl15 synechococc
O45228 caenorhabdi
Q8ate3 ciona intes
Q8di88 synechococc
Q8tki7 methanosarc
Q6hac7 serratia en
Q7qds8 anopheles g

DE Hypothetical 36.8 kDa protein (ORFs) (Retron EC67).

OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=562;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=O1:NM / Cl-1;

RX MEDLINE=91067724; PubMed=1701261;

RA Hsu M.-Y., Inouye M., Inouye S.;

RT "Retron for the 67-base multicopy single-stranded DNA from Escherichia coli: a potential transposable element encoding both reverse transcriptase and Dam methylase functions.";

RT Proc. Natl. Acad. Sci. U.S.A. 87:9454-9458(1990).

CC -!- SIMILARITY: Strong, to the phase P2 presumed portal vertex protein.

CC -----

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CC -----

DR EMBL; M55249; AAA23404.1; -.

DR PIR; JQ0855; JQ0855.

DR InterPro; IPR006944; Phage portal.

DR InterPro; IPR006430; Portal_PBSX.

DR Pfam; PF04860; Phage_portal_1.

DR TIGRFAMs; TIGR01540; portal_PBSX; 1.

RW Hypothetical protein; Transposable element.

SQ SEQUENCE 326 AA; 36819 MW; 80A67F9A238173E0 CRC64;

Query Match 80.9%; Score 38; DB 1; Length 326;

Best Local Similarity 87.5%; Pred. No. 24;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LEPAIAKY 9

Db 126 LEPALAKY 133

RESULT 3

Q62MU7

ID Q62MU7 PRELIMINARY; PRT; 337 AA.

AC Q62MU7

DT 25-OCT-2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Portal protein, PBSX family.

GN ORFNames=BMA0128;

OS Burkholderia mallei ATCC 23344.

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;

OC Burkholderiaceae; Burkholderia.

OX NCBI_TaxID=243160;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 23344;

RA Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E., Feldblyum T., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C., Davidson T.D., Deboy R.T., Dmitrov G., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R., Mohammed Y., Nelson W.C., Radune D., Romero C.M., Sarria S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N., Zhou L., Fraser C.M.;

RT "Structural flexibility in the Burkholderia mallei genome.";

RT Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).

RL EMBL; CP000010; AAU48678.1; -.

SQ SEQUENCE 337 AA; 38300 MW; AC77382B0D4776F4 CRC64;

Query Match 80.9%; Score 38; DB 2; Length 337;

Best Local Similarity 87.5%; Pred. No. 25;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LEPAIAKY 9

Db 126 LEPALAKY 133

RESULT 5

Q8FJ15

ID Q8FJ15 PRELIMINARY; PRT; 345 AA.

AC Q8FJ15

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Probable capsid portal protein.

GN OrderedLocuNames=c0947;

OS Escherichia coli O6.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LEPAIAKY 9

Db 117 LEPALAKY 124

RESULT 4

Q8Z359

ID Q8Z359 PRELIMINARY; PRT; 345 AA.

AC Q8Z359; Q7C6S5;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Probable capsid portal protein.

GN OrderedLocuNames=STY3674, t3416;

OS Salmonella typhi.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Salmonella.

OX NCBI_TaxID=601;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CT18;

RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;

RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Baker S., Basham D., Brooks K., Chillingworth T., Connor P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

RT "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";

RT Nature 413:848-852(2001).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=TY2 / ATCC 700931;

RX MEDLINE=22531367; PubMed=12644504;

RX DOI=10.1128/JB.185.7.2330-2337.2003;

RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J., Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;

RA "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18.";

RL J. Bacteriol. 185:2330-2337(2003).

DR EMBL; AL627279; CAD09435.1; -.

DR EMBL; AE016845; AA070939.1; -.

DR Pfam; PF04860; Phage_portal; 1.

DR TIGRFAMs; TIGR01540; portal_PBSX; 1.

KW Complete proteome.

SQ SEQUENCE 345 AA; 39308 MW; 2FFBF4F3C7B6F26A CRC64;

Query Match 80.9%; Score 38; DB 2; Length 345;

Best Local Similarity 87.5%; Pred. No. 26;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LEPAIAKY 9

Db 126 LEPALAKY 133

RESULT 5

Q8FJ15

ID Q8FJ15 PRELIMINARY; PRT; 345 AA.

AC Q8FJ15

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Probable capsid portal protein.

GN OrderedLocuNames=c0947;

OS Escherichia coli O6.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=217992;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O6:H1 / CFT073 / ATCC 700928 / UPEC;
 RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
 RA Raeko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
 RT "Extensive mosaic structure revealed by the complete genome sequence
 of uropathogenic *Escherichia coli*."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
 DR EMBL; AE016758; AAN79420.1; -;
 DR InterPro; IPR009027; L9_N_like.
 DR InterPro; IPR006944; Phage_portal.
 DR InterPro; IPR006430; Portal_PBSX.
 DR Pfam; PF04860; Phage_portal; 1.
 DR TIGRFAMs; TIGR01540; portal_PBSX; 1.
 DR Complete proteome.
 KW SEQUENCE 345 AA; 39126 MW; F841C15B20DB0D28 CRC64;
 SQ SEQUENCE 348 AA; 39710 MW; 68F1A713B73778A4 CRC64;
 Query Match 80.9%; Score 38; DB 2; Length 345;
 Best Local Similarity 87.5%; Pred. No. 26;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 LEPAIAKY 9
 Db 127 LEPALAKY 134
 RESULT 6
 Q821E6 PRELIMINARY; PRT; 348 AA.
 AC Q821E6; O7C5B5;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Probable capsid portal protein.
 GN OrderedLocusNames=STY4628, t4321;
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrell B.G.;
 RT "Complete genome sequence of a multiple drug resistant *Salmonella*
 enterica serovar Typhi CT18."
 RL Nature 413:848-852(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ty2 / ATCC 700931;
 RX MEDLINE=22531367; PubMed=12644504;
 RX DOI=10.1128/JB.185.7.2330-2337.2003;
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
 RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
 RT "Comparative genomics of *Salmonella enterica* serovar Typhi strains Ty2
 and CT18."
 RL J. Bacteriol. 185:2330-2337(2003).
 RL EMBL; AL627283; CAD06750.1; -;
 DR EMBL; AE016848; AAO71777.1; -;
 DR Pfam; PF04860; Phage_portal; 1.
 DR TIGRFAMs; TIGR01540; portal_PBSX; 1.
 KW Complete proteome.

SQ SEQUENCE 348 AA; 39710 MW; 68F1A713B73778A4 CRC64;
 Query Match 80.9%; Score 38; DB 2; Length 348;
 Best Local Similarity 87.5%; Pred. No. 26;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 LEPAIAKY 9
 Db 129 LEPALAKY 136
 RESULT 7
 Q62GG0 PRELIMINARY; PRT; 351 AA.
 AC Q62GG0;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Phage portal protein, PBSX family.
 GN ORFNames=BMA2691;
 GN ORFNames=ATCC 23344.
 OS Burkholderia mallei ATCC 23344.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia.
 OX NCBI_TaxID=243160;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 23344;
 RA Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.B.,
 RA Feldblyum T., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C.,
 RA Davidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S.,
 RA Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R.,
 RA Mohammad Y., Nelson W.C., Radune D., Romero C.M., Sarria S.,
 RA Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N.,
 RA Zhou L., Fraser C.M.;
 RT "Structural flexibility in the Burkholderia mallei genome."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).
 DR EMBL; CP000010; AAU48261.1; -;
 SQ SEQUENCE 351 AA; 39616 MW; E90D7F6EF9B87729 CRC64;
 Query Match 80.9%; Score 38; DB 2; Length 351;
 Best Local Similarity 87.5%; Pred. No. 26;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 LEPAIAKY 9
 Db 131 LEPALAKY 138
 RESULT 8
 Q63LE8 PRELIMINARY; PRT; 351 AA.
 ID Q63LE8
 AC Q63LE8;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Putative phage protein.
 GN ORFNames=BPSS1062;
 OS Burkholderia pseudomallei K96243.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia.
 OX NCBI_TaxID=272560;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K96243;
 RX PubMed=15377794;
 RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,
 RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
 RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
 RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
 RA Chillingworth T., Cronin A., Crosset B., Davis P., DeShazer D.,
 RA Feltwell T., Fraser A., Hance Z., Hauser H., Holtroyd S., Jagels K.,
 RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
 RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,

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RA Songsilvilai S., Stevens K., Tumapa S., Vesaratchavest M.,
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT "Genomic plasticity of the causative agent of melioidosis,
RL Burkholderia pseudomallei.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004) .
DR EMBL; BX571966; CAH38528.1; -.
SQ SEQUENCE 351 AA; 39489 MW; EADD83CC39BA2BED CRC64;

Query Match      80.9%; Score 38; DB 2; Length 351;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LEPALAKY 9
      |||||:|
Db      131 LEPALAKY 138

RESULT 9
Q63YL4 PRELIMINARY; PRT; 351 AA.
ID Q63YL4
AC Q63YL4
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Putative phage portal vertex protein.
GN ORFNames=BPSL0173;
OS Burkholderia pseudomallei K96243.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=272560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K96243;
RX PubMed=15377794;
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crosset B., Davis P., Deshazer D.,
RA Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA Songsilvilai S., Stevens K., Tumapa S., Vesaratchavest M.,
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT "Genomic plasticity of the causative agent of melioidosis,
RL Burkholderia pseudomallei.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004) .
DR EMBL; BX571965; CAH34160.1; -.
SQ SEQUENCE 351 AA; 39441 MW; BB5D1A854843ED6A CRC64;

Query Match      80.9%; Score 38; DB 2; Length 351;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LEPALAKY 9
      |||||:|
Db      131 LEPALAKY 138

RESULT 10
Q63YS8 PRELIMINARY; PRT; 370 AA.
ID Q63YS8
AC Q63YS8
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Probable portal protein.
GN ORFNames=BPSL0111;
OS Burkholderia pseudomallei K96243.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=272560;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=K96243;
RX PubMed=15377794;
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crosset B., Davis P., Deshazer D.,
RA Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA Songsilvilai S., Stevens K., Tumapa S., Vesaratchavest M.,
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT "Genomic plasticity of the causative agent of melioidosis,
RL Burkholderia pseudomallei.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004) .
DR EMBL; BX571965; CAH34096.1; -.
SQ SEQUENCE 370 AA; 41640 MW; E9F5FF9F77ABF86B CRC64;

Query Match      80.9%; Score 38; DB 2; Length 370;
Best Local Similarity 87.5%; Pred. No. 28;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      2 LEPALAKY 9
      |||||:|
Db      150 LEPALAKY 157

RESULT 11
Q8W5J7 PRELIMINARY; PRT; 468 AA.
ID Q8W5J7
AC Q8W5J7
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative monoterpene synthase.
GN Name=OSJNB0049A16.6;
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Moffat K.S., Hill J.N.,
RA Gansberger K., Brenner M., Burgess S., Hance M., Shvartsbeyn M.,
RA Tsitrin T., Riggs F., Hsiao J., Ziemann V., Blunt S., Pai G.,
RA VanAken S.E., Utterback T.R., Feldblyum T.V., Kalb E., Quackenbush J.,
RA Salzberg S.L., White O., Fraser C.M.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Buell R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC090120; AAL31055.1; -.
DR HSSP; O81192; INIZ.
DR Gramene; Q8W5J7; -.
DR GO; GO:0016829; F:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR Pfam; PF01397; Terpene synthase; 1.
DR Pfam; PF03936; Terpene synthase; 1.
SQ SEQUENCE 468 AA; 53441 MW; 81D9E5B891305C05 CRC64;

Query Match      80.9%; Score 38; DB 2; Length 468;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 YLEPALAKY 9
      |||||:|
Db      115 YLEPALAKY 123

RESULT 12

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DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative monoterpene synthase.
GN ORFNames=OSJNB0049A16.6;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriocarpaceae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA The Rice Chromosome 10 Sequencing Consortium;
RT "In-depth view of structure, activity, and evolution of rice
chromosome 10."
RL Science 300:1566-1569(2003).
RN [2]
RP SEQUENCE FROM N.A.
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017107; AAP84380.1; -;
DR Gramene; Q7XD63; -;
DR GO; GO:0016829; P:lyase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth C.
DR InterPro; IPR008949; Terpenoid synth.
DR InterPro; IPR008930; Terp_cyc toroid.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene synth; 1.
DR Pfam; PF03936; Terpene synth C; 1.
SQ SEQUENCE 468 AA; 53441 MW; 81D95B891305C05 CRC64;
Query Match 80.9%; Score 38; DB 2; Length 468;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YLEPAIAKY 9
Db 115 YLEPGLARY 123
RESULT 13
Q7SG62
ID Q7SG62 PRELIMINARY; PRT; 505 AA.
AC Q7SG62;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative terpene synthase.
GN Name=B1288B10.7;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriocarpaceae; Oryzae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
RA Vanaken S.S., Riedmuller S.B., Uterback T.T., Feldblyum T.V.,
RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Buell R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC146481; AAR87368.1; -;
GO; GO:0016829; P:lyase activity; IEA.

DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR005630; Terpene synth C.
DR InterPro; IPR008949; Terpenoid synth.
DR InterPro; IPR008930; Terp_cyc toroid.
DR InterPro; IPR001906; Terp_synth-like.
DR Pfam; PF01397; Terpene synth; 1.
DR Pfam; PF03936; Terpene synth C; 1.
SQ SEQUENCE 505 AA; 57549 MW; DE64A54C6DEACAC92 CRC64;
Query Match 80.9%; Score 38; DB 2; Length 505;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YLEPAIAKY 9
Db 152 YLEPGLARY 160
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ID Q87KR7 PRELIMINARY; PRT; 534 AA.
AC Q87KR7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein VP2909.
GN OrderedLocNames=VP2909;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae".
RL Lancet 361:743-749(2003).
DR EMBL; AP005083; BAC61172.1; -;
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0015074; P:DNA integration; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR InterPro; IPR011010; DNA_brk_join_enz.
DR InterPro; IPR002104; Phage_integrase.
DR Pfam; PF00589; Phage_integrase; 1.
KW Complete proteome.
SQ SEQUENCE 534 AA; 61597 MW; E1F3187F1DECA81C CRC64;
Query Match 80.9%; Score 38; DB 2; Length 534;
Best Local Similarity 77.8%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YLEPAIAKY 9
Db 457 YLEPAVACY 465
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ID Q6VY34 PRELIMINARY; PRT; 261 AA.
AC Q6VY34;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Capsid protein (Fragment).
OS Turkey astrovirus 2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Astroviridae;
OC Avastrovirus.
OX NCBI_TaxID=246343;
RN [1]

RP SEQUENCE FROM N.A.
RA Guy J.S., Miles A., Smith L.G., Fuller F., Schultz-Cherry S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY320042; AAQ8297.1; -.
FT NON TER 1 261
SQ SEQUENCE 261 AA; 29740 MW; 8E36C789F52D733D CRC64;

Query Match 78.7%; Score 37; DB 2; Length 261;
Best Local Similarity 77.8%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YLEPAIAKY 9
| | | | |
Db 110 YTEPAIOKY 118

Search completed: June 29, 2005, 01:34:54
Job time : 57.2473 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 05:18:25 ; Search time 53.8517 Seconds
(without alignments)
64.268 Million cell updates/sec

Title: US-08-170-344-76

Perfect score: 47

Sequence: 1 YLEPAIYAKY 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	9	8 US-08-344-824-10	Sequence 10, Appl
2	47	100.0	9	15 US-10-149-138-4188	Sequence 4188, Ap
3	47	100.0	9	15 US-10-149-135-2175	Sequence 2175, Ap
4	47	100.0	9	16 US-10-149-138-4188	Sequence 4188, Ap
5	47	100.0	9	17 US-10-654-601-2486	Sequence 2486, Ap
6	47	100.0	9	17 US-10-751-845-117	Sequence 117, App
7	39	83.0	129	16 US-10-425-115-240653	Sequence 240653,
8	38	80.9	468	16 US-10-437-963-142246	Sequence 142246,
9	37	78.7	313	15 US-10-282-122A-48180	Sequence 48180, A
10	37	78.7	377	15 US-10-369-493-5776	Sequence 5776, Ap
11	37	78.7	724	17 US-10-684-129-9	Sequence 9, Appli

12	36	76.6	527	16	US-10-437-963-172470	Sequence 172470,
13	36	76.6	1139	15	US-10-259-194A-78	Sequence 78, Appl
14	34	72.3	320	14	US-10-076-157-13	Sequence 13, Appl
15	34	72.3	564	15	US-10-369-493-6219	Sequence 6219, Ap
16	34	72.3	689	15	US-10-369-493-10443	Sequence 10443, A
17	34	72.3	909	16	US-10-437-963-149025	Sequence 149025,
18	33	70.2	67	16	US-10-437-963-164967	Sequence 164967,
19	33	70.2	79	16	US-10-425-115-368932	Sequence 368932,
20	33	70.2	102	16	US-10-425-115-295827	Sequence 295827,
21	33	70.2	249	16	US-10-437-963-177259	Sequence 177259,
22	33	70.2	254	16	US-10-425-115-280016	Sequence 280016,
23	33	70.2	258	9	US-09-815-242-5680	Sequence 5680, Ap
24	33	70.2	286	15	US-10-282-122A-44430	Sequence 44430, A
25	33	70.2	293	16	US-10-437-963-176423	Sequence 176423,
26	33	70.2	300	9	US-09-815-242-12173	Sequence 12173, A
27	33	70.2	312	15	US-10-282-122A-49943	Sequence 49943, A
28	33	70.2	338	15	US-10-282-122A-52673	Sequence 52673, A
29	33	70.2	401	15	US-10-424-599-161628	Sequence 161628,
30	33	70.2	462	16	US-10-437-963-177252	Sequence 177252,
31	33	70.2	464	16	US-10-689-200-2	Sequence 2, Appli
32	33	70.2	477	9	US-09-876-224-2	Sequence 2, Appli
33	33	70.2	477	9	US-09-876-221-2	Sequence 2, Appli
34	33	70.2	477	14	US-10-302-904-2	Sequence 2, Appli
35	33	70.2	477	14	US-10-323-968-2	Sequence 2, Appli
36	33	70.2	477	17	US-10-732-923-15052	Sequence 15052, A
37	33	70.2	477	17	US-10-732-923-15053	Sequence 15053, A
38	33	70.2	713	16	US-10-437-963-171800	Sequence 171800,
39	33	70.2	730	16	US-10-437-963-121286	Sequence 121286,
40	33	70.2	764	16	US-10-437-963-177266	Sequence 177266,
41	33	70.2	1031	17	US-10-732-923-21567	Sequence 21567, A
42	33	70.2	1080	16	US-10-437-963-177258	Sequence 177258,
43	33	70.2	1119	16	US-10-437-963-177254	Sequence 177254,
44	33	70.2	1249	16	US-10-437-963-133630	Sequence 133630,
45	33	70.2	1355	16	US-10-437-963-154052	Sequence 154052,

ALIGNMENTS

RESULT 1
US-08-344-824-10
; Sequence 10, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; STREET: Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:

```
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-344-824-10

Query Match 100.0%; Score 47; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YLEPAIAKY 9
Db 1 YLEPAIAKY 9

RESULT 2
US-10-149-138-4188
; Sequence 4188, Application US/10149138
; Publication No. US20040018971A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10149,138
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4188
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4188

Query Match 100.0%; Score 47; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 YLEPAIAKY 9

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; Publication No. US20040053822A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0130001
; CURRENT APPLICATION NUMBER: US/10149,135
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: PCT/US00/33545
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,298
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; NUMBER OF SEQ ID NOS: 2479
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2175
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-135-2175

Query Match 100.0%; Score 47; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YLEPAIAKY 9
Db 1 YLEPAIAKY 9

RESULT 4
US-10-149-138-4188
; Sequence 4188, Application US/10149138
; Publication No. US20040121946A9
; GENERAL INFORMATION:
; APPLICANT: Fikes, John
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa
; TITLE OF INVENTION: Inducing Cellular Immune Responses to
; TITLE OF INVENTION: HER2/neu Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0140001
; CURRENT APPLICATION NUMBER: US/10149,138
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: PCT/US00/33591
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/458,299
; PRIOR FILING DATE: 1999-12-11
; NUMBER OF SEQ ID NOS: 4641
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4188
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Peptide
US-10-149-138-4188

Query Match 100.0%; Score 47; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YLEPAIAKY 9
Db 1 YLEPAIAKY 9
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Db      1 YLEPAIAKY 9
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RESULT 5
US-10-654-601-2486
; Sequence 2486, Application US/10654601
; Publication No. US20050063983A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidnev, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitiello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Eptimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0060007
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/09/239,043
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2486
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Standard peptide that binds to HLA A*0101
US-10-654-601-2486
Query Match      100.0%; Score 47; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YLEPAIAKY 9
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RESULT 6
US-10-751-845-117
; Sequence 117, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0060007
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/09/239,043
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2486
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Standard peptide that binds to HLA A*0101
US-10-654-601-2486
Query Match      100.0%; Score 47; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YLEPAIAKY 9
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RESULT 7
US-10-425-115-240653
; Sequence 240653, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 240653
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_151055C.1.pep
US-10-425-115-240653
Query Match      83.0%; Score 39; DB 16; Length 129;
Best Local Similarity 77.8%; Pred. No. 8.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YLEPAIAKY 9
|||||
RESULT 8
US-10-437-963-142246
; Sequence 142246, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
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; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 142246
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_43270C.1.pep
US-10-437-963-142246

Query Match 80.9%; Score 38; DB 16; Length 468;
Best Local Similarity 66.7%; Pred. No. 51;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YLEPAIAKY 9
|||:|
Db 115 YLEGLARY 123

RESULT 9
US-10-282-122A-48180
; Sequence 48180, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48180
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Burkholderia cepacia
US-10-282-122A-48180

Query Match 78.7%; Score 37; DB 15; Length 313;
Best Local Similarity 77.8%; Pred. No. 53;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 YLEPAIAKY 9
|||:|
Db 106 YLVPAlARY 114

RESULT 10
US-10-369-493-5776
; Sequence 5776, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkie, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5776
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5776

Query Match 78.7%; Score 37; DB 15; Length 377;
Best Local Similarity 77.8%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YLEPAIAKY 9
|||:|
Db 204 YAEPAILKY 212

RESULT 11
US-10-684-129-9
; Sequence 9, Application US/10684129
; Publication No. US20050079485A1
; GENERAL INFORMATION:
; APPLICANT: Schultz-Cherry, Stacey L.
; APPLICANT: Koki, Matthew
; APPLICANT: WARF - Wisconsin Alumni Research Foundation
; TITLE OF INVENTION: Method to Detect Antibodies Specific for Type-2 Turkey Astrovirus
; FILE REFERENCE: 800.039US1
; CURRENT APPLICATION NUMBER: US/10/684,129
; CURRENT FILING DATE: 2003-10-10
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Turkey astrovirus
US-10-684-129-9

Query Match 78.7%; Score 37; DB 17; Length 724;
Best Local Similarity 77.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YLEPAIAKY 9
|||:|
Db 534 YTEPAIQKY 542

RESULT 12
US-10-437-963-172470
; Sequence 172470, Application US/10437963
; Publication No. US20040123343A1

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/ GENERAL INFORMATION:
/ APPLICANT: La Rosa, Thomas J.
/ APPLICANT: Kovalic, David K.
/ APPLICANT: Zhou, Yihua
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Wu, Wei
/ APPLICANT: Boukharov, Andrey A.
/ APPLICANT: Barbazuk, Brad
/ APPLICANT: Li, Ping
/ TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
/ FILE REFERENCE: 38-21(53221)B
/ CURRENT APPLICATION NUMBER: US/10/437,963
/ CURRENT FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 204966
/ SEQ ID NO 172470
/ LENGTH: 527
/ TYPE: PRT
/ ORGANISM: Oryza sativa
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT4530_70602C.1.pep
US-10-437-963-172470

Query Match      76.6%; Score 36; DB 16; Length 527;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 YLEPAIAKY 9
Db      159 YLEPNLARY 167

RESULT 13
US-10-259-194A-78
/ Sequence 78, Application US/10259194A
/ Publication No. US20040010815A1
/ GENERAL INFORMATION:
/ APPLICANT: Lange, Markus B.
/ APPLICANT: Ghassemian, Majid
/ APPLICANT: Briggs, Steven P.
/ APPLICANT: Cooper, Bret
/ APPLICANT: Glazebrook, Jane
/ APPLICANT: Goff, Stephen A.
/ APPLICANT: Katagiri, Fumiaki
/ APPLICANT: Kreps, Joel
/ APPLICANT: Moughamer, Todd
/ APPLICANT: Provart, Nicholas
/ APPLICANT: Ricke, Darrell
/ APPLICANT: Zhu, Tong
/ TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
/ FILE REFERENCE: 70029-NP
/ CURRENT APPLICATION NUMBER: US/10/259,194A
/ CURRENT FILING DATE: 2003-01-07
/ PRIOR APPLICATION NUMBER: US 60/325,277
/ PRIOR FILING DATE: 2001-09-26
/ PRIOR APPLICATION NUMBER: US 60/370,743
/ PRIOR FILING DATE: 2002-04-04
/ PRIOR APPLICATION NUMBER: US 60/370,620
/ PRIOR FILING DATE: 2002-04-04
/ NUMBER OF SEQ ID NOS: 662
/ SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
/ SEQ ID NO 78
/ LENGTH: 1139
/ TYPE: PRT
/ ORGANISM: Oryza sativa
US-10-259-194A-78

Query Match      76.6%; Score 36; DB 15; Length 1139;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 YLEPAIAKY 9
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Db      227 YLEPNLARY 235

RESULT 14
US-10-076-157-13
/ Sequence 13, Application US/10076157
/ Publication No. US20030027309A1
/ GENERAL INFORMATION:
/ APPLICANT: Pompejus, Markus
/ APPLICANT: Suelberger, Harald
/ APPLICANT: Joeffken, Hans Wolfgang
/ APPLICANT: Doval, Jose Luis Revuelta
/ APPLICANT: Jimenez, Alberto;
/ APPLICANT: Garcia, Maria Angeles Santos
/ TITLE OF INVENTION: Genes of purine biosynthesis from Ashbya Gossypii and the use th
/ TITLE OF INVENTION: in
/ FILE REFERENCE: 48684DIV
/ CURRENT APPLICATION NUMBER: US/10/076,157
/ CURRENT FILING DATE: 2002-02-15
/ PRIOR APPLICATION NUMBER: US 09/212,247
/ PRIOR FILING DATE: 1998-12-16
/ NUMBER OF SEQ ID NOS: 21
/ SOFTWARE: WordPerfect v. 6.1
/ SEQ ID NO 13
/ LENGTH: 320
/ TYPE: PRT
/ ORGANISM: Ashbya gossypii
US-10-076-157-13

Query Match      72.3%; Score 34; DB 14; Length 320;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 YLEPAIAKY 9
      |||| :|||
Db      149 YAEPSVVKY 157

RESULT 15
US-10-369-493-6219
/ Sequence 6219, Application US/10369493
/ Publication No. US20030233675A1
/ GENERAL INFORMATION:
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Hinkle, Gregory J.
/ APPLICANT: Slater, Steven C.
/ APPLICANT: Goldman, Barry S.
/ APPLICANT: Chen, Xianfeng
/ TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
/ FILE REFERENCE: 38-10(52052)B
/ CURRENT APPLICATION NUMBER: US/10/369,493
/ CURRENT FILING DATE: 2003-02-28
/ PRIOR APPLICATION NUMBER: US 60/360,039
/ PRIOR FILING DATE: 2002-02-21
/ NUMBER OF SEQ ID NOS: 47374
/ SEQ ID NO 6219
/ LENGTH: 564
/ TYPE: PRT
/ ORGANISM: Caenorhabditis elegans
US-10-369-493-6219

Query Match      72.3%; Score 34; DB 15; Length 564;
Best Local Similarity 75.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YLEPAIAK 8
      |||| :|||
Db      344 YLQPAISK 351

Search completed: June 29, 2005, 05:48:16
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Job time : 53.8517 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:37:59 ; Search time 16.8626 Seconds
(without alignments)
39.842 Million cell updates/sec

Title: US-08-170-344-76

Perfect score: 47

Sequence: 1 YLEPAIARY 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	9	1	US-08-186-266-3
2	47	100.0	9	3	US-08-159-339A-126
3	47	100.0	9	4	US-09-543-608A-42
4	47	100.0	9	4	US-09-239-043D-2486
5	37	78.7	724	4	US-09-900-920-62
6	34	72.3	320	3	US-09-212-247C-13
7	33	70.2	187	4	US-09-270-767-45328
8	33	70.2	477	4	US-09-876-221-2
9	32	68.1	90	4	US-09-270-767-38985
10	32	68.1	90	4	US-09-270-767-54202
11	32	68.1	104	4	US-09-513-999C-5453
12	32	68.1	174	4	US-09-248-796A-24410
13	32	68.1	744	4	US-09-248-796A-18090
14	31	66.0	68	3	US-09-905-223-279
15	31	66.0	72	4	US-09-513-999C-6819
16	31	66.0	117	4	US-09-902-540-13629
17	31	66.0	124	4	US-09-134-000C-3784
18	31	66.0	169	4	US-09-270-767-33370
19	31	66.0	169	4	US-09-270-767-48587
20	31	66.0	175	4	US-09-270-767-39569
21	31	66.0	175	4	US-09-270-767-54786
22	31	66.0	207	1	US-08-557-917A-2
23	31	66.0	207	3	US-09-084-153-2
24	31	66.0	207	3	US-09-084-079-2
25	31	66.0	218	3	US-09-084-079-5
26	31	66.0	218	4	US-09-949-016-11677
27	31	66.0	230	4	US-09-503-110-2824

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28 31 66.0 233 4 US-09-248-796A-21348 Sequence 21348, A
29 31 66.0 249 4 US-09-107-433-4980 Sequence 4980, Ap
30 31 66.0 259 4 US-09-270-767-59221 Sequence 59221, A
31 31 66.0 317 4 US-09-538-092-882 Sequence 882, App
32 31 66.0 318 4 US-09-919-497-91 Sequence 91, Appl
33 31 66.0 321 4 US-09-949-016-7474 Sequence 7474, Ap
34 31 66.0 332 4 US-09-248-796A-17382 Sequence 17382, A
35 31 66.0 347 4 US-09-270-767-41519 Sequence 41519, A
36 31 66.0 349 3 US-09-134-001C-4519 Sequence 4519, Ap
37 31 66.0 349 4 US-09-710-279-932 Sequence 932, App
38 31 66.0 430 4 US-09-270-767-43819 Sequence 43819, A
39 31 66.0 469 4 US-09-949-016-8245 Sequence 8245, Ap
40 31 66.0 485 4 US-09-949-016-10455 Sequence 10455, A
41 31 66.0 622 4 US-09-328-352-4844 Sequence 4844, Ap
42 31 66.0 703 4 US-09-134-000C-5072 Sequence 5072, Ap
43 31 66.0 749 4 US-09-902-540-10608 Sequence 10608, A
44 31 66.0 768 4 US-09-540-236-3811 Sequence 3811, Ap
45 31 66.0 1622 4 US-09-231-8999-72 Sequence 72, Appl

```

ALIGNMENTS

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RESULT 1
US-08-186-266-3
; Sequence 3, Application US/08186266
; Patent No. 5662907
; GENERAL INFORMATION:
; APPLICANT: KUBO, Ralph T.
; APPLICANT: GREY, Howard M.
; APPLICANT: SETTE, Alessandro
; APPLICANT: CELIS, Esteban
; TITLE OF INVENTION: INDUCTION OF ANTI-TUMOR CYTOTOXIC
; T LYMPHOCYTES IN HUMANS USING
; TITLE OF INVENTION: SYNTHETIC PEPTIDE EPITOPES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,266
; FILING DATE: 25-JAN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/159,339
; FILING DATE: 29-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-50-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-186-266-3

Query Match 100.0%; Score 47; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YLEPAIAKY 9
Db 1 YLEPAIAKY 9

RESULT 2
US-08-159-339A-126
; Sequence 126, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 126:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-126

Query Match 100.0%; Score 47; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YLEPAIAKY 9
Db 1 YLEPAIAKY 9

Db 1 YLEPAIAKY 9

RESULT 3
US-09-543-608A-42
; Sequence 42, Application US/09543608A
; Patent No. 6602510
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Celis, Esteban
; APPLICANT: Keogh, Elissa A.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: HLA Class I A2 Tumor Associated Antigen
; TITLE OF INVENTION: Peptides and Vaccine Compositions
; FILE REFERENCE: 018623-015710US
; CURRENT APPLICATION NUMBER: US/09/543,608A
; CURRENT FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Standard Peptide 944.02
US-09-543-608A-42

Query Match 100.0%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YLEPAIAKY 9
Db 1 YLEPAIAKY 9

RESULT 4
US-09-239-043D-2486
; Sequence 2486, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitiello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824

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; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2486
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Standard peptide that binds to HLA A*0101
US-09-239-043D-2486

Query Match      100.0%; Score 47; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4;le+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YLEPAIAKY 9
      |||||
Db      1 YLEPAIAKY 9

RESULT 5
US-09-900-920-62
; Sequence 62, Application US/09900920
; Patent No. 6696562
; GENERAL INFORMATION:
; APPLICANT: Schultz-Cherry, Stacey
; APPLICANT: Kelley, Laura
; APPLICANT: Koci, Matthew
; APPLICANT: Seal, Bruce
; TITLE OF INVENTION: No. 6696562el Avian Astrovirus
; FILE REFERENCE: turkeyastrovirus
; CURRENT APPLICATION NUMBER: US/09/900,920
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,312
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Turkey astrovirus
US-09-900-920-62

Query Match      78.7%; Score 37; DB 4; Length 724;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 YLEPAIAKY 9
      |||||
Db      534 YTEPAIQKY 542

RESULT 6
US-09-212-247C-13
; Sequence 13, Application US/09212247C
; Patent No. 6391603
; GENERAL INFORMATION:
; APPLICANT: FOMPEJUS, Markus; SUELBURGER, Harald; JOEFFKEN, Hans
; Wolfgang; DOVAL, Jose Luis Revuelta; JIMENEZ, Alberto;
; and GARCIA, Maria Angeles Santos
; TITLE OF INVENTION: Genes of purine biosynthesis from Ashbya Gossypii
; and the use thereof in microbial riboflavin
; synthesis
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Keil & Weinkauff
```

```
; STREET: 1101 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM AT-compatible, Pentium processor
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect version 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/212,247C
; FILING DATE: 16-Dec-1998
; CLASSIFICATION: <Unknown>
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 320 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-212-247C-13

Query Match      72.3%; Score 34; DB 3; Length 320;
Best Local Similarity 55.6%; Pred. No. 44;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 YLEPAIAKY 9
      |||||
Db      149 YAEPSVVKY 157

RESULT 7
US-09-270-767-45328
; Sequence 45328, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45328
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-45328

Query Match      70.2%; Score 33; DB 4; Length 187;
Best Local Similarity 55.6%; Pred. No. 40;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 YLEPAIAKY 9
      |||||
Db      162 YYRPSVAKY 170

RESULT 8
US-09-876-221-2
; Sequence 2, Application US/09876221
; Patent No. 6555329
; GENERAL INFORMATION:
; APPLICANT: Jenuwein, Thomas
; APPLICANT: Rea, Stephen
; APPLICANT: Eisenhaber, Frank
; APPLICANT: O'Carroll, Donal
; TITLE OF INVENTION: Method for identifying compounds altering higher-order chromatin
; stability
; FILE REFERENCE: 0652.2240001
; CURRENT APPLICATION NUMBER: US/09/876,221
; CURRENT FILING DATE: 2001-06-08
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; PRIOR APPLICATION NUMBER: EP 00 112 345.4
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: EP 00 112 479.1
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: US 60/224,220
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-876-221-2

Query Match 70.2%; Score 33; DB 4; Length 477;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YLEPAIAKY 9
|:|||||:
Db 186 LQPAIAEY 193

RESULT 9
US-09-270-767-38985
; Sequence 38985, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38985
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-38985

Query Match 68.1%; Score 32; DB 4; Length 90;
Best Local Similarity 55.6%; Pred. No. 30;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YLEPAIAKY 9
|:|||||:
Db 45 YLQPMIGRY 53

RESULT 10
US-09-270-767-54202
; Sequence 54202, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54202
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-54202

Query Match 68.1%; Score 32; DB 4; Length 90;

Best Local Similarity 55.6%; Pred. No. 30;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YLEPAIAKY 9
|:|||||:
Db 45 YLQPMIGRY 53

RESULT 11
US-09-513-999C-5453
; Sequence 5453, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5453
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-5453

Query Match 68.1%; Score 32; DB 4; Length 104;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LEPAlAKY 9
|:|||||:
Db 59 LKPAIAEY 66

RESULT 12
US-09-248-796A-24410
; Sequence 24410, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICA
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 24410
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-24410

Query Match 68.1%; Score 32; DB 4; Length 174;
Best Local Similarity 55.6%; Pred. No. 60;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YLEPAIAKY 9
|:|||||:
Db 95 YFDPISIQY 103

RESULT 13
US-09-248-796A-18090

```
; Sequence 18090, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18090
; LENGTH: 744
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18090

Query Match      68.1%; Score 32; DB 4; Length 744;
Best Local Similarity 55.6%; Pred. No. 2.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      1 YLEPAIAKY 9
Db      470 YLEPDLSKF 478

RESULT 14
US-08-905-223-279
; Sequence 279, Application US/08905223
; Patent No. 6222029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duclert, Americ
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,223
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 279:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 68 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; TISSUE TYPE: Brain
; FEATURE:
; NAME/KEY: sig_peptide

; Sequence 18090, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18090
; LENGTH: 744
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18090

Query Match      68.1%; Score 32; DB 4; Length 744;
Best Local Similarity 55.6%; Pred. No. 2.8e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      1 YLEPAIAKY 9
Db      470 YLEPDLSKF 478

RESULT 15
US-09-513-999C-6819
; Sequence 6819, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6819
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-6819

Query Match      66.0%; Score 31; DB 4; Length 72;
Best Local Similarity 55.6%; Pred. No. 38;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 YLEPAIAKY 9
Db      16 YLEPGIGRH 24

Search completed: June 29, 2005, 01:44:30
Job time : 17.9126 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:32:21 ; Search time 11.2747 Seconds
(without alignments)
76.805 Million cell updates/sec

Title: US-08-170-344-75

Perfect score: 45

Sequence: 1 ATELOTTIH 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	91.1	158	1 W6WLHS	protein E6 - human
2	36	80.0	334	2 A72217	Holliday junction
3	35	77.8	138	2 I59767	lamin-like protein
4	35	77.8	394	2 A82168	cytochrome c-type
5	35	77.8	2155	2 AD2742	conserved hypotet
6	35	77.8	2155	2 C97523	hypothetical prote
7	34	75.6	248	1 LNDGPS	pulmonary surfacta
8	34	75.6	438	2 A70544	probable histidino
9	34	75.6	1317	2 F83310	conserved hypotet
10	33	73.3	116	1 EVECBA	boIA protein - Esc
11	33	73.3	116	2 A90690	probable murein ge
12	33	73.3	116	2 E85540	hypothetical prote
13	33	73.3	189	2 C95022	hypothetical prote
14	33	73.3	189	2 F97893	hypothetical prote
15	32	71.1	108	2 T34436	hypothetical prote
16	32	71.1	201	2 D81919	hypothetical prote
17	32	71.1	201	2 G81182	hypothetical prote
18	32	71.1	259	2 T26298	hypothetical prote
19	32	71.1	431	2 T45246	probable histidino
20	32	71.1	449	2 C87056	histidinol dehydro
21	32	71.1	540	2 AC2353	peptide-chain-rele
22	32	71.1	769	2 E97092	glycosyltransferas
23	32	71.1	773	2 H70108	hypothetical prote
24	32	71.1	982	2 T06576	probable protein k
25	31	68.9	280	1 VPXRNN	outer capsid prote
26	31	68.9	335	4 A26718	retrovirus-related
27	31	68.9	381	2 H88028	protein F46P5.2 [i
28	31	68.9	591	2 T45713	hypothetical prote
29	31	68.9	617	2 T15104	hypothetical prote

ALIGNMENTS

RESULT 1

W6WLHS

protein E6 - human papillomavirus type 16

C;Species: human papillomavirus type 16

C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C;Accession: A03682; T10427

R;Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virology 145, 181-185, 1985

A;Title: Human papillomavirus type 16 DNA sequence.

A;Reference number: A22355; MUID:85246220; PMID:2990099

A;Accession: A03682

A;Molecule type: DNA

A;Residues: 1-158 <SEE>

A;Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G3330303

R;Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A;Title: A negative element in the human poapillomavirus type 16 genome acts at the lev

A;Reference number: Z17014; MUID:91162763; PMID:1848319

A;Accession: T10427

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-158 <KEN>

A;Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G33303032

C;Genetics:

A;Gene: E6

C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; zinc finger

F;37-73/Region: zinc finger CCCC motif

F;110-146/Region: zinc finger CCCC motif

Query Match 91.1%; Score 41; DB 1; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.19;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TELOTTIH 9

|||||

Db 24 TELOTTIH 31

RESULT 2

A72217

Holliday junction DNA helicase - Thermotoga maritima (strain MSB8)

C;Species: Thermotoga maritima

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: A72217

R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Dodson, R.J.; Haft, D.H.; Hicke

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.

C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome se

A;Reference number: A72200; MUID:99287316; PMID:10360571

A;Accession: A72217

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-334 <ARN>
A;Cross-references: UNIPROT:Q5G313; GB:AB001812; GB:AB000512; NID:G4982302; PIDN:AAD3679
A;Experimental source: strain MSB8
C;Genetics:
A;Gene: TMI730
C;Superfamily: ruvB protein

Query Match 80.0%; Score 36; DB 2; Length 334;
Best Local Similarity 77.8%; Pred. No. 5.4;
Matches 7; Conservative 1; Mismatches 0; Gaps 0;

QY 1 ATELQTTIH 9
|:|||||
72 ASELQTNIH 80
|:|||||

RESULT 3
159767
lamin-like protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 159767
R;Bloom, D.C.; Massung, R.F.; Savage, L.; Morrison, D.K.; Moyer, R.W.
Virology 169, 115-126, 1989
A;Title: Recruitment to the cytoplasm of a cellular lamin-like protein from the nucleus
A;Reference number: 159767; MUID:89163245; PMID:2538026
A;Accession: 159767
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-138 <RES>
A;Cross-references: UNIPROT:Q14755; GB:M24732; NID:G187176; PIDN:AAA36178.1; PID:G187177
C;Superfamily: pol polyprotein

Query Match 77.8%; Score 35; DB 2; Length 138;
Best Local Similarity 87.5%; Pred. No. 3.3;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATELQTTY 8
|:|||||
124 ATEIQTTI 131
|:|||||

RESULT 4
H82168
cytochrome c-type protein TorC VCI693 [imported] - Vibrio cholerae (strain N16961 serog
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 21-Jul-2003
C;Accession: H82168
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Basse, S.; Qin, H.; Dragoi, I.; Sellers, F
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: H82168
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-394 <HEI>
A;Cross-references: GB:AE004247; GB:AE003852; NID:G9656204; PIDN:AAF94843.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VCI693
A;Map position: 1
C;Superfamily: membrane-bound tetraheme cytochrome TorC/yeck; nirt homology

Query Match 77.8%; Score 35; DB 2; Length 394;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 ELQTTIH 9
|:|||||

Db 65 ELQTTVH 71

RESULT 5
AD2742
conserved hypothetical protein Atul348 [imported] - Agrobacterium tumefaciens (strain C
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AD2742
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClel
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AD2742
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2155 <KUR>
A;Cross-references: UNIPROT:Q8UFP9; GB:AB008688; PIDN:AAL42354.1; PID:G17739760; GSPDB:
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atul348
A;Map position: circular chromosome

Query Match 77.8%; Score 35; DB 2; Length 2155;
Best Local Similarity 66.7%; Pred. No. 71;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATELQTTIH 9
|:|||||
257 ATELETLVH 265
|:|||||

Db 257 ATELETLVH 265

RESULT 6
C97523
hypothetical protein AGR_C_2490 [imported] - Agrobacterium tumefaciens (strain C58, Cer
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: C97523
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: C97523
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2155 <KUR>
A;Cross-references: UNIPROT:Q8UFP9; GB:AB007869; PIDN:AAK87140.1; PID:G15156408; GSPDB:
C;Genetics:
A;Gene: AGR C_2490
A;Map position: circular chromosome

Query Match 77.8%; Score 35; DB 2; Length 2155;
Best Local Similarity 66.7%; Pred. No. 71;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATELQTTIH 9
|:|||||
257 ATELETLVH 265
|:|||||

Db 257 ATELETLVH 265

RESULT 7
LNDQPS
Pulmonary surfactant protein A precursor - dog
N;Alternate names: pulmonary surfactant 32K approtein; pulmonary surfactant-associated
C;Species: Canis lupus familiaris (dog)
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
C;Accession: A25296; A61227; A60142
R;Benson, B.; Hawgood, S.; Schilling, J.; Clements, J.; Damm, D.; Cordell, B.; White, R

C;Comment: This protein causes round morphology of the organism when overexpressed.

C;Genetics:

A;Gene: *bolA*

C;Function:

A;Description: involved in the morphogenetic pathways; probably involved in the induction of DNA binding; transcription regulation

C;Superfamily: *bolA* protein

C;Keywords: DNA binding; status predicted <DBI>

F;37-56/Domain: DNA binding #status predicted <DBI>

Query Match 73.3%; Score 33; DB 1; Length 116;

Best Local Similarity 66.7%; Pred. No. 7.5;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATELOTTIH 9

76 AEELSTTVH 84

RESULT 11

A90690 probable regulator of murein genes [imported] - Escherichia coli (strain O157:H7, subsp. *Escherichia coli*)

C;Species: *Escherichia coli*

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C;Accession: A90690

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic reference sequence

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: A90690

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-116 <HAY>

A;Cross-references: UNIPROT:Q8XE61; GB:BA000007; PIDN:BA033912.1; PID:G13359946; GSPDB:G13359946

A;Experimental source: strain O157:H7, substrain RMD 0509952

C;Genetics:

A;Gene: EC0489

C;Superfamily: *bolA* protein

Query Match 73.3%; Score 33; DB 2; Length 116;

Best Local Similarity 66.7%; Pred. No. 7.5;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATELOTTIH 9

76 AEELSTTVH 84

RESULT 12

E85540 probable murein genes regulator *bolA* [imported] - Escherichia coli (strain O157:H7, subsp. *Escherichia coli*)

C;Species: *Escherichia coli*

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C;Accession: E85540

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: E85540

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-116 <STO>

A;Cross-references: UNIPROT:Q8XE61; GB:AE005174; NID:G12513294; PIDN:AAG54785.1; GSPDB:G12513294

A;Experimental source: strain O157:H7, substrain EDL933

C;Genetics:

A;Gene: *bolA*

C;Superfamily: *bolA* protein

Query Match 73.3%; Score 33; DB 2; Length 116;

Best Local Similarity 66.7%; Pred. No. 7.5;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATELOTTIH 9

76 AEELSTTVH 84

RESULT 13

C95022

hypothetical protein SP0191 [imported] - Streptococcus pneumoniae (strain TIGR4)

C;Species: Streptococcus pneumoniae

C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004

C;Accession: C95022

R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Hej

son, J.D.; Umeyam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzap

Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison

A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: C95022

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-189 <KUR>

A;Cross-references: UNIPROT:Q97SX2; GB:AE005672; PIDN:AAK74372.1; PID:G14971659; GSPDB:

A;Experimental source: strain TIGR4

C;Genetics:

A;Gene: SP0191

Query Match 73.3%; Score 33; DB 2; Length 189;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATELOTT 7

136 ATELOTT 142

RESULT 14

F97893

hypothetical protein spr0174 [imported] - Streptococcus pneumoniae (strain R6)

C;Species: Streptococcus pneumoniae

C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004

C;Accession: F97893

R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.;

e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;

Y, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.

A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A;Reference number: A97872; MUID:21429245; PMID:11544234

A;Accession: F97893

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-189 <KUR>

A;Cross-references: UNIPROT:Q8CZ90; GB:AE007317; PIDN:AAK98978.1; PID:G15457717; GSPDB:

C;Genetics:

A;Gene: spr0174

Query Match 73.3%; Score 33; DB 2; Length 189;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATELOTT 7

136 ATELOTT 142

RESULT 15

T34436

hypothetical protein K11H12.1 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004

C;Accession: T34436

R;Bradehaw, H.

submitted to the EMBL Data Library, February 1997
A;Description: The sequence of C. elegans cosmid K11H12.
A;Reference number: Z21526
A;Accession: T34436
A;Status: Preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-108 <BRA>
A;Cross-references: UNIPROT:P91375; EMBL:U88168; PIDN:AAC24398.1; GSPDB:GN00022; CESP:K11H12
A;Experimental source: strain Bristol N2; clone K11H12
C;Genetics:
A;Gene: CESP:K11H12.1
A;Map position: 4
A;Introns: 22/3; 61/3
C;Superfamily: b01A protein

Query Match 71.1%; Score 32; DB 2; Length 108;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ATELQTTIH 9
| | | | |
Db 71 AKELATTWH 79

Search completed: June 29, 2005, 01:38:52
Job time : 13.2747 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:28:22 ; Search time 54.2473 Seconds
(without alignments)
84.958 Million cell updates/sec

Title: US-08-170-344-75
Perfect score: 45
Sequence: 1 ATELQTTIH 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	91.1	138	2	Q919D2 human papil
2	41	91.1	143	2	Q919B6 human papil
3	41	91.1	143	2	Q919C4 human papil
4	41	91.1	151	2	O12335 human papil
5	41	91.1	151	2	O12336 human papil
6	41	91.1	151	2	Q76T50 human papil
7	41	91.1	151	2	Q77816 human papil
8	41	91.1	151	2	Q77E16 human papil
9	41	91.1	151	2	Q77JC7 human papil
10	41	91.1	151	2	Q77ZJ5 human papil
11	41	91.1	151	2	Q80963 human papil
12	41	91.1	151	2	Q80966 human papil
13	41	91.1	151	2	Q89640 human papil
14	41	91.1	151	2	Q89648 human papil
15	41	91.1	151	2	Q89708 human papil
16	41	91.1	151	2	Q89755 human papil
17	41	91.1	151	2	Q89852 human papil
18	41	91.1	151	2	Q89887 human papil
19	41	91.1	151	2	Q8B564 human papil
20	41	91.1	151	2	Q8BB19 human papil
21	41	91.1	151	2	Q8BB20 human papil
22	41	91.1	151	2	Q8BB21 human papil
23	41	91.1	151	2	Q8W8C3 human papil
24	41	91.1	151	2	Q9W931 human papil
25	41	91.1	151	2	Q9WMP2 human papil
26	41	91.1	151	2	Q9WMP3 human papil
27	41	91.1	151	2	Q9WMP4 human papil
28	41	91.1	151	2	Q9WMP5 human papil
29	41	91.1	158	1	V56_HPV16
30	41	91.1	158	2	Q8JMU8 human papil
31	41	91.1	158	2	Q8QHNO human papil

32 41 91.1 158 2 Q8QHP5 human papil
33 41 91.1 158 2 Q8QHT0 human papil
34 41 91.1 158 2 Q8QRD5 human papil
35 41 91.1 158 2 Q8QRD6 human papil
36 41 91.1 158 2 Q8QRD7 human papil
37 41 91.1 158 2 Q8QRD8 human papil
38 41 91.1 158 2 Q8QRD9 human papil
39 41 91.1 158 2 Q8QRE0 human papil
40 41 91.1 158 2 Q8QRE1 human papil
41 41 91.1 158 2 Q71B17 human papil
42 41 91.1 158 2 Q9QDH3 human papil
43 41 91.1 158 2 Q9QDH5 human papil
44 41 91.1 158 2 Q9QDH9 human papil
45 41 91.1 158 2 Q9WH13 human papil

ALIGNMENTS

RESULT 1

Q919D2 PRELIMINARY; PRT; 138 AA.
AC Q919D2; 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404694; AAL01345.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1 1
SQ SEQUENCE 138 AA; 16696 MW; 481B5AEA90895FC2 CRC64;

Query Match 91.1%; Score 41; DB 2; Length 138;

Best Local Similarity 100.0%; Pred. No. 1.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TELQTTIH 9

DB 4 TELQTTIH 11

RESULT 2

Q919B6 PRELIMINARY; PRT; 143 AA.
AC Q919B6; 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).

DR EMBL; AF404702; AAL01361.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1 1
SQ SEQUENCE 143 AA; 17272 MW; 071F14BE3E6BE2AC CRC64;

Query Match 91.1%; Score 41; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TELQTTIH 9
|||||
Db 9 TELQTTIH 16

RESULT 3

O12336 PRELIMINARY; PRT; 143 AA.
AC Q19C4
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=21846229; PubMed=11857370;
RX Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RA "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404698; AAL01353.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1 1
SQ SEQUENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;

Query Match 91.1%; Score 41; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TELQTTIH 9
|||||
Db 9 TELQTTIH 16

RESULT 4

O12335 PRELIMINARY; PRT; 151 AA.
AC O12335;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=97437474; PubMed=9292007;
RX Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RA "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003015; AAB70732.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.

DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18238 MW; BEF32A8B016CC88B CRC64;

Query Match 91.1%; Score 41; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TELQTTIH 9
|||||
Db 17 TELQTTIH 24

RESULT 5

O12336 PRELIMINARY; PRT; 151 AA.
AC O12336;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=97437474; PubMed=9292007;
RX Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RA "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003016; AAB70733.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;

Query Match 91.1%; Score 41; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TELQTTIH 9
|||||
Db 17 TELQTTIH 24

RESULT 6

O76TSO PRELIMINARY; PRT; 151 AA.
AC O76TSO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=96079021; PubMed=7494284;
RX Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RA "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RL L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.

RA Farmer A.D.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U34114; AA91661.1; -;
 DR EMBL; U34125; AA91672.1; -;
 DR EMBL; U34130; AA91677.1; -;
 DR EMBL; U34131; AA91678.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;

Query Match 91.1%; Score 41; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TELQTTIH 9
 |||||
 Db 17 TELQTTIH 24

RESULT 7

Q77816 ID Q77816 PRELIMINARY; PRT; 151 AA.
 AC Q77816;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE E6 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20112892; PubMed=10644829;
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F., Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
 RT "Analysis of human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
 RT J. Gen. Virol. 81:317-325(2000).
 DR EMBL; AJ388056; CAB45104.1; -;
 DR EMBL; AJ388061; CAB45114.1; -;
 DR EMBL; AJ388066; CAB45124.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18334 MW; PF8F2A2FCBA6C02 CRC64;

Query Match 91.1%; Score 41; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TELQTTIH 9
 |||||
 Db 17 TELQTTIH 24

RESULT 8

Q77E16 ID Q77E16 PRELIMINARY; PRT; 151 AA.
 AC Q77E16;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE E6 oncoprotein (E6 protein).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Ponglikitmongkol M., Vaeteewoottacharn K.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20112892; PubMed=10644829;
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F., Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
 RT "Analysis of human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
 RT J. Gen. Virol. 81:317-325(2000).
 DR EMBL; AF469197; AA015691.1; -;
 DR EMBL; AJ388063; CAB45118.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CFIP CRC64;

Query Match 91.1%; Score 41; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TELQTTIH 9
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 Db 17 TELQTTIH 24

RESULT 9

Q77JC7 ID Q77JC7 PRELIMINARY; PRT; 151 AA.
 AC Q77JC7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Early transforming protein E6 variant (Transforming protein E6).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Xinjiang;
 RA Ma Z., Qian D., Ma J., Lin R., Ming W., Zhong Z., Zhang Q., Zhang F.;
 RT "Cloning and Sequencing of HPV16 E6 gene from Cervical Carcinoma Biopsies in Xinjiang."
 RL Sheng Wu Hua Xue Yu Sheng Wu Wu Li Jin Zhan 0:0-0(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20112892; PubMed=10644829;
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F., Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
 RT "Analysis of human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
 RT J. Gen. Virol. 81:317-325(2000).
 DR EMBL; AF469197; AA015691.1; -;
 DR EMBL; AJ388063; CAB45118.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CFIP CRC64;

RESULT 10

Q77E16 ID Q77E16 PRELIMINARY; PRT; 151 AA.
 AC Q77E16;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE E6 oncoprotein (E6 protein).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.

DR EMBL; AY089951; AAM11875.1; -;
 DR EMBL; AY089954; AAM11881.1; -;
 DR EMBL; AY112683; AAM51854.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18320 MW; 617D2A2FDB4F8C17 CRC64;

Query Match 91.1%; Score 41; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TELQTTIH 9
 |||||
 Db 17 TELQTTIH 24

RESULT 10

Q7725 Q77ZJ5 PRELIMINARY; PRT; 151 AA.
 AC Q77ZJ5;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE E6 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OC NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97437474; PubMed=9292007;
 RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
 RA Beth-Giraldo E., Giraldo G.;
 RT "Sequence variations and viral genomic state of human papillomavirus
 type 16 in penile carcinomas from Ugandan patients.";
 RL J. Gen. Virol. 78:2199-2208(1997).
 DR EMBL; AF003019; AAB70735.1; -;
 DR EMBL; AF003018; AAB70735.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18221 MW; 60CD2A34DAF48CB7 CRC64;

Query Match 91.1%; Score 41; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TELQTTIH 9
 |||||
 Db 17 TELQTTIH 24

RESULT 11

Q80963 Q80963 PRELIMINARY; PRT; 151 AA.
 AC Q80963;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Early transforming protein E6.
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OC NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96079021; PubMed=7494284;
 RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
 RA Jenison S.A.;
 RT "Human papillomavirus type 16 variant lineages in United States

RT populations characterized by nucleotide sequence analysis of the E6,
 RT L2, and L1 coding segments";
 RL J. Virol. 69:7743-7753(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Farmer A.D.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 RL EMBL; U34122; AAA91669.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18291 MW; 97C7028D5169382D CRC64;

Query Match 91.1%; Score 41; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TELQTTIH 9
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 Db 17 TELQTTIH 24

RESULT 12

Q80966 Q80966 PRELIMINARY; PRT; 151 AA.
 AC Q80966; O12650; O12651; O12652; O12925; O12926; O12927; Q80962;
 AC Q80964; Q80965;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE E6 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OC NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97437474; PubMed=9292007;
 RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
 RA Beth-Giraldo E., Giraldo G.;
 RT "Sequence variations and viral genomic state of human papillomavirus
 type 16 in penile carcinomas from Ugandan patients.";
 RL J. Gen. Virol. 78:2199-2208(1997).
 DR EMBL; AF003019; AAB70735.1; -;
 DR EMBL; AF003017; AAB70734.1; -;
 DR EMBL; AF472508; AAO15697.1; -;
 DR EMBL; AJ388068; CAB45128.1; -;
 DR EMBL; AF003013; AAB70730.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;

Query Match 91.1%; Score 41; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 1.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TELQTTIH 9
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Db 17 TELQTTIH 24

RESULT 13
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AC Q89640;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A. PubMed=7494284;
RX MEDLINE=96079021; Halpern A.L., Stewart A.C., Hildesheim A.,
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RT J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RA Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EMBL; U34129; AAA91676.1; -.
DR EMBL; AF469198; AA015693.1; -.
DR EMBL; U34115; AAA91662.1; -.
DR EMBL; U34120; AAA91667.1; -.
DR EMBL; U34124; AAA91671.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18348 MW; F83F2A2FCF0A6CB2 CRC64;

Query Match 91.1%; Score 41; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TELQTTIH 9
Db 17 TELQTTIH 24

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AC Q89648; O12653; O12654; O12928; O12929;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RT J. Virol. 69:7743-7753(1995).
RN [2]
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RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RA Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EMBL; U34110; AAA91657.1; -.
DR EMBL; U34109; AAA91656.1; -.
DR EMBL; U34113; AAA91660.1; -.
DR EMBL; U34135; AAA91682.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18221 MW; 60CD2A34DAF48CE7 CRC64;

Query Match 91.1%; Score 41; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TELQTTIH 9
Db 17 TELQTTIH 24

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AC Q89708;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RT J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RA Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EMBL; U34128; AAA91675.1; -.
DR EMBL; U34117; AAA91664.1; -.
DR EMBL; U34118; AAA91665.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CF1F CRC64;

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Qy 2 TELQTTIH 9
Db 17 TELQTTIH 24

Search completed: June 29, 2005, 01:34:51
Job time : 54.2473 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:37:59 ; Search time 16.8626 Seconds
(without alignments)
39.842 Million cell updates/sec

Title: US-08-170-344-75
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	41	91.1	20	2 US-08-934-915-159	Sequence 159, App
3	41	91.1	30	1 US-08-363-586-4	Sequence 4, Appli
4	41	91.1	30	4 US-09-980-523A-4	Sequence 4, Appli
5	41	91.1	158	4 US-09-980-523A-2	Sequence 2, Appli
6	41	91.1	162	1 US-08-316-239B-3	Sequence 3, Appli
7	41	91.1	162	1 US-08-316-239B-4	Sequence 4, Appli
8	41	91.1	172	3 US-08-860-165-14	Sequence 14, Appl
9	41	91.1	172	3 US-09-359-382-14	Sequence 14, Appl
10	41	91.1	182	1 US-08-117-083-10	Sequence 10, Appl
11	41	91.1	266	3 US-08-860-165-10	Sequence 10, Appl
12	41	91.1	266	3 US-09-359-382-10	Sequence 10, Appl
13	41	91.1	266	4 US-08-367-309A-1	Sequence 1, Appli
14	41	91.1	273	3 US-09-485-885-4	Sequence 4, Appli
15	41	91.1	292	3 US-09-485-885-10	Sequence 10, Appl
16	41	91.1	371	3 US-09-485-885-6	Sequence 6, Appli
17	41	91.1	390	3 US-09-485-885-14	Sequence 14, Appl
18	34	75.6	1128	4 US-09-252-991A-31032	Sequence 31032, A
19	33	73.3	189	4 US-09-583-110-4167	Sequence 4167, Ap
20	33	73.3	196	4 US-09-107-433-4096	Sequence 4096, Ap
21	31	68.9	9	1 US-08-787-547-102	Sequence 102, App
22	31	68.9	9	3 US-08-159-339A-248	Sequence 248, App
23	31	68.9	50	3 US-09-065-474-165	Sequence 165, App
24	31	68.9	50	3 US-09-557-034-165	Sequence 165, App
25	31	68.9	213	4 US-09-107-532A-3797	Sequence 3797, Ap
26	31	68.9	302	2 US-09-031-485-38	Sequence 38, Appl
27	31	68.9	302	2 US-08-847-429A-38	Sequence 38, Appl

28	31	68.9	302	3	US-09-065-474-38	Sequence 38, Appl
29	31	68.9	302	3	US-09-557-034-38	Sequence 38, Appl
30	31	68.9	303	2	US-09-031-485-23	Sequence 23, Appl
31	31	68.9	303	2	US-08-847-429A-23	Sequence 23, Appl
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33	31	68.9	303	3	US-09-557-034-23	Sequence 23, Appl
34	31	68.9	352	3	US-09-065-474-139	Sequence 139, App
35	31	68.9	352	3	US-09-557-034-139	Sequence 139, App
36	31	68.9	937	3	US-09-005-180A-4	Sequence 4, Appli
37	31	68.9	944	4	US-09-538-092-452	Sequence 452, App
38	31	68.9	1745	2	US-09-031-485-33	Sequence 33, Appl
39	31	68.9	1745	2	US-08-847-429A-33	Sequence 33, Appl
40	31	68.9	1745	3	US-09-065-474-33	Sequence 33, Appl
41	31	68.9	1745	3	US-09-557-034-33	Sequence 33, Appl
42	30	66.7	59	1	US-08-118-270-256	Sequence 256, App
43	30	66.7	59	5	PCT-US93-08528-256	Sequence 256, App
44	30	66.7	108	4	US-09-489-039A-12134	Sequence 12134, A
45	30	66.7	230	4	US-09-252-991A-22090	Sequence 22090, A

ALIGNMENTS

RESULT 1
US-07-909-122-3
; Sequence 3, Application US/07909122
; Patent No. 5415995
; GENERAL INFORMATION:
; APPLICANT: SCHOOLNIK, GARY K.
; APPLICANT: PALEFSKY, JOEL M.
; TITLE OF INVENTION: DIAGNOSTIC PEPTIDES OF HUMAN PAPILLOMA
; TITLE OF INVENTION: VIRUS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/909,122
; FILING DATE: 19920706
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: BENZ, WILLIAM H.
; REGISTRATION NUMBER: 25,952
; REFERENCE/DOCKET NUMBER: 28600-20105.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-909-122-3

Query Match 91.1%; Score 41; DB 1; Length 14;
Best Local Similarity 100.0%; Pred.No. 0.055;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TELQTTIH 9

Db 1 TELQTTIH 8

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; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,586
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/909,296
; FILING DATE: 09-JUL-1992
; APPLICATION NUMBER: EP 9111720.8
; FILING DATE: 13-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wadler, Linda A.
; REGISTRATION NUMBER: 33,218
; REFERENCE/DOCKET NUMBER: 02481-1195-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 4:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-363-586-4

Query Match 91.1%; Score 41; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TELQTTIH 9
Db 17 TELQTTIH 24

RESULT 4
US-09-980-523A-4
; Sequence 4, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO81 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Human Papillomavirus
; US-09-980-523A-4

Query Match 91.1%; Score 41; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,586
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/909,296
; FILING DATE: 09-JUL-1992
; APPLICATION NUMBER: EP 9111720.8
; FILING DATE: 13-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wadler, Linda A.
; REGISTRATION NUMBER: 33,218
; REFERENCE/DOCKET NUMBER: 02481-1195-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 4:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-363-586-4

Query Match 91.1%; Score 41; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TELQTTIH 9
Db 17 TELQTTIH 24

RESULT 4
US-09-980-523A-4
; Sequence 4, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO81 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Human Papillomavirus
; US-09-980-523A-4

Query Match 91.1%; Score 41; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 2 TELQTTIH 9
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Db 10 TELQTTIH 17

RESULT 5
US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCES
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO/01 AO INS
; CURRENT APPLICATION NUMBER: US/09/980.523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 91.1%; Score 41; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.81; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TELQTTIH 9
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Db 24 TELQTTIH 31

RESULT 6
US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316.239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 91.1%; Score 41; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.83; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TELQTTIH 9

; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 91.1%; Score 41; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.83; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TELQTTIH 9
| | | | |
Db 24 TELQTTIH 31

RESULT 7
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Cancer
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316.239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

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Db          24 TELQTTIH 31
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RESULT 8
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14
Query Match          91.1%; Score 41; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          2 TELQTTIH 9
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Db          93 TELQTTIH 100
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RESULT 9
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14
Query Match          91.1%; Score 41; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          2 TELQTTIH 9
|||||
Db          93 TELQTTIH 100
|||||
RESULT 10
US-08-117-083-10
; Sequence 10, Application US/08117083
; Patent No. 5715054
; GENERAL INFORMATION:
; APPLICANT: Bournsnel, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
; OTHER INFORMATION: /note= "Xaa refers to stop codon in
; OTHER INFORMATION: the open reading frame."
US-08-117-083-10
Query Match          91.1%; Score 41; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.94;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          2 TELQTTIH 9
|||||
Db          25 TELQTTIH 32
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RESULT 11
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
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; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; PRIOR FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match          91.1%; Score 41; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TELQTTIH 9
Db 24 TELQTTIH 31

RESULT 12
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match          91.1%; Score 41; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TELQTTIH 9
Db 24 TELQTTIH 31

RESULT 13
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
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; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
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; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match          91.1%; Score 41; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TELQTTIH 9
Db 24 TELQTTIH 31

RESULT 14
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match          91.1%; Score 41; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TELQTTIH 9
Db 130 TELQTTIH 137

RESULT 15
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10

Query Match      91.1%; Score 41; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 TELQTTIH 9
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Db      149 TELQTTIH 156

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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Title: US-08-170-344-75

Perfect score: 45

Sequence: 1 ATELQTTIH 9

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- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
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- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	41	91.1	21	16	US-10-476-570-8
5	41	91.1	30	16	US-10-476-570-53
6	41	91.1	30	17	US-10-858-384-4
7	41	91.1	32	16	US-10-476-570-9
8	41	91.1	33	16	US-10-476-570-19
9	41	91.1	151	14	US-10-177-390-6
10	41	91.1	151	17	US-10-484-063-20
11	41	91.1	151	17	US-10-484-063-27

12	41	91.1	158	17	US-10-858-384-2	Sequence 2, Appli
13	41	91.1	158	17	US-10-367-057-16	Sequence 16, Appl
14	41	91.1	171	16	US-10-472-724-2	Sequence 2, Appli
15	41	91.1	266	9	US-09-367-309A-1	Sequence 1, Appli
16	41	91.1	273	13	US-10-000-903-4	Sequence 4, Appli
17	41	91.1	273	17	US-10-899-771-4	Sequence 4, Appli
18	41	91.1	292	13	US-10-000-903-10	Sequence 10, Appl
19	41	91.1	292	17	US-10-899-771-10	Sequence 10, Appl
20	41	91.1	371	13	US-10-000-903-6	Sequence 6, Appli
21	41	91.1	371	17	US-10-899-771-6	Sequence 6, Appli
22	41	91.1	390	13	US-10-000-903-14	Sequence 14, Appl
23	41	91.1	390	17	US-10-899-771-14	Sequence 14, Appl
24	41	91.1	536	15	US-10-367-095-10	Sequence 10, Appl
25	41	91.1	536	16	US-10-368-046-10	Sequence 10, Appl
26	41	91.1	536	16	US-10-367-367-10	Sequence 10, Appl
27	41	91.1	536	17	US-10-918-337-10	Sequence 10, Appl
28	36	80.0	126	17	US-10-484-063-2	Sequence 2, Appli
29	35	77.8	120	16	US-10-767-701-50300	Sequence 50300, A
30	34	75.6	120	16	US-10-767-701-52305	Sequence 52305, A
31	34	75.6	472	15	US-10-424-599-165549	Sequence 165549,
32	34	75.6	1317	9	US-09-815-242-5118	Sequence 5118, Ap
33	34	75.6	1317	15	US-10-282-122A-43495	Sequence 43495, A
34	33	73.3	47	16	US-10-437-963-128975	Sequence 128975,
35	33	73.3	74	16	US-10-425-115-223782	Sequence 223782,
36	33	73.3	74	16	US-10-425-115-264586	Sequence 264586,
37	33	73.3	121	16	US-10-425-115-240437	Sequence 240437,
38	33	73.3	176	14	US-10-156-761-8767	Sequence 8767, Ap
39	33	73.3	189	16	US-10-474-776-223	Sequence 223, App
40	33	73.3	189	17	US-10-472-928-192	Sequence 192, App
41	33	73.3	258	15	US-10-264-237-1481	Sequence 1481, Ap
42	33	73.3	995	15	US-10-094-749-2626	Sequence 2626, Ap
43	32	71.1	201	15	US-10-275-026A-182	Sequence 182, App
44	32	71.1	222	15	US-10-369-493-15948	Sequence 15948, A
45	32	71.1	267	16	US-10-425-115-223163	Sequence 223163,

ALIGNMENTS

RESULT 1

US-10-476-570-20
; Sequence 20, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from B6 and/or E7
; TITLE OF INVENTION: Papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 17-31
US-10-476-570-20

Query Match 91.1%; Score 41; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TELQTTIH 9
|||||
Db 8 TELQTTIH 15

RESULT 2

US-10-476-570-21
; Sequence 21, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 20-34
US-10-476-570-21

Query Match 91.1%; Score 41; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.28; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0;

QY 2 TELQTTIH 9
|||||
Db 5 TELQTTIH 12

RESULT 3

US-10-476-570-22
; Sequence 22, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 24-38
US-10-476-570-22

Query Match 91.1%; Score 41; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.28; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0;

QY 2 TELQTTIH 9
|||||
Db 1 TELQTTIH 8

RESULT 4

US-10-476-570-8
; Sequence 8, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 21
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-34
US-10-476-570-8

Query Match 91.1%; Score 41; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.41; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0;

QY 2 TELQTTIH 9
|||||
Db 11 TELQTTIH 18

RESULT 5

US-10-476-570-53
; Sequence 53, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 30

; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 15-44
US-10-476-570-53

Query Match 91.1%; Score 41; DB 16; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TELQTTIH 9
| | | | |
Db 10 TELQTTIH 17

RESULT 6
US-10-858-384-4
; Sequence 4, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
; OTHER INFORMATION: for E6 of HPV
US-10-858-384-4

Query Match 91.1%; Score 41; DB 17; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TELQTTIH 9
| | | | |
Db 10 TELQTTIH 17

RESULT 7
US-10-476-570-9
; Sequence 9, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04

; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 32
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-45
US-10-476-570-9

Query Match 91.1%; Score 41; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TELQTTIH 9
| | | | |
Db 11 TELQTTIH 18

RESULT 8
US-10-476-570-19
; Sequence 19, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 33
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-46
US-10-476-570-19

Query Match 91.1%; Score 41; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TELQTTIH 9
| | | | |
Db 11 TELQTTIH 18

RESULT 9
US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerps Innovatiecentrum
; TITLE OF INVENTION: Improved transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6

; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6

Query Match 91.1%; Score 41; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TELQTTIH 9
| | | | |
Db 17 TELQTTIH 24

RESULT 10
US-10-484-063-20
; Sequence 20, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; TITLE OF INVENTION: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-20

Query Match 91.1%; Score 41; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TELQTTIH 9
| | | | |
Db 17 TELQTTIH 24

RESULT 11
US-10-484-063-27
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-484-063-27

Query Match 91.1%; Score 41; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TELQTTIH 9
| | | | |
Db 17 TELQTTIH 24

RESULT 12
US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US2005003025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match 91.1%; Score 41; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TELQTTIH 9
| | | | |
Db 24 TELQTTIH 31

RESULT 13
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match 91.1%; Score 41; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TELQTTIH 9
| | | | |

Db 24 TELQTTIH 31

RESULT 14

US-10-472-724-2

; Sequence 2, Application US/10472724

; Publication No. US20040171806A1

; GENERAL INFORMATION:

; APPLICANT: Cid-Arregui, Angel

; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination

; FILE REFERENCE: 4121-154

; CURRENT APPLICATION NUMBER: US/10/472.724

; CURRENT FILING DATE: 2003-09-17

; PRIOR APPLICATION NUMBER: PCT/EP02/03271

; PRIOR FILING DATE: 2002-03-22

; PRIOR APPLICATION NUMBER: EP 01107271.7

; PRIOR FILING DATE: 2001-03-23

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2

; LENGTH: 171

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetic Construct

US-10-472-724-2

Query Match 91.1%; Score 41; DB 16; Length 171;

Best Local Similarity 100.0%; Pred. No. 3.9;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TELQTTIH 9

Db 29 TELQTTIH 36

RESULT 15

US-09-367-309A-1

; Sequence 1, Application US/09367309A

; Publication No. US20020081329A1

; GENERAL INFORMATION:

; APPLICANT: MACFARLAN, RODERICK I.

; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES

; FILE REFERENCE: 017227/0149

; CURRENT APPLICATION NUMBER: US/09/367.309A

; CURRENT FILING DATE: 1999-08-11

; PRIOR APPLICATION NUMBER: PCT/AU98/00080

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: AU PO 5178

; PRIOR FILING DATE: 1997-02-19

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 266

; TYPE: PRT

; ORGANISM: Human papillomavirus type 16

US-09-367-309A-1

Query Match 91.1%; Score 41; DB 9; Length 266;

Best Local Similarity 100.0%; Pred. No. 6.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TELQTTIH 9

Db 24 TELQTTIH 31

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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:28:22 ; Search time 54.2473 Seconds
(without alignments)
84.958 Million cell updates/sec

Title: US-08-170-344-74
Perfect score: 49
Sequence: 1 RAHYNIVTF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	65	2 Q8B563	Q8B563 human papil
2	49	100.0	77	2 Q8B5P5	Q8B5P5 human papil
3	49	100.0	93	2 Q9QDH2	Q9QDH2 human papil
4	49	100.0	93	2 Q9QDH4	Q9QDH4 human papil
5	49	100.0	93	2 Q9QDH6	Q9QDH6 human papil
6	49	100.0	93	2 Q9QDH8	Q9QDH8 human papil
7	49	100.0	94	2 Q8B5P6	Q8B5P6 human papil
8	49	100.0	98	1 VE7 HPV16	P03129 human papil
9	49	100.0	98	2 O11650	O11650 human papil
10	49	100.0	98	2 O12337	O12337 human papil
11	49	100.0	98	2 O12338	O12338 human papil
12	49	100.0	98	2 Q9QDH2	Q9QDH2 human papil
13	49	100.0	98	2 Q9QDH3	Q9QDH3 human papil
14	49	100.0	98	2 Q9QDH4	Q9QDH4 human papil
15	49	100.0	98	2 Q9QDH6	Q9QDH6 human papil
16	49	100.0	98	2 Q9QDH8	Q9QDH8 human papil
17	49	100.0	98	2 Q778H5	Q778H5 human papil
18	39	79.6	405	2 Q9UXV2	Q9UXV2 pyrococcus
19	38	77.6	651	2 Q91821	Q91821 xenopus lae
20	37	75.5	162	2 Q81PX2	Q81PX2 bacillus an
21	37	75.5	611	1 GLMS_NE1MA	O9JWN9 n glucosami
22	37	75.5	611	1 GLMS_NE1MB	Q9K1P9 n glucosami
23	37	75.5	1452	2 Q27028	Q27028 theileria p
24	36	73.5	196	2 Q988D2	Q988D2 thizobium l
25	36	73.5	279	1 XJ86 YEAST	P47153 saccharomyc
26	36	73.5	727	1 VP4 RDVA	P22474 rice dwarf
27	36	73.5	727	1 VP4 RDVF	Q85436 rice dwarf
28	36	73.5	867	2 Q7WZ88	Q7WZ88 nonomurea
29	36	73.5	10287	2 Q6LEZ3	Q6LEZ3 plasmodium
30	35	71.4	266	2 Q8KWG0	Q8KWG0 staphylococ
31	35	71.4	290	2 Q93197	Q93197 staphylococ

32 35 71.4 355 2 Q6ANS6 Q6ans6 desulfotale
33 35 71.4 479 2 Q75F99 Q75f99 ashbya goss
34 34 69.4 61 2 Q6WU90 Q6wu90 lactobacill
35 34 69.4 98 1 VE7 HPV31 P17387 human papil
36 34 69.4 98 2 Q6T377 Q6t377 human papil
37 34 69.4 163 2 Q88XV6 Q88xv6 lactobacill
38 34 69.4 233 2 Q8IIV5 Q8iiv5 plasmodium
39 34 69.4 240 2 Q8RE78 Q8re78 fusobacteri
40 34 69.4 306 2 Q716C2 Q716c2 bacterioph
41 34 69.4 307 2 Q8GJ20 Q8gj20 escherichia
42 34 69.4 350 2 Q7UDN7 Q7udn7 shigella fl
43 34 69.4 357 2 Q6A8F3 Q6a8f3 propionibac
44 34 69.4 390 2 Q8GJ19 Q8gj19 escherichia
45 34 69.4 391 2 Q8GJ14 Q8gj14 escherichia

ALIGNMENTS

RESULT 1

Q8B563 ID Q8B563 PRELIMINARY; PRT; 65 AA.
AC Q8B563;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE E7 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF548023; AA016240.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 65
SQ SEQUENCE 65 AA; 7373 MW; E9D74D7923700195 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
Db 49 RAHYNIVTF 57

RESULT 2

Q8B5P5 ID Q8B5P5 PRELIMINARY; PRT; 77 AA.
AC Q8B5P5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE E7 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF469198; AA015694.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 77
SQ SEQUENCE 77 AA; 8782 MW; CSDE3A7E546AC31B CRC64;

Query Match 100.0%; Score 49; DB 2; Length 77;

Best Local Similarity 100.0%; Pred. No. 0.031; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 RAHYNIVTF 9
| | | | | | | |
Db 49 RAHYNIVTF 57

RESULT 3

ID Q9QDH2 PRELIMINARY; PRT; 93 AA.
AC Q9QDH2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187869; AAF13399.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 49; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
| | | | | | | |
Db 49 RAHYNIVTF 57

RESULT 4

ID Q9QDH4 PRELIMINARY; PRT; 93 AA.
AC Q9QDH4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187868; AAF13397.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 49; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
| | | | | | | |
Db 49 RAHYNIVTF 57

RESULT 5

ID Q9QDH6 PRELIMINARY; PRT; 93 AA.

AC Q9QDH6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187867; AAF13395.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10513 MW; 92C7054341326A1F CRC64;

Query Match 100.0%; Score 49; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
| | | | | | | |
Db 49 RAHYNIVTF 57

RESULT 6

ID Q9QDH8 PRELIMINARY; PRT; 93 AA.
AC Q9QDH8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187866; AAF13393.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 49; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
| | | | | | | |
Db 49 RAHYNIVTF 57

RESULT 7

ID Q8B5P6 PRELIMINARY; PRT; 94 AA.
AC Q8B5P6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE E7 oncoprotein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.

RA Ponglikitmongkol M., Vaeteewoottacharn K.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF469197; AAO15692.1; -
 DR InterPro: IPR000148; Papvi_E7.
 DR Pfam: PF00527; E7; 1;
 FT NON_TER 94 94
 SQ SEQUENCE 94 AA; 10555 MW; 7CC3281BB2AE2C8A CRC64;

Query Match 100.0%; Score 49; DB 2; Length 94;
 Best Local Similarity 100.0%; Pred. No. 0.039;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
 |||||
 Db 49 RAHYNIVTF 57

RESULT 8
 ID VE7 HPV16 STANDARD; PRT; 98 AA.
 AC P03129;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE E7 protein.
 GN Name=E7;
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85246220; PubMed=2990099;
 RA Seedorf K., Krammer G., Durst M., Suhai S., Rowkamp W.G.;
 RT "Human papillomavirus type 16 DNA sequence.";
 RL Virology 145:181-185(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90218027; PubMed=2157796;
 RA Schneider-Maunoury S., Pebau-Arnaudet G., Breitburd F., Orth G.;
 RT "Expression of the human papillomavirus type 16 genome in SK-v cells,
 a line derived from a vulvar intraepithelial neoplasia.";
 RL J. Gen. Virol. 71:809-817(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Lee H.P.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
 RA Beth-Giraldo E., Giraldo G.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP FUNCTION.

RA Phelps W.C., Yee C.L., Munger K., Howley P.M.;
 RL "The human papillomavirus type 16 E7 gene encodes transactivation and
 RT transformation functions similar to those of adenovirus E1A.";
 RL Cell 53:539-547(1988).
 CC -1- FUNCTION: E7 protein has both transforming and trans-activating
 CC activities.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; K02718; AAA46940.1; -
 DR EMBL; D00735; BAA06633.1; -
 DR EMBL; U76411; AAB18962.1; -

DR EMBL; U76412; AAB18963.1; -
 DR EMBL; U76413; AAB18964.1; -
 DR EMBL; AF003020; AAB70737.1; -
 DR EMBL; AF003023; AAB70740.1; -
 DR EMBL; AF003024; AAB70741.1; -
 DR EMBL; AF003025; AAB70742.1; -
 DR EMBL; AF003026; AAB70743.1; -
 DR PIR; A03688; W7WLHS.
 DR InterPro: IPR000148; Papvi_E7.
 DR Pfam: PF00527; E7; 1;
 KW DNA-binding; Early protein; Oncogene; Trans-acting factor;
 KW Transcription regulation.
 FT SITE 58 61 C-XX-C motif-1.
 FT SITE 91 94 C-XX-C motif-2.
 SQ SEQUENCE 98 AA; 11022 MW; 98D612534CD2C9EB CRC64;

Query Match 100.0%; Score 49; DB 1; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.041;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
 |||||
 Db 49 RAHYNIVTF 57

RESULT 9
 ID O11650 PRELIMINARY; PRT; 98 AA.
 AC O11650;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Putative transforming protein E7.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97407827; PubMed=9264576; DOI=10.1006/gyno.1997.4756;
 RA Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Chang W.H.,
 RA Lee H.P.;
 RT "Major sequence variants in E7 gene of human papillomavirus type 16
 RL from cervical cancerous and noncancerous lesions of Korean women.";
 RL Gynecol. Oncol. 66:275-281(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Song Y.-S., Kee S.-H., Kim J.-W., Park N.-H., Kang S.-B., Chang W.-H.,
 RA Lee H.-P.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Terai M., Ma Z., Burk R.D.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22192962; PubMed=12195358;
 RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
 RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
 RT "Human papillomavirus type 16 intratypic variant infection and risk
 RL for cervical neoplasia in southern China.";
 RL J. Infect. Dis. 186:696-700(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Terai M., Fu L., Ma Z., Burk R.D.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U76404; AAC58243.1; -
 DR EMBL; AF472509; AAO15706.1; -
 DR EMBL; AF486326; AAL96631.1; -
 DR EMBL; AF486327; AAL96632.1; -
 DR EMBL; AF486330; AAL96635.1; -
 DR EMBL; AF486331; AAL96636.1; -
 DR EMBL; AF486332; AAL96637.1; -

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DR EMBL; AF486333; AAL96638.1; -
DR EMBL; AF486334; AAL96639.1; -
DR EMBL; AF486336; AAL96641.1; -
DR EMBL; AF486338; AAL96643.1; -
DR EMBL; AF486346; AAL96651.1; -
DR EMBL; AF486350; AAL96655.1; -
DR EMBL; AF486351; AAL96656.1; -
DR EMBL; AF534061; AAQ10404.1; -
DR InterPro; IPR00148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 100.0%; Score 49; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
Db 49 RAHYNIVTF 57

RESULT 10
O12337
ID O12337 PRELIMINARY; PRT; 98 AA.
AC O12337;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003021; AAB70738.1; -
DR InterPro; IPR00148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11056 MW; 19DEB8F14CD2C705 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
Db 49 RAHYNIVTF 57

RESULT 11
O12338
ID O12338 PRELIMINARY; PRT; 98 AA.
AC O12338;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003022; AAB70739.1; -
DR EMBL; AF477385; AAM03025.1; -
DR InterPro; IPR00148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10969 MW; 9BD612534CCBA59B CRC64;

Query Match 100.0%; Score 49; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
Db 49 RAHYNIVTF 57

RESULT 12
Q8QRD2
ID Q8QRD2 PRELIMINARY; PRT; 98 AA.
AC Q8QRD2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486345; AAL96650.1; -
DR InterPro; IPR00148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11045 MW; 9C4F8C534CD76C4B CRC64;

Query Match 100.0%; Score 49; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
Db 49 RAHYNIVTF 57

RESULT 13
Q8QRD3
ID Q8QRD3 PRELIMINARY; PRT; 98 AA.
AC Q8QRD3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk

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RT for cervical neoplasia in southern China." ;
RL J. Infect. Dis. 186:696-700(2002) .
RR EMBL; AF486344; AAL96649.1; - .
DR InterPro: IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11021 MW; 9BD6125946D2C3E1 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
Db 49 RAHYNIVTF 57

RESULT 14

Q8QRD4 Q8QRD4 PRELIMINARY; PRT; 98 AA.
AC Q8QRD4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
for cervical neoplasia in southern China." ;
RL J. Infect. Dis. 186:696-700(2002) .
RR EMBL; AF486329; AAL96634.1; - .
DR InterPro: IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11025 MW; 86E24B234CC3281B CRC64;

Query Match 100.0%; Score 49; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
Db 49 RAHYNIVTF 57

RESULT 15

Q8VLJ0 Q8VLJ0 PRELIMINARY; PRT; 98 AA.
AC Q8VLJ0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Jinhu X., Xinxiang W., Yun T.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RR EMBL; AF461264; AAL66736.1; - .
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10997 MW; 9BD610834CCEA59B CRC64;

Query Match 100.0%; Score 49; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
Db 49 RAHYNIVTF 57

Search completed: June 29, 2005, 01:34:51
Job time : 56.2473 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:32:21 ; Search time 11.2747 Seconds
(without alignments)
76.805 Million cell updates/sec

Title: US-08-170-344-74

Perfect score: 49

Sequence: 1 RAHYNIVTF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79.*

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	98	1 W7WLS	E7 protein - human
2	39	79.6	405	2 G75027	alanyl-tRNA synthe
3	38	77.6	651	2 S82244	p9Eg3 protein - A
4	37	75.5	612	2 B81246	glutamine-fructose
5	37	75.5	612	2 H82022	glutamine-fructose
6	37	75.5	1452	2 T29107	polymorphic antigen
7	36	73.5	279	2 S57139	probable membrane
8	36	73.5	727	1 A45342	nonstructural prot
9	36	73.5	727	2 A58457	segment S4 protein
10	34	69.4	98	1 W7WLS	E7 protein - human
11	34	69.4	447	2 G82244	response regulator
12	34	69.4	720	2 A44819	alpha-galactosidase
13	34	69.4	735	2 S18623	hypothetical prote
14	34	69.4	1149	2 T18515	adenosinetriphosph
15	33	67.3	421	2 H89490	formylmethanofuran
16	33	67.3	424	2 S57458	formylmethanofuran
17	33	67.3	437	2 A69075	formylmethanofuran
18	33	67.3	456	2 C71402	probable glucosylt
19	33	67.3	579	2 T16237	hypothetical prote
20	33	67.3	593	2 S30958	gene 13 protein -
21	33	67.3	658	2 T33418	hypothetical prote
22	33	67.3	891	2 T40137	hypothetical serin
23	33	67.3	893	2 S64926	probable membrane
24	33	67.3	1149	2 T30869	probable adenosine
25	32.5	66.3	349	2 B82256	probable porin VCO
26	32	65.3	117	2 C95203	ioiap-related prot
27	32	65.3	117	2 C98070	conserved hypothet
28	32	65.3	181	2 E82448	probable cytochrom
29	32	65.3	245	2 D64147	hypothetical prote

RESULT 1

W7WLS

E7 protein - human papillomavirus type 16

C/Species: human papillomavirus type 16

C/Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C/Accession: A03688; S12367; T10428

R/Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virology 145, 181-185, 1985

A/Title: Human papillomavirus type 16 DNA sequence.

A/Reference number: A22355; MUID:85246220; PMID:2990099

A/Accession: A03688

A/Molecule type: DNA

A/Residues: 1-98 <SER>

A/Cross-references: UNIPROT:P03129; GB:K02718; NID:G333031; PIDN:AAA46940.1; PID:G33303

R/Barbosa, M.S.; Edmonds, C.; Fisher, C.; Schiller, J.T.; Lowy, D.R.; Vousden, K.H.

EMBO J. 9, 153-160, 1990

A/Title: The region of the HPV E7 oncoprotein homologous to adenovirus E1a and SV40 la

A/Reference number: S12367; MUID:90107938; PMID:2153075

A/Accession: S12367

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-98 <BAR>

R/Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A/Title: A negative element in the human poapillomavirus type 16 genome acts at the le

A/Reference number: Z17014; MUID:91162763; PMID:1848319

A/Accession: T10428

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-98 <KEN>

A/Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46940.1; PID:G333033

C/Genetics:

A/Gene: E7

C/Superfamily: papillomavirus E7 protein

C/Keywords: DNA binding; early protein; transcription regulation; zinc finger

P:58-94/Region: zinc finger CCCC motif

Query Match 100.0%; Score 49; DB 1; Length 98;

Best Local Similarity 100.0%; Pred. No. 0.01;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9

Db 49 RAHYNIVTF 57

|||||

|||||

RESULT 2

G75027

alanyl-tRNA synthetase related protein PAB1190 - Pyrococcus abyssi (strain Orsay)

C/Species: Pyrococcus abyssi

C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C/Accession: G75027

R;anonymous, Genoscope
 submitted to the EMBL Data Library, July 1999
 A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
 A;Reference number: A75001
 A;Accession: G75027
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-405 <KAW>
 A;Cross-references: UNIPROT:Q9UKV2; GB:AJ248288; GB:AL096836; NID:G5458960; PIDN:CAB5066
 A;Experimental source: strain Orsay
 C;Genetics:
 A;Gene: PAB1190

Query Match 79.6%; Score 39; DB 2; Length 405;
 Best Local Similarity 85.7%; Pred. No. 4.7;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 3 HYNIVTF 9
 |||||:
 Db 307 HYNVTF 313

RESULT 3
 S52244
 P69893 protein - African clawed frog
 C;Species: Xenopus laevis (African clawed frog)
 C;Date: 07-May-1995 #sequence_revision 03-Aug-1995 #text_change 16-Aug-2004
 C;Accession: S52244
 R;Roghi, C.; le Guellec, R.; Paris, J.; Couturier, A.; Philippe, M.
 submitted to the EMBL Data Library, October 1992
 A;Description: Eg3, selected by differential screening encodes a new Xenopus protein kinase
 A;Reference number: S52243
 A;Accession: S52244
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-651 <ROG>
 A;Cross-references: UNIPROT:Q91821; EMBL:Z17205; NID:G609283; PIDN:CAA78913.1; PID:G609283
 C;Superfamily: protein kinase homology
 C;Keywords: ATP
 F;11-265/Domain: protein kinase ATP-binding motif
 F;19-27/Region: protein kinase ATP-binding motif

Query Match 77.6%; Score 38; DB 2; Length 651;
 Best Local Similarity 75.0%; Pred. No. 12;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RAHYNIVT 8
 |||||:
 Db 558 RAHYNVTF 565

RESULT 4
 B81246
 glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) NMB0031 [similar
 N;Alternate names: glucosamine fructose-6-phosphate aminotransferase [misnomer]
 C;Species: Neisseria meningitidis
 C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C;Accession: B81246
 R;Tetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
 Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
 Xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Massignani, V.; Pizza, M.
 Science 287, 1809-1815, 2000
 A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Vitti
 A;Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.
 A;Reference number: A81000; MUID:20175755; PMID:10710307
 A;Accession: B81246
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-612 <TET>
 A;Cross-references: UNIPROT:Q9K1P9; GB:AE002361; GB:AE002098; NID:G7225245; PIDN:AAF4050
 A;Experimental source: serogroup B, strain MC58
 C;Genetics:
 A;Gene: NMB0031

C;Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)
 C;Keywords: aminotransferase; isomerase
 F;2-612/Product: glutamine-fructose-6-phosphate transaminase (isomerizing) #status predicted
 F;2/Active site: Cys #status predicted

Query Match 75.5%; Score 37; DB 2; Length 612;
 Best Local Similarity 66.7%; Pred. No. 18;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RAHYNIVTF 9
 |||||:
 Db 9 RAHNVVDF 17

RESULT 5
 H82022
 glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) NMA0276 [similar
 N;Alternate names: glucosamine fructose-6-phosphate aminotransferase [misnomer]
 C;Species: Neisseria meningitidis
 C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
 C;Accession: H82022
 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; More
 ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream
 Nature 404, 502-506, 2000
 A;Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491.
 A;Reference number: A81775; MUID:20222556; PMID:10761919
 A;Accession: H82022
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-612 <PAR>
 A;Cross-references: UNIPROT:Q9UWN9; GB:AL162752; GB:AL157959; NID:G7378778; PIDN:CAB835
 A;Experimental source: serogroup A, strain Z2491
 C;Genetics:
 A;Gene: glms; NMA0276
 C;Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)
 C;Keywords: aminotransferase; isomerase
 F;2-612/Product: glutamine-fructose-6-phosphate transaminase (isomerizing) #status predicted
 F;2/Active site: Cys #status predicted

Query Match 75.5%; Score 37; DB 2; Length 612;
 Best Local Similarity 66.7%; Pred. No. 18;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 RAHYNIVTF 9
 |||||:
 Db 9 RAHNVVDF 17

RESULT 6
 T29107
 polymorphic antigen p150 precursor - *Theileria parva*
 C;Species: *Theileria parva*
 C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T29107
 R;Skilton, R.; Iams, K.P.; Macklin, M.D.; Gobright, E.
 submitted to the EMBL Data Library, September 1995
 A;Description: Characterisation of a polymorphic 150 kilodalton antigen of *Theileria parva*
 A;Reference number: Z20571
 A;Accession: T29107
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-1452 <SKI>
 A;Cross-references: UNIPROT:Q27028; EMBL:L47230; NID:G986990; PID:G986991; PIDN:AAA7542
 A;Experimental source: strain Muguga; sep. parva
 C;Genetics:
 A;Note: P150
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-1452/Product: polymorphic antigen #status predicted <MAT>

Query Match 75.5%; Score 37; DB 2; Length 1452;
 Best Local Similarity 75.0%; Pred. No. 46;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHYNIWTF 9
 ||:||||
 Db 836 AHENILTF 843

RESULT 7

S57139 probable membrane protein YJRI16w - yeast (*Saccharomyces cerevisiae*)
 N;Alternate names: hypothetical protein J2031
 C;Species: *Saccharomyces cerevisiae*
 C;Date: 23-Aug-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
 C;Accession: S57139
 R;Rose, M.; Koetter, P.; Entian, K.D.
 submitted to the Protein Sequence Database, September 1995
 A;Reference number: S56848
 A;Accession: S57139
 A;Molecule type: DNA
 A;Residues: 1-279 <ROS>
 A;Cross-references: UNIPROT:P47153; EMBL:Z49616; NID:G1015834; PID:G1015835; GSPDB:GN000
 C;Genetics:
 A;Gene: MIPS:YJRI16w
 A;Cross-references: SGD:S0003877
 A;Map position: 10R
 C;Keywords: transmembrane protein

Query Match 73.5%; Score 36; DB 2; Length 279;
 Best Local Similarity 71.4%; Pred. No. 13;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HYNIVTF 9
 ||:||||
 Db 101 HYNVTV 107

RESULT 8

A45342 nonstructural protein Pns4 - rice dwarf virus
 C;Species: rice dwarf virus
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C;Accession: A45342
 R;Suzuki, N.; Watanabe, Y.; Kusano, T.; Kitagawa, Y.
 Virology 179, 446-454, 1990
 A;Title: Sequence analysis of rice dwarf phytoereovirus genome segments S4, S5, and S6:
 A;Reference number: A45342; MUID:91021049; PMID:2219732
 A;Accession: A45342
 A;Molecule type: genomic RNA
 A;Residues: 1-727 <SUZ>
 A;Cross-references: UNIPROT:P22474; GB:X54622; NID:G61469; PIDN:CAA38442.1; PID:G61470
 C;Genetics:

A;Map position: segment 4
 C;Superfamily: wound tumor virus nonstructural protein Pns4
 C;Keywords: glycoprotein; nonstructural protein

F;2,94,138,161,176,283,402,537,600,644/Binding site: carbohydrate (Asn) (covalent) #stat
 Query Match 73.5%; Score 36; DB 1; Length 727;
 Best Local Similarity 66.7%; Pred. No. 35;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RAHYNIVTF 9
 ||:||||
 Db 84 ROHWNIMTF 92

RESULT 9

A58457 segment S4 protein - rice dwarf virus
 C;Species: rice dwarf virus
 C;Date: 30-Sep-1993 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
 C;Accession: A58457
 R;Zhao, X.; Li, Y.; Liu, Y.; Liang, X.; Chen, Z.
 Acta Microbiol. Sin. 36, 93-102, 1996
 A;Title: Sequencing and function analysis of the deduced protein of rice dwarf virus gen
 A;Reference number: A58457

A;Accession: A58457
 A;Molecule type: mRNA
 A;Residues: 1-727 <ZHA>
 A;Cross-references: UNIPROT:Q85436
 C;Superfamily: wound tumor virus nonstructural protein Pns4
 C;Keywords: GNP binding; nucleotide binding; P-loop; zinc finger
 F;33-40/Region: nucleotide-binding motif A (P-loop)

Query Match 73.5%; Score 36; DB 2; Length 727;
 Best Local Similarity 66.7%; Pred. No. 35;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RAHYNIVTF 9
 ||:||||
 Db 84 ROHWNIMTF 92

RESULT 10

W7ML31 E7 protein - human papillomavirus type 31
 C;Species: human papillomavirus type 31
 A;Note: host Homo sapiens (man)
 C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
 C;Accession: B32444
 R;Goldaborough, M.D.; Disilvestre, D.; Temple, G.F.; Lorincz, A.T.
 Virology 171, 306-311, 1989
 A;Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-ass

A;Accession: B32444
 A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-98 <GOL>

A;Cross-references: UNIPROT:P17387; GB:J04353; NID:G333048; PIDN:AAA46951.1; PID:G45991
 C;Comment: This protein may be involved in the oncogenic potential of this virus.

C;Superfamily: papillomavirus E7 protein
 C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
 F;58-94/Region: zinc finger CCCC motif

Query Match 69.4%; Score 34; DB 1; Length 98;
 Best Local Similarity 75.0%; Pred. No. 11;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 AHYNIWTF 9
 ||:||||
 Db 50 SNTNIWTF 57

RESULT 11

G82244 response regulator VC1087 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)
 C;Species: *Vibrio cholerae*
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 12-Jul-2004
 C;Accession: G82244
 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
 chardson, D.; Ermlaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,
 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 405, 477-483, 2000
 A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: G82244

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-447 <HEI>

A;Cross-references: GB:AE004189; GB:AE003852; NID:G9655541; PIDN:AAF94246.1; GSPDB:GN00

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC1087

A;Map position: 1

C;Superfamily: response regulator with HD-GYP domain; response regulator homology; sens
 Query Match 69.4%; Score 34; DB 2; Length 447;
 Best Local Similarity 66.7%; Pred. No. 53;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
Db 31 RMDYNNVTF 39

RESULT 12

A44819 alpha-galactosidase (EC 3.2.1.22) - Streptococcus mutans

C;Species: Streptococcus mutans
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: A44819; A44673

R;Aduse-Opoku, J.; Tao, L.; Ferretti, J.J.; Russell, R.R.
J. Gen. Microbiol. 137, 2271-2272, 1991

A;Reference number: A44819; MUID:92085044; PMID:1650918

A;Contents: erratum; strain Ingbritt

A;Accession: A44819

A;Molecule type: DNA

A;Residues: 1-720 <ADU>

A;Cross-references: UNIPROT:P27756; GB:M77351; EMBL:M60777; NID:g153734; PIDN:AAA26933.1
A;Note: sequence extracted from NCBI backbone (NCBIN:70487, NCBI:P:70488)

R;Aduse-Opoku, J.; Tao, L.; Ferretti, J.J.; Russell, R.R.B.

J. Gen. Microbiol. 137, 757-764, 1991

A;Title: Biochemical and genetic analysis of Streptococcus mutans alpha-galactosidase.

A;Reference number: A44673; MUID:91311378; PMID:1649890

A;Contents: annotation

A;Note: this sequence has been revised in reference A44819

C;Genetics:

A;Gene: aga

C;Superfamily: alpha-galactosidase II

C;Keywords: glycosidase; hydrolase

Query Match 69.4%; Score 34; DB 2; Length 720;
Best Local Similarity 50.0%; Pred. No. 87;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AHYNIVTF 9
Db 182 SHYDVITF 189

RESULT 13

S18623

hypothetical protein 1 (ntrC 3' region) - Azorhizobium caulinodans

C;Species: Azorhizobium caulinodans

C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004

C;Accession: S18623

R;Pawlowski, K.; Klose, U.; de Bruijn, F.J.

Mol. Gen. Genet. 231, 124-138, 1991

A;Title: Characterization of a novel Azorhizobium caulinodans ORS571 two-component regul

A;Reference number: S18622; MUID:92092954; PMID:1661370

A;Accession: S18623

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-735 <PAW>

A;Cross-references: UNIPROT:Q04855; GB:X63841; GB:S71362; NID:g38734; PIDN:CAA45329.1; F

Query Match 69.4%; Score 34; DB 2; Length 735;
Best Local Similarity 62.5%; Pred. No. 89;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AHYNIVTF 9
Db 123 SHYGVVTF 130

RESULT 14

T18515

adenosinetriphosphatase (EC 3.6.1.3) - bovine

C;Alternate names: chromaffin granule ATPase II; P-type ATPase

C;Species: Bos primigenius taurus (cattle)

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T18515

R;Williamson, P.; Halleck, M.
submitted to the EMBL Data Library, January 1999

A;Reference number: Z18940

A;Accession: T18515

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-1149 <WIL>

A;Cross-references: UNIPROT:Q29449; EMBL:U51100; NID:g4115340; PID:g4115341; PIDN:AAD03

C;Keywords: hydrolase

Query Match 69.4%; Score 34; DB 2; Length 1149;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AHYNIVTF 9
Db 57 AKYNIITF 64

RESULT 15

H69490

formylmethanofuran dehydrogenase (tungsten) chain B homolog (fwdB-2) - Archaeoglobus

C;Species: Archaeoglobus fulgidus

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C;Accession: H69490

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiaich, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Woese, C.R.; Venter, J.C.

A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae

A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: H69490

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-421 <KLE>

A;Cross-references: UNIPROT:O28350; GB:AE000970; GB:AE000782; NID:g2689293; PIDN:AAB893

C;Superfamily: formylmethanofuran dehydrogenase (molybdenum) beta chain

C;Keywords: iron-sulfur protein; metalloprotein; molybdenum; molybdopterin

Query Match 67.3%; Score 33; DB 2; Length 421;
Best Local Similarity 71.4%; Pred. No. 79;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RAHYNIV 7
Db 279 RGHYNNV 285

Search completed: June 29, 2005, 01:38:50

Job time : 12.2747 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 05:18:25 ; Search time 53.8517 Seconds
(without alignments)

64.268 Million cell updates/sec

Title: US-08-170-344-74

Perfect score: 49

Sequence: 1 RAHYNIVTF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	9	9 US-09-891-823-48	Sequence 48, Appl
2	49	100.0	9	9 US-09-888-721-4	Sequence 4, Appl
3	49	100.0	9	10 US-09-077-439A-1	Sequence 1, Appl
4	49	100.0	9	14 US-10-227-789-3	Sequence 3, Appl
5	49	100.0	9	14 US-10-115-620-3	Sequence 3, Appl
6	49	100.0	9	14 US-10-365-908-48	Sequence 48, Appl
7	49	100.0	9	15 US-10-406-818-3	Sequence 3, Appl
8	49	100.0	9	15 US-10-367-580-93	Sequence 93, Appl
9	49	100.0	9	15 US-10-367-593-93	Sequence 93, Appl
10	49	100.0	9	15 US-10-367-594-93	Sequence 93, Appl
11	49	100.0	9	15 US-10-367-654-93	Sequence 93, Appl

12	49	100.0	9	15 US-10-367-658-93	Sequence 93, Appl
13	49	100.0	9	15 US-10-367-668-93	Sequence 93, Appl
14	49	100.0	9	16 US-10-367-674-93	Sequence 93, Appl
15	49	100.0	9	16 US-10-777-053-331	Sequence 331, Appl
16	49	100.0	9	16 US-10-306-541-49	Sequence 49, Appl
17	49	100.0	9	16 US-10-837-217-331	Sequence 331, Appl
18	49	100.0	9	16 US-10-871-138-48	Sequence 48, Appl
19	49	100.0	9	17 US-10-484-063-15	Sequence 15, Appl
20	49	100.0	9	17 US-10-844-711-9	Sequence 9, Appl
21	49	100.0	9	17 US-10-751-845-109	Sequence 109, Appl
22	49	100.0	9	17 US-10-835-662-22	Sequence 22, Appl
23	49	100.0	10	9 US-09-891-823-32	Sequence 32, Appl
24	49	100.0	10	14 US-10-365-908-32	Sequence 32, Appl
25	49	100.0	10	16 US-10-306-541-53	Sequence 53, Appl
26	49	100.0	10	16 US-10-871-138-32	Sequence 32, Appl
27	49	100.0	12	16 US-10-654-200-51	Sequence 51, Appl
28	49	100.0	13	16 US-10-654-200-52	Sequence 52, Appl
29	49	100.0	14	16 US-10-654-200-53	Sequence 53, Appl
30	49	100.0	14	16 US-10-654-200-54	Sequence 54, Appl
31	49	100.0	14	17 US-10-751-845-68	Sequence 68, Appl
32	49	100.0	15	16 US-10-654-200-55	Sequence 55, Appl
33	49	100.0	15	16 US-10-476-570-63	Sequence 63, Appl
34	49	100.0	15	16 US-10-306-541-61	Sequence 61, Appl
35	49	100.0	15	16 US-10-306-541-62	Sequence 62, Appl
36	49	100.0	15	16 US-10-306-541-64	Sequence 64, Appl
37	49	100.0	15	16 US-10-306-541-74	Sequence 74, Appl
38	49	100.0	17	17 US-10-858-384-16	Sequence 16, Appl
39	49	100.0	19	16 US-10-654-200-56	Sequence 56, Appl
40	49	100.0	19	17 US-10-484-063-14	Sequence 14, Appl
41	49	100.0	20	15 US-10-432-465-48	Sequence 48, Appl
42	49	100.0	20	16 US-10-654-200-57	Sequence 57, Appl
43	49	100.0	20	16 US-10-890-526-73	Sequence 73, Appl
44	49	100.0	21	16 US-10-306-541-107	Sequence 107, Appl
45	49	100.0	66	9 US-09-870-759-149	Sequence 149, Appl

ALIGNMENTS

RESULT 1
US-09-891-823-48
; Sequence 48, Application US/09891823
; Publication No. US20020110566A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/09/891,823
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-09-891-823-48

Query Match 100.0%; Score 49; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9

Db 1 RAHYNIVTF 9

RESULT 2

US-09-888-721-4
; Sequence 4, Application US/09888721
; Patent No. US20020132990A1
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Wils, Pierre
; APPLICANT: Zhu, Quan
; APPLICANT: Laurent, Olivier
; APPLICANT: Marasco, Wayne A.
; APPLICANT: Scherman, Daniel
; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
; TITLE OF INVENTION: DELIVERY
; FILE REFERENCE: 23611-A USA
; CURRENT APPLICATION NUMBER: US/09/888,721
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: 60/213,653
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-09-888-721-4

Query Match 100.0%; Score 49; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
| | | | | | | |
Db 1 RAHYNIVTF 9

RESULT 3
US-09-077-439A-1
; Sequence 1, Application US/09077439A
; Publication No. US20030202989A1
; GENERAL INFORMATION:
; APPLICANT: Collier, R. John
; APPLICANT: Blanke, Steven R.
; APPLICANT: Milne, Jill C.
; APPLICANT: Benson, Ericka L.
; APPLICANT: Ballard, Jimmy D.
; APPLICANT: Starnbach, Michael N.
; TITLE OF INVENTION: Use of Toxin Peptides and/or Affinity
; TITLE OF INVENTION: Handles for Delivering Compounds into Cells
; FILE REFERENCE: 00246/187002
; CURRENT APPLICATION NUMBER: US/09/077,439A
; CURRENT FILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: PCT/US96/20463
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: US 60/019,275
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 60/008,518
; PRIOR FILING DATE: 1995-12-13
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-077-439A-1

Query Match 100.0%; Score 49; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
| | | | | | | |
Db 1 RAHYNIVTF 9

RESULT 4
US-10-227-789-3
; Sequence 3, Application US/10227789
; Publication No. US20030022860A1
; GENERAL INFORMATION:
; APPLICANT: MELIEF, Cornelius
; APPLICANT: Schoenberger, Stephen
; APPLICANT: Offringa, Rienk
; APPLICANT: Toes, Rene
; TITLE OF INVENTION: CD-40 Binding Molecules and CTL Peptides for Treating
; TITLE OF INVENTION: Tumors
; FILE REFERENCE: TNX 98-04
; CURRENT APPLICATION NUMBER: US/10/227,789
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US/09/316,935
; PRIOR FILING DATE: 1999-05-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma Virus Type 16 E7 derived peptide
US-10-227-789-3

Query Match 100.0%; Score 49; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
| | | | | | | |
Db 1 RAHYNIVTF 9

RESULT 5
US-10-115-620-3
; Sequence 3, Application US/10115620
; Publication No. US20030118588A1
; GENERAL INFORMATION:
; APPLICANT: MELIEF, Cornelius
; APPLICANT: Schoenberger, Stephen
; APPLICANT: Offringa, Rienk
; APPLICANT: Toes, Rene
; TITLE OF INVENTION: CD-40 Binding Molecules and CTL Peptides for Treating Tumors
; FILE REFERENCE: TNX 98-04
; CURRENT APPLICATION NUMBER: US/10/115,620
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US/09/316,935
; PRIOR FILING DATE: 1999-05-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma Virus Type 16 E7 derived peptide
US-10-115-620-3

Query Match 100.0%; Score 49; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
| | | | | | | |
Db 1 RAHYNIVTF 9

RESULT 6
US-10-365-908-48
; Sequence 48, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.

```
; APPLICANT: Goldstone, Stephen E.
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-48
```

```
Query Match 100.0%; Score 49; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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Qy 1 RAHYNIVTF 9
Db 1 RAHYNIVTF 9
|||||
```

```
RESULT 7
US-10-406-818-3
; Sequence 3, Application US/10406818
; Publication No. US20040005711A1
; GENERAL INFORMATION:
; APPLICANT: Regts, Geesje D.
; APPLICANT: Holtrop, Marijke
; APPLICANT: Wilschut, Christiaan J.
; APPLICANT: Daemen, Arnoldine C.
; TITLE OF INVENTION: GENETIC IMMUNIZATION AGAINST CERVICAL CARCINOMA
; FILE REFERENCE: 2183-5920
; CURRENT APPLICATION NUMBER: US/10/406,818
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: PCT/NL01/00740
; PRIOR FILING DATE: 2001-10-08
; PRIOR APPLICATION NUMBER: EP 00203472.6
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthesized peptide originating from E7, binds to HPV16 H-2Db
US-10-406-818-3
```

```
Query Match 100.0%; Score 49; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 RAHYNIVTF 9
Db 1 RAHYNIVTF 9
|||||
```

```
RESULT 8
US-10-367-580-93
; Sequence 93, Application US/10367580
; Publication No. US20040071720A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
```

```
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461061
; CURRENT APPLICATION NUMBER: US/10/367,580
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/794,832
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 93
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-580-93
```

```
Query Match 100.0%; Score 49; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 RAHYNIVTF 9
Db 1 RAHYNIVTF 9
|||||
```

```
RESULT 9
US-10-367-593-93
; Sequence 93, Application US/10367593
; Publication No. US20040071721A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461012
; CURRENT APPLICATION NUMBER: US/10/367,593
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 93
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-367-593-93
```

```
Query Match 100.0%; Score 49; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 RAHYNIVTF 9
Db 1 RAHYNIVTF 9
|||||
```

Db 1 RAHYNIVTF 9

RESULT 10

US-10-367-594-93
; Sequence 93, Application US/10367594
; Publication No. US2004007172A1

; GENERAL INFORMATION:

; APPLICANT: Rothman, James E.

; APPLICANT: Hartl, F. Ulrich

; APPLICANT: Hoe, Mee H.

; APPLICANT: Houghton, Alan

; APPLICANT: Takechi, Yoshizumi

; APPLICANT: Mayhew, Mark

; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies

; FILE REFERENCE: 11746/461041

; CURRENT APPLICATION NUMBER: US/10/367,594

; CURRENT FILING DATE: 2003-02-14

; PRIOR APPLICATION NUMBER: US 09/680,806

; PRIOR FILING DATE: 2000-10-05

; PRIOR APPLICATION NUMBER: US 09/011,645

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: PCT/US96/13363

; PRIOR FILING DATE: 1996-08-16

; PRIOR APPLICATION NUMBER: US 60/002,490

; PRIOR FILING DATE: 1995-08-18

; PRIOR APPLICATION NUMBER: US 60/002,479

; PRIOR FILING DATE: 1995-08-18

; NUMBER OF SEQ ID NOS: 349

; SOFTWARE: WordPerfect 8.0 for Windows

; SEQ ID NO 93

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: synthetic peptide

US-10-367-594-93

Query Match 100.0%; Score 49; DB 15; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9

|||||

Db 1 RAHYNIVTF 9

RESULT 11

US-10-367-654-93

; Sequence 93, Application US/10367654

; Publication No. US2004007172A1

; GENERAL INFORMATION:

; APPLICANT: Rothman, James E.

; APPLICANT: Hartl, F. Ulrich

; APPLICANT: Hoe, Mee H.

; APPLICANT: Houghton, Alan

; APPLICANT: Takechi, Yoshizumi

; APPLICANT: Mayhew, Mark

; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies

; FILE REFERENCE: 11746/461032

; CURRENT APPLICATION NUMBER: US/10/367,654

; CURRENT FILING DATE: 2003-02-14

; PRIOR APPLICATION NUMBER: US 10/171,734

; PRIOR FILING DATE: 2002-06-13

; PRIOR APPLICATION NUMBER: US 09/636,295

; PRIOR FILING DATE: 2000-08-10

; PRIOR APPLICATION NUMBER: US 09/011,645

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: PCT/US96/13363

; PRIOR FILING DATE: 1996-08-16

; PRIOR APPLICATION NUMBER: US 60/002,490

; PRIOR FILING DATE: 1995-08-18

; PRIOR APPLICATION NUMBER: US 60/002,479

; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 93

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: synthetic peptide

US-10-367-654-93

Query Match 100.0%; Score 49; DB 15; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9

|||||

Db 1 RAHYNIVTF 9

RESULT 12

US-10-367-658-93

; Sequence 93, Application US/10367658

; Publication No. US2004007172A1

; GENERAL INFORMATION:

; APPLICANT: Rothman, James E.

; APPLICANT: Hartl, F. Ulrich

; APPLICANT: Hoe, Mee H.

; APPLICANT: Houghton, Alan

; APPLICANT: Takechi, Yoshizumi

; APPLICANT: Mayhew, Mark

; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies

; FILE REFERENCE: 11746/461051

; CURRENT APPLICATION NUMBER: US/10/367,658

; CURRENT FILING DATE: 2003-02-14

; PRIOR APPLICATION NUMBER: US 09/794,529

; PRIOR FILING DATE: 2001-02-27

; PRIOR APPLICATION NUMBER: US 09/011,645

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: PCT/US96/13363

; PRIOR FILING DATE: 1996-08-16

; PRIOR APPLICATION NUMBER: US 60/002,490

; PRIOR FILING DATE: 1995-08-18

; PRIOR APPLICATION NUMBER: US 60/002,479

; PRIOR FILING DATE: 1995-08-18

; NUMBER OF SEQ ID NOS: 349

; SOFTWARE: WordPerfect 8.0 for Windows

; SEQ ID NO 93

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: synthetic peptide

US-10-367-658-93

Query Match 100.0%; Score 49; DB 15; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9

|||||

Db 1 RAHYNIVTF 9

RESULT 13

US-10-367-668-93

; Sequence 93, Application US/10367668

; Publication No. US2004007172A1

; GENERAL INFORMATION:

; APPLICANT: Rothman, James E.

; APPLICANT: Hartl, F. Ulrich

; APPLICANT: Hoe, Mee H.

; APPLICANT: Houghton, Alan

; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/461072
; CURRENT APPLICATION NUMBER: US/10/367,668
; CURRENT FILING DATE: 2003-02-14
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 09/794,517
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 93
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; US-10-367-668-93

Query Match 100.0%; Score 49; DB 15; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
Db 1 RAHYNIVTF 9

RESULT 14
US-10-367-674-93
; Sequence 93, Application US/10367674
; Publication No. US20040127684A1
; GENERAL INFORMATION:
; APPLICANT: Rothman, James E.
; APPLICANT: Hartl, F. Ulrich
; APPLICANT: Hoe, Mee H.
; APPLICANT: Houghton, Alan
; APPLICANT: Takechi, Yoshizumi
; APPLICANT: Mayhew, Mark
; TITLE OF INVENTION: Heat Shock Protein-Based Vaccines and Immunotherapies
; FILE REFERENCE: 11746/4610211
; CURRENT APPLICATION NUMBER: US/10/367,674
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 10/170,738
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 09/552,868
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 09/011,645
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: PCT/US96/13363
; PRIOR FILING DATE: 1996-08-16
; PRIOR APPLICATION NUMBER: US 60/002,490
; PRIOR FILING DATE: 1995-08-18
; PRIOR APPLICATION NUMBER: US 60/002,479
; PRIOR FILING DATE: 1995-08-18
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 93
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; US-10-367-674-93

Query Match 100.0%; Score 49; DB 16; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RAHYNIVTF 9
Db 1 RAHYNIVTF 9

RESULT 15
US-10-777-053-331
; Sequence 331, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANNK.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 331
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papillomavirus 16
; US-10-777-053-331

Query Match 100.0%; Score 49; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
Db 1 RAHYNIVTF 9

Search completed: June 29, 2005, 05:48:15
Job time : 53.8517 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:37:59 ; Search time 16.8626 Seconds
(without alignments)
39.842 Million cell updates/sec

Title: US-08-170-344-74

Perfect score: 49

Sequence: 1 RAHYNIVTF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	9	3	US-08-159-339A-138
2	49	100.0	9	4	US-09-593-870A-25
3	49	100.0	9	4	US-09-000-003A-5
4	49	100.0	9	4	US-09-501-097A-5
5	49	100.0	9	4	US-10-365-908-48
6	49	100.0	10	4	US-10-365-908-32
7	49	100.0	14	3	US-08-075-541D-4
8	49	100.0	14	3	US-08-075-541D-29
9	49	100.0	14	3	US-08-075-541D-56
10	49	100.0	15	3	US-08-075-541D-18
11	49	100.0	15	4	US-09-601-729-279
12	49	100.0	17	3	US-08-075-541D-25
13	49	100.0	17	4	US-09-980-523A-16
14	49	100.0	18	3	US-08-075-541D-30
15	49	100.0	19	3	US-08-075-541D-3
16	49	100.0	20	2	US-08-934-915-48
17	49	100.0	20	2	US-08-934-915-155
18	49	100.0	20	3	US-08-075-541D-10
19	49	100.0	20	4	US-09-980-177A-73
20	49	100.0	26	3	US-08-075-541D-20
21	49	100.0	30	2	US-08-934-915-52
22	49	100.0	30	4	US-09-486-394-3
23	49	100.0	32	3	US-08-075-541D-7
24	49	100.0	32	3	US-08-075-541D-8
25	49	100.0	38	4	US-09-501-097A-6
26	49	100.0	59	3	US-09-390-027-6
27	49	100.0	98	1	US-08-406-248-6

28 49 100.0 98 3 US-08-075-541D-42 Sequence 42, Appl
29 49 100.0 98 3 US-09-382-616A-1 Sequence 1, Appl
30 49 100.0 98 3 US-08-944-368A-4 Sequence 4, Appl
31 49 100.0 98 3 US-09-820-764-4 Sequence 4, Appl
32 49 100.0 98 4 US-09-613-303-8 Sequence 8, Appl
33 49 100.0 98 4 US-09-566-420-19 Sequence 19, Appl
34 49 100.0 98 4 US-09-986-118A-4 Sequence 4, Appl
35 49 100.0 98 4 US-09-728-466-1 Sequence 1, Appl
36 49 100.0 98 4 US-09-824-017-4 Sequence 4, Appl
37 49 100.0 98 4 US-10-267-311-8 Sequence 8, Appl
38 49 100.0 98 4 US-10-201-764-19 Sequence 19, Appl
39 49 100.0 98 4 US-09-637-746-3 Sequence 3, Appl
40 49 100.0 98 4 US-09-501-097A-7 Sequence 7, Appl
41 49 100.0 98 4 US-09-980-523A-12 Sequence 12, Appl
42 49 100.0 121 4 US-09-613-303-12 Sequence 12, Appl
43 49 100.0 121 4 US-10-267-311-12 Sequence 12, Appl
44 49 100.0 172 3 US-08-860-165-12 Sequence 12, Appl
45 49 100.0 172 3 US-08-860-165-14 Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-159-339A-138
; Sequence 138, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 138:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

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US-08-159-339A-138
Query Match      100.0%; Score 49; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
   |||||
Db 1 RAHYNIVTF 9

RESULT 2
US-09-593-870A-25
; Sequence 25, Application US/09593870A
; Patent No. 6548643
; GENERAL INFORMATION:
; APPLICANT: McKenzie, Ian F.C.
; APPLICANT: Apostolopoulos, Vasso
; APPLICANT: Pietersz, Geoff Allan
; TITLE OF INVENTION: Antigen Carbohydrate Compounds and Their
; FILE REFERENCE: 2368-McKenzie
; CURRENT APPLICATION NUMBER: US/09/593,870A
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: 09/223,043
; PRIOR FILING DATE: 1998-12-30
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-593-870A-25

Query Match      100.0%; Score 49; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
   |||||
Db 1 RAHYNIVTF 9

RESULT 3
US-09-000-003A-5
; Sequence 5, Application US/09000003A
; Patent No. 6652850
; GENERAL INFORMATION:
; APPLICANT: Philip, Ramila
; APPLICANT: Lebkowski, Jane S.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRAL LIPOSOMES AND
; THEIR USE IN TRANSFECTING DENDRITIC CELLS TO STIMULATE
; SPECIFIC IMMUNITY
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Alexis Barron, Esq.
; STREET: Suite 2600 Aramark Tower, 1101 Market Street
; CITY: Philadelphia
; STATE: PA
; COUNTRY: United States of America
; ZIP: 19107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/000,003A
; FILING DATE: 15-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/12012
; FILING DATE: 19-JUL-1996
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; APPLICATION NUMBER: US 60/001,312
; FILING DATE: 21-JUL-1995
; APPLICATION NUMBER: US 60/007,184
; FILING DATE: 01-NOV-1995
; APPLICATION NUMBER: US 08/566,286
; FILING DATE: 01-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Barron, Alexis
; REGISTRATION NUMBER: 22,702
; REFERENCE/DOCKET NUMBER: 20,846-K USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 923-4466
; TELEFAX: (215) 923-2189
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-000-003A-5

Query Match      100.0%; Score 49; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
   |||||
Db 1 RAHYNIVTF 9

RESULT 4
US-09-501-097A-5
; Sequence 5, Application US/09501097A
; Patent No. 6734173
; GENERAL INFORMATION:
; APPLICANT: Tzyy-Choo Wu
; APPLICANT: Chien-Fu Hung
; TITLE OF INVENTION: IMPROVED HSP DNA VACCINES
; FILE REFERENCE: 2240-169349
; CURRENT APPLICATION NUMBER: US/09/501,097A
; CURRENT FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 9
; TYPE: PRT
; ORGANISM: human papillomavirus
US-09-501-097A-5

Query Match      100.0%; Score 49; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
   |||||
Db 1 RAHYNIVTF 9

RESULT 5
US-10-365-908-48
; Sequence 48, Application US/10365908
; Patent No. 6797491
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Wilmott, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
```


; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-48

Query Match 100.0%; Score 49; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
Db 1 RAHYNIVTF 9

RESULT 6
US-10-365-908-32

; Sequence 32, Application US/10365908
; Patent No. 6797491
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-32

Query Match 100.0%; Score 49; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
Db 2 RAHYNIVTF 10

RESULT 7

US-08-075-541D-4
; Sequence 4, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA

; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-4

Query Match 100.0%; Score 49; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
Db 6 RAHYNIVTF 14

RESULT 8

US-08-075-541D-29
; Sequence 29, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-29

Query Match 100.0%; Score 49; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0038; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 RAHYNIVTF 9
| | | | |
Db 1 RAHYNIVTF 9

RESULT 9
US-08-075-541D-56
; Sequence 56, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
US-08-075-541D-56

Query Match 100.0%; Score 49; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0038; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 RAHYNIVTF 9
| | | | |
Db 5 RAHYNIVTF 13

RESULT 10
US-08-075-541D-18
; Sequence 18, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-18

Query Match 100.0%; Score 49; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0041; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 RAHYNIVTF 9
| | | | |
Db 2 RAHYNIVTF 10

RESULT 11
US-09-601-729-279
; Sequence 279, Application US/09601729

;; CITY: PHILADELPHIA
;; STATE: PENNSYLVANIA
;; COUNTRY: USA
;; ZIP: 19103-2398
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/075.541D
;; FILING DATE: 10-JUN-1993
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: AU pk 3876
;; FILING DATE: 12-DEC-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: pct/au91/00575
;; FILING DATE: 12-DEC-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: NADEL, ALAN S
;; REGISTRATION NUMBER: 27,363
;; REFERENCE/DOCKET NUMBER: 8795-4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-567-2020
;; TELEFAX: 215-567-2991
;; INFORMATION FOR SEQ ID NO: 30:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-075-541D-30

Query Match 100.0%; Score 49; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
Db 5 RAHYNIVTF 13
|||||

RESULT 15
US-08-075-541D-3
; Sequence 3, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075.541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876

;; FILING DATE: 12-DEC-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: pct/au91/00575
;; FILING DATE: 12-DEC-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: NADEL, ALAN S
;; REGISTRATION NUMBER: 27,363
;; REFERENCE/DOCKET NUMBER: 8795-4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-567-2020
;; TELEFAX: 215-567-2991
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 19 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-075-541D-3

Query Match 100.0%; Score 49; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.0052;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RAHYNIVTF 9
Db 6 RAHYNIVTF 14
|||||

Search completed: June 29, 2005, 01:44:28
Job time : 16.9126 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:32:21 ; Search time 11.2747 Seconds
(without alignments)
76.805 Million cell updates/sec

Title: US-08-170-344-73
Perfect score: 56
Sequence: 1 RFHNRGRW 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	158	1 W6WLS	protein E6 - human
2	50	89.3	148	2 A61237	E6 protein - human
3	50	89.3	148	2 S36573	E6 protein - human
4	50	89.3	149	1 W6WLS3	E6 protein - human
5	50	89.3	149	1 W6WLS8	E6 protein - human
6	50	89.3	159	1 S15614	E6 protein - human
7	50	89.3	159	2 S36497	E6 protein - human
8	49	87.5	149	1 W6WLS1	E6 protein - human
9	49	87.5	149	1 W6WLS35	E6 protein - human
10	44	78.6	151	1 W6WLS1	E6 protein - human
11	40	71.4	150	2 S36544	E6 protein - human
12	40	71.4	153	1 S15621	E6 protein - human
13	40	71.4	191	1 W6WLS1	E6 protein - human
14	39	69.6	274	2 E69423	branched-chain ami
15	39	69.6	340	2 H71479	probable outer mem
16	39	69.6	340	2 H81742	major outer membra
17	38	67.9	138	2 S36567	E6 protein - human
18	38	67.9	321	2 B75366	probable pseudouri
19	37	66.1	155	1 W6WLS8	E6 protein - human
20	37	66.1	157	2 S36538	E6 protein - human
21	37	66.1	197	1 Q3BEB6	HRF6 protein - hu
22	37	66.1	395	2 H72222	conserved hypothet
23	37	66.1	466	2 F81302	hypothetical prote
24	37	66.1	1449	2 T30857	glucosyltransferas
25	37	66.1	1449	2 T30552	glucosyltransferas
26	36	64.3	114	2 H71155	hypothetical prote
27	36	64.3	158	1 W6WLS8	E6 protein - human
28	36	64.3	211	2 S18463	lysosyme (EC 3.2.1
29	36	64.3	556	2 B83847	cytochrome c bioge

ALIGNMENTS

RESULT 1

W6WLS

protein E6 - human papillomavirus type 16

C;Species: human papillomavirus type 16

C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C;Accession: A03682; T10427

R;Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virology 145, 181-195, 1985

A;Title: Human papillomavirus type 16 DNA sequence.

A;Reference number: A22355; MUID:85246220; PMID:2990099

A;Accession: A03682

A;Molecule type: DNA

A;Residues: 1-158 <SEE>

A;Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G33303

R;Kennedy, I.M.; Hadow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A;Title: A negative element in the human poapillomavirus type 16 genome acts at the lev

A;Reference number: Z17014; MUID:91162763; PMID:1848319

A;Accession: T10427

A;Status: preliminary; translated from GB/EMBL/DBD

A;Molecule type: DNA

A;Residues: 1-158 <KEN>

A;Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

C;Genetics:

C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; zinc finger

F;37-73/Region: zinc finger CCCC motif

F;110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 56; DB 1; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.0044;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFHNRGRW 9

Db 131 RFHNRGRW 139

RESULT 2

A61237

E6 protein - human papillomavirus type 52

C;Species: human papillomavirus type 52

C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 03-May-1996

C;Accession: A61237

R;Takami, Y.; Kondoh, G.; Saito, K.; Sudiro, T.M.; Sjahrurachman, A.; Warsa,

Int. J. Cancer 48, 516-522, 1991

A;Title: Cloning and characterization of human papillomavirus type 52 from cervical ca

A;Reference number: A61237; MUID:91258022; PMID:1646174

A;Accession: A61237

A;Status: preliminary

A;Molecule type: DNA

nudel protein prec
phage integrase (p
hypothetical prote
ribosomal protein
conserved hypothet
E6 protein - human
probable integrase
probable integrase
integrase - phage
prophage DLP12 int
A33497
hypothetical prote
hypothetical prote
probable sugar tra
seizure-related me
SNF2 helicase homo
probable helicase

A;Residues: 1-148 <TAK>
C;Superfamily: papillomavirus E6 protein

Query Match 89.3%; Score 50; DB 2; Length 148;
Best Local Similarity 88.9%; Pred. No. 0.053;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RFHNIRGRW 9
Db 124 RFHNIGRW 132

RESULT 3
S36573
E6 protein - human papillomavirus type 52
C;Species: human papillomavirus type 52
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36573
R;Delius, H.; Hofmann, B.
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36573
A;Molecule type: DNA
A;Residues: 1-148
A;Cross-references: UNIPROT:P36814; EMBL:X74481; NID:g337038; PIDN:CAA52585.1; PID:g3970
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 89.3%; Score 50; DB 2; Length 148;
Best Local Similarity 88.9%; Pred. No. 0.053;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RFHNIRGRW 9
Db 124 RFHNIGRW 132

RESULT 4
W6WL33
E6 protein - human papillomavirus type 33
C;Species: human papillomavirus type 33
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C;Accession: A03683
F;Cole, S.T.; Strebeck, R.E.
J. Virol. 58, 991-995, 1986
A;Title: Genome organization and nucleotide sequence of human papillomavirus type 33, wh
A;Reference number: A93020; MUID:86200464; PMID:3009902
A;Accession: A03683
A;Molecule type: DNA
A;Residues: 1-149 <COL>
A;Cross-references: UNIPROT:P06427; GB:IM12732; NID:g333049; PIDN:AAA46958.1; PID:g463177
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif

Query Match 89.3%; Score 50; DB 1; Length 149;
Best Local Similarity 88.9%; Pred. No. 0.054;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RFHNIRGRW 9
Db 124 RFHNIGRW 132

RESULT 5
W6WL58
E6 protein - human papillomavirus type 58
C;Species: human papillomavirus type 58
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: E36779

R;Kirii, Y.; Iwamoto, S.; Matsukura, T.
Virology 185, 424-427, 1991
A;Title: Human papillomavirus type 58 DNA sequence.
A;Reference number: A36779; MUID:92024102; PMID:1656594
A;Accession: E36779
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-149 <KIR>
A;Cross-references: UNIPROT:P26555; GB:D90400; NID:g222386; PIDN:BAA31845.1; PID:g33370
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif

Query Match 89.3%; Score 50; DB 1; Length 149;
Best Local Similarity 88.9%; Pred. No. 0.054;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RFHNIRGRW 9
Db 124 RFHNIGRW 132

RESULT 6
S15614
E6 protein - human papillomavirus type 2a
C;Species: human papillomavirus type 2a
A;Note: host Homo sapiens (man)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: S15614
R;Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.
Virus Res. 18, 81-98, 1990
A;Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and
A;Reference number: S15614; MUID:91188699; PMID:1964523
A;Accession: S15614
A;Molecule type: DNA
A;Residues: 1-159 <HIR>
A;Cross-references: UNIPROT:P25484; EMBL:X55964
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;35-71/Region: zinc finger CCCC motif
F;108-144/Region: zinc finger CCCC motif

Query Match 89.3%; Score 50; DB 1; Length 159;
Best Local Similarity 88.9%; Pred. No. 0.057;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RFHNIRGRW 9
Db 129 RFHNIGRW 137

RESULT 7
S36497
E6 protein - human papillomavirus type 27
C;Species: human papillomavirus type 27
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36497
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36497
A;Molecule type: DNA
A;Residues: 1-159
A;Cross-references: UNIPROT:P36808; EMBL:X74473; NID:g396964; PIDN:CAA52536.1; PID:g396
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 89.3%; Score 50; DB 2; Length 159;
Best Local Similarity 88.9%; Pred. No. 0.057;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 RFHNIRGRW 9
||||| |||
Db      129 RFHNISGRW 137

RESULT 8
W6WLJ1
E6 protein - human papillomavirus type 31
C:Species: human papillomavirus type 31
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: A32444
R:Goldsborough, M.D.; Disilvestre, D.; Temple, G.F.; Lorincz, A.T.
Virology 171, 306-311, 1989
A:Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associated
A:Reference number: A94398; MUID:89299478; PMID:2545036
A:Accession: A32444
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-149 <GOL>
A:Cross-references: UNIPROT:P17386; GB:J04353; NID:G333048; PIDN:AAA46950.1; PID:G459916
C:Comment: This protein may be involved in the oncogenic potential of this virus.
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match      87.5%; Score 49; DB 1; Length 149;
Best Local Similarity 88.9%; Pred. No. 0.082;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy      1 RFHNIRGRW 9
||||| |||
Db      124 RFHNIGRW 132

RESULT 9
W6WLJ5
E6 protein - human papillomavirus type 35
C:Species: human papillomavirus type 35
A:Note: host Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: E40824; S36521
R:Marich, J.E.; Pontsgler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776, 1992
A:Title: The phylogenetic relationship and complete nucleotide sequence of human papillomavirus
A:Reference number: A40824; MUID:92124753; PMID:1310198
A:Accession: E40824
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-149 <MAR>
A:Cross-references: UNIPROT:P27228; GB:M74117; NID:G333050; PIDN:AAA46966.1; PID:G333051
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36521
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-149 <DEL>
A:Cross-references: EMBL:X74477; NID:G396997; PIDN:CAA52561.1; PID:G396998
A:Experimental source: strain 35H
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match      87.5%; Score 49; DB 1; Length 149;
Best Local Similarity 88.9%; Pred. No. 0.082;
Matches 8; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

Qy      1 RFHNIRGRW 9
||||| |||
```

```
Db      124 RFHNIGRW 132

RESULT 10
W6WL51
E6 protein - human papillomavirus type 51
C:Species: human papillomavirus type 51
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: E40415
R:Lungu, O.; Crum, C.P.; Silverstein, S.J.
J. Virol. 65, 4216-4225, 1991
A:Title: Biologic properties and nucleotide sequence analysis of human papillomavirus
A:Reference number: A40415; MUID:91303675; PMID:1649326
A:Accession: E40415
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-151 <LUN>
A:Cross-references: UNIPROT:P26554; GB:MG2877
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match      78.6%; Score 44; DB 1; Length 151;
Best Local Similarity 77.8%; Pred. No. 0.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 RFHNIRGRW 9
||||| |||
Db      124 RFHEIAGRW 132

RESULT 11
S36544
E6 protein - human papillomavirus type 26
C:Species: human papillomavirus type 26
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36544
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36544
A:Molecule type: DNA
A:Residues: 1-150 <DEL>
A:Cross-references: UNIPROT:P36807; EMBL:X74472; NID:G396956; PIDN:CAA52530.1; PID:G396957
C:Superfamily: papillomavirus E6 protein
C:Keywords: early protein; zinc finger

Query Match      71.4%; Score 40; DB 2; Length 150;
Best Local Similarity 66.7%; Pred. No. 3.8;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 RFHNIRGRW 9
||||| |||
Db      124 RFHEIAGRW 132

RESULT 12
S15621
E6 protein - human papillomavirus type 57
C:Species: human papillomavirus type 57
A:Note: host Homo sapiens (man)
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C:Accession: S15621
R:Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.
Virus Res. 18, 81-98, 1990
A:Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and
A:Reference number: S15614; MUID:91188699; PMID:1964523
A:Accession: S15621
A:Molecule type: DNA
A:Residues: 1-153 <HIR>
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A;Cross-references: UNIPROT:P22158; EMBL:X55965; NID:g60882; PIDN:CAA39430.1; PID:g60883
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;29-65/Region: zinc finger CCCC motif
F;102-138/Region: zinc finger CCCC motif

Query Match 71.4%; Score 40; DB 1; Length 153;
Best Local Similarity 66.7%; Pred. No. 3.9;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RFHNRGRW 9
||| | | |
Db 123 RFHKISGW 131

RESULT 13
W6WLR1
E6 protein - rhesus papillomavirus (type 1)
C;Species: rhesus papillomavirus
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: A38503
R;Ostrow, R.S.; LaBresh, K.V.; Faras, A.J.
Virology 181, 424-429, 1991
A;Title: Characterization of the complete RHPV 1 genomic sequence and an integration loc
A;Reference number: A38503; MUID:91135018; PMID:1847267
A;Accession: A38503
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-191 <OST>
A;Cross-references: UNIPROT:P22159; EMBL:M37717
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;60-96/Region: zinc finger CCCC motif
F;133-169/Region: zinc finger CCCC motif

Query Match 71.4%; Score 40; DB 1; Length 191;
Best Local Similarity 66.7%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RFHNRGRW 9
||| | | |
Db 154 RFHRIAGW 162

RESULT 14
E69423
branched-chain amino acid ABC transporter, ATP-binding protein (braF-4) homolog - Archae
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Aug-2004
C;Accession: E69423
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: E69423
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-274 <KLE>
A;Cross-references: GB:AE001008; GB:AE000782; NID:g2689331; PIDN:AB89855.1; PID:g264918
C;Superfamily: ATP-binding cassette homology
C;Keywords: ATP; nucleotide binding; P-loop
F;36-241/Domain: ATP-binding cassette homology <ABC>
F;53-60/Region: nucleotide-binding motif A (P-loop)

Query Match 69.6%; Score 39; DB 2; Length 274;
Best Local Similarity 62.5%; Pred. No. 11;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FHNIRGRW 9

||: |||
Db 128 FHSVSGRW 135

RESULT 15

H71479

probable outer membrane protein analog - Chlamydia trachomatis (serotype D, strain UW3/
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C;Accession: H71479
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra
A;Reference number: A71570; MUID:9900809; PMID:9784136
A;Accession: H71479
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-340 <ARN>
A;Cross-references: UNIPROT:P38006; GB:AE001342; GB:AE001273; NID:g3329166; PIDN:AA6683
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: ompB

Query Match 69.6%; Score 39; DB 2; Length 340;
Best Local Similarity 62.5%; Pred. No. 13;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FHNIRGRW 9

||: |||
Db 319 FYNVEGRW 326

Search completed: June 29, 2005, 01:38:49
Job time : 12.2747 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:28:22 ; Search time 54.2473 Seconds
(without alignments)
84.958 Million cell updates/sec

Title: US-08-170-344-73
Perfect score: 56
Sequence: 1 RFHNRGRW 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	91	2 Q80887	Q80887 human papil
2	56	100.0	103	2 Q919D6	Q919D6 human papil
3	56	100.0	130	2 Q919B4	Q919B4 human papil
4	56	100.0	130	2 Q919B8	Q919B8 human papil
5	56	100.0	130	2 Q919C0	Q919C0 human papil
6	56	100.0	130	2 Q919C2	Q919C2 human papil
7	56	100.0	130	2 Q919C8	Q919C8 human papil
8	56	100.0	130	2 Q919D0	Q919D0 human papil
9	56	100.0	138	2 Q919D2	Q919D2 human papil
10	56	100.0	143	2 Q919B6	Q919B6 human papil
11	56	100.0	143	2 Q919C4	Q919C4 human papil
12	56	100.0	151	2 Q12335	Q12335 human papil
13	56	100.0	151	2 Q12336	Q12336 human papil
14	56	100.0	151	2 Q76TS0	Q76TS0 human papil
15	56	100.0	151	2 Q77816	Q77816 human papil
16	56	100.0	151	2 Q77E16	Q77E16 human papil
17	56	100.0	151	2 Q77JC7	Q77JC7 human papil
18	56	100.0	151	2 Q77ZJ5	Q77ZJ5 human papil
19	56	100.0	151	2 Q80963	Q80963 human papil
20	56	100.0	151	2 Q80966	Q80966 human papil
21	56	100.0	151	2 Q89640	Q89640 human papil
22	56	100.0	151	2 Q89648	Q89648 human papil
23	56	100.0	151	2 Q89708	Q89708 human papil
24	56	100.0	151	2 Q89755	Q89755 human papil
25	56	100.0	151	2 Q89852	Q89852 human papil
26	56	100.0	151	2 Q89887	Q89887 human papil
27	56	100.0	151	2 Q8B564	Q8B564 human papil
28	56	100.0	151	2 Q8BB19	Q8BB19 human papil
29	56	100.0	151	2 Q8BB20	Q8BB20 human papil
30	56	100.0	151	2 Q8BB21	Q8BB21 human papil
31	56	100.0	151	2 Q9W8C3	Q9W8C3 human papil

32	56	100.0	151	2 Q9W931	Q9W931 human papil
33	56	100.0	151	2 Q9WMP2	Q9WMP2 human papil
34	56	100.0	151	2 Q9WMP3	Q9WMP3 human papil
35	56	100.0	151	2 Q9WMP4	Q9WMP4 human papil
36	56	100.0	151	2 Q9WMP5	Q9WMP5 human papil
37	56	100.0	158	1 VE6_HPVI6	P3126 human papil
38	56	100.0	158	2 Q8JMU8	Q8JMU8 human papil
39	56	100.0	158	2 Q8JMU0	Q8JMU0 human papil
40	56	100.0	158	2 Q8QHP5	Q8QHP5 human papil
41	56	100.0	158	2 Q8QHT0	Q8QHT0 human papil
42	56	100.0	158	2 Q8QRD5	Q8QRD5 human papil
43	56	100.0	158	2 Q8QRD6	Q8QRD6 human papil
44	56	100.0	158	2 Q8QRD7	Q8QRD7 human papil
45	56	100.0	158	2 Q8QRD8	Q8QRD8 human papil

ALIGNMENTS

RESULT 1

Q80887 PRELIMINARY; PRT; 91 AA.
AC Q80887;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Hager D.G.; Galuira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U14516; AAB60570.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR NON_TER 1
FT NON TER 91
SQ SEQUENCE 91 AA; 11136 MW; 22PDF3EA185ACBA7 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFHNRGRW 9
|||
Db 83 RFHNRGRW 91

RESULT 2

Q919D6 PRELIMINARY; PRT; 103 AA.
AC Q919D6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RL "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
Int. J. Cancer 97:868-874(2002).

```
DR EMBL; AF404692; AAL01342.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 103 AA; 12422 MW; 6F90CBAF1F25449B CRC64;

Query Match 100.0%; Score 56; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. NO. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFHNRGRW 9
Db 76 RFHNRGRW 84

RESULT 3
Q919B4 ID Q919B4 PRELIMINARY; PRT; 130 AA.
AC Q919B4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404703; AAL01363.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227BEDDC CRC64;

Query Match 100.0%; Score 56; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. NO. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFHNRGRW 9
Db 103 RFHNRGRW 111

RESULT 4
Q919B8 ID Q919B8 PRELIMINARY; PRT; 130 AA.
AC Q919B8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404701; AAL01359.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
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DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15775 MW; 92D3C07BF96B092F CRC64;

Query Match 100.0%; Score 56; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. NO. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFHNRGRW 9
Db 103 RFHNRGRW 111

RESULT 5
Q919C0 ID Q919C0 PRELIMINARY; PRT; 130 AA.
AC Q919C0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404700; AAL01357.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. NO. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFHNRGRW 9
Db 103 RFHNRGRW 111

RESULT 6
Q919C2 ID Q919C2 PRELIMINARY; PRT; 130 AA.
AC Q919C2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404699; AAL01355.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
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Query Match      100.0%; Score 56; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFHNRGRW 9
Db 103 RFHNRGRW 111

RESULT 7
ID Q919C8 PRELIMINARY; PRT; 130 AA.
AC Q919C8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404696; AA01349.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;

Query Match      100.0%; Score 56; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFHNRGRW 9
Db 103 RFHNRGRW 111

RESULT 8
ID Q919D0 PRELIMINARY; PRT; 130 AA.
AC Q919D0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404695; AA01347.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15735 MW; 9FB30EEDCA21AF3 CRC64;

Query Match      100.0%; Score 56; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFHNRGRW 9
Db 103 RFHNRGRW 111

RESULT 9
ID Q919D2 PRELIMINARY; PRT; 138 AA.
AC Q919D2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404694; AA01345.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 138 AA; 16696 MW; 481ESA90895FC2 CRC64;

Query Match      100.0%; Score 56; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFHNRGRW 9
Db 111 RFHNRGRW 119

RESULT 10
ID Q919B6 PRELIMINARY; PRT; 143 AA.
AC Q919B6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404702; AA01361.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;

Query Match      100.0%; Score 56; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFHNRGRW 9
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Db |||||
116 RFNIRGRW 124

RESULT 11
Q919C4 PRELIMINARY; PRT; 143 AA.
ID Q919C4
AC Q919C4
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846223; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404698; AAL01353.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFNIRGRW 9
|||
Db 116 RFNIRGRW 124

RESULT 12
ID Q12335 PRELIMINARY; PRT; 151 AA.
AC Q12335
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003015; AAB70732.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18238 MW; BFF32A8B016CC88B CRC64;

Query Match 100.0%; Score 56; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFNIRGRW 9
|||
Db 124 RFNIRGRW 132

RESULT 13
O12336 PRELIMINARY; PRT; 151 AA.
ID O12336
AC O12336
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003016; AAB70733.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;

Query Match 100.0%; Score 56; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFNIRGRW 9
|||
Db 124 RFNIRGRW 132

RESULT 14
Q76TS0 PRELIMINARY; PRT; 151 AA.
ID Q76TS0
AC Q76TS0
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RE EMBL; U34114; AAA91661.1; -.
DR EMBL; U34125; AAA91672.1; -.
DR EMBL; U34130; AAA91677.1; -.
DR EMBL; U34131; AAA91678.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFHNRGRW 9
Db 124 RFHNRGRW 132

RESULT 15

Q778I6 PRELIMINARY; PRT; 151 AA.
AC Q778I6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388056; CAB45104.1; -;
DR EMBL; AJ388061; CAB45114.1; -;
DR EMBL; AJ388066; CAB45124.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18334 MW; FF8F2A2FCEBA6C02 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFHNRGRW 9
Db 124 RFHNRGRW 132

Search completed: June 29, 2005, 01:34:49
Job time : 54.2473 secs

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OM protein - protein search, using sw model

Run on: June 29, 2005, 05:18:25 ; Search time 53.8517 Seconds
(without alignments)
64.268 Million cell updates/sec

Title: US-08-170-344-73

Perfect score: 56

Sequence: 1 RFNIRGRW 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	15	16	US-10-476-570-43
2	56	100.0	20	16	US-10-476-570-41
3	56	100.0	22	16	US-10-476-570-56
4	56	100.0	22	17	US-10-858-384-10
5	56	100.0	23	16	US-10-476-570-40
6	56	100.0	151	14	US-10-177-390-6
7	56	100.0	151	17	US-10-484-063-20
8	56	100.0	151	17	US-10-484-063-27
9	56	100.0	158	17	US-10-858-384-2
10	56	100.0	158	17	US-10-367-057-16
11	56	100.0	171	16	US-10-472-724-2

12	56	100.0	266	9	US-09-367-309A-1	Sequence 1, Appli
13	56	100.0	273	13	US-10-000-903-4	Sequence 4, Appli
14	56	100.0	273	17	US-10-899-771-4	Sequence 4, Appli
15	56	100.0	292	13	US-10-000-903-10	Sequence 10, Appli
16	56	100.0	292	17	US-10-899-771-10	Sequence 10, Appli
17	56	100.0	371	13	US-10-000-903-6	Sequence 6, Appli
18	56	100.0	371	17	US-10-899-771-6	Sequence 6, Appli
19	56	100.0	390	13	US-10-000-903-14	Sequence 14, Appli
20	56	100.0	390	17	US-10-899-771-14	Sequence 14, Appli
21	45	80.4	14	16	US-10-476-570-42	Sequence 42, Appli
22	41	73.2	317	17	US-10-774-355A-1752	Sequence 1752, Ap
23	40	71.4	114	16	US-10-767-701-60553	Sequence 60553, A
24	40	71.4	557	15	US-10-424-599-182541	Sequence 182541,
25	39	69.6	18	14	US-10-094-407A-33	Sequence 33, Appli
26	39	69.6	20	17	US-10-938-249-534	Sequence 534, App
27	39	69.6	126	16	US-10-425-115-290549	Sequence 290549,
28	39	69.6	340	9	US-09-775-195-2	Sequence 2, Appli
29	39	69.6	340	9	US-09-775-195-5	Sequence 5, Appli
30	39	69.6	340	9	US-09-775-195-6	Sequence 6, Appli
31	39	69.6	340	14	US-10-155-947-2	Sequence 2, Appli
32	39	69.6	340	14	US-10-155-947-5	Sequence 5, Appli
33	39	69.6	340	14	US-10-155-947-6	Sequence 6, Appli
34	39	69.6	340	14	US-10-094-407A-2	Sequence 2, Appli
35	39	69.6	340	14	US-10-094-407A-5	Sequence 5, Appli
36	39	69.6	340	14	US-10-094-407A-6	Sequence 6, Appli
37	39	69.6	340	16	US-10-467-534-2	Sequence 2, Appli
38	39	69.6	340	16	US-10-467-534-17	Sequence 17, Appli
39	39	69.6	340	17	US-10-498-327-201	Sequence 201, App
40	39	69.6	407	15	US-10-425-114-44733	Sequence 44733, A
41	39	69.6	423	15	US-10-425-114-36574	Sequence 36574, A
42	39	69.6	616	16	US-10-425-115-207255	Sequence 207255,
43	38	67.9	20	17	US-10-938-249-537	Sequence 537, App
44	38	67.9	260	16	US-10-437-963-133492	Sequence 133492,
45	38	67.9	290	16	US-10-425-115-241846	Sequence 241846,

ALIGNMENTS

RESULT 1

US-10-476-570-43
; Sequence 43, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from B6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 130-144

Query Match 100.0%; Score 56; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFNIRGRW 9
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Db 2 RFNIRGRW 10

RESULT 2
US-10-476-570-41
; Sequence 41, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 20
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 121-140
US-10-476-570-41

Query Match 100.0%; Score 56; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.013; Length 20;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFNIRGRW 9
| | | | | | | |
Db 11 RFNIRGRW 19

RESULT 3
US-10-476-570-56
; Sequence 56, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 22
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 118-139
US-10-476-570-56

Query Match 100.0%; Score 56; DB 16; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.014; Length 22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFNIRGRW 9
| | | | | | | |
Db 14 RFNIRGRW 22

RESULT 4
US-10-858-384-10
; Sequence 10, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 10
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
; OTHER INFORMATION: for E6 of HPV
US-10-858-384-10

Query Match 100.0%; Score 56; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.014; Length 22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFNIRGRW 9
| | | | | | | |
Db 14 RFNIRGRW 22

RESULT 5
US-10-476-570-40
; Sequence 40, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 23
; TYPE: PRT

; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 118-140

US-10-476-570-40

Query Match 100.0%; Score 56; DB 16; Length 23;

Best Local Similarity 100.0%; Pred. No. 0.015;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFHNRGRW 9

Db 14 RFHNRGRW 22

RESULT 6

US-10-177-390-6

; Sequence 6, Application US/10177390

; Publication No. US20030143743A1

; GENERAL INFORMATION:

; APPLICANT: Schuler, Gerold

; APPLICANT: N.V. Antwerp Innovatiecentrum

; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear

; TITLE OF INVENTION: Polynucleotides by Electroporation

; FILE REFERENCE: 021505wo/JH/ml

; CURRENT APPLICATION NUMBER: US/10/177,390

; CURRENT FILING DATE: 2002-06-20

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6

; LENGTH: 151

; TYPE: PRT

; ORGANISM: Human papillomavirus type 16

US-10-177-390-6

Query Match 100.0%; Score 56; DB 14; Length 151;

Best Local Similarity 100.0%; Pred. No. 0.078;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFHNRGRW 9

Db 124 RFHNRGRW 132

RESULT 7

US-10-484-063-20

; Sequence 20, Application US/10484063

; Publication No. US20050048467A1

; GENERAL INFORMATION:

; APPLICANT: SASTRY, K. JAGANNADHA

; APPLICANT: TORTOLERO-LUNA, GUILLERMO

; APPLICANT: FOLLEN, MICHELE

; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED

; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN

; FILE REFERENCE: UTSC:560US

; CURRENT APPLICATION NUMBER: US/10/484,063

; CURRENT FILING DATE: 2004-01-16

; PRIOR APPLICATION NUMBER: PCT/US02/23198

; PRIOR FILING DATE: 2002-07-19

; PRIOR APPLICATION NUMBER: 60/306,809

; PRIOR FILING DATE: 2001-07-20

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 20

; LENGTH: 151

; TYPE: PRT

; ORGANISM: Human papillomavirus

US-10-484-063-20

Query Match 100.0%; Score 56; DB 17; Length 151;

Best Local Similarity 100.0%; Pred. No. 0.078;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFHNRGRW 9

Db 124 RFHNRGRW 132

RESULT 8

US-10-484-063-27

; Sequence 27, Application US/10484063

; Publication No. US20050048467A1

; GENERAL INFORMATION:

; APPLICANT: SASTRY, K. JAGANNADHA

; APPLICANT: TORTOLERO-LUNA, GUILLERMO

; APPLICANT: FOLLEN, MICHELE

; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED

; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN

; FILE REFERENCE: UTSC:560US

; CURRENT APPLICATION NUMBER: US/10/484,063

; CURRENT FILING DATE: 2004-01-16

; PRIOR APPLICATION NUMBER: PCT/US02/23198

; PRIOR FILING DATE: 2002-07-19

; PRIOR APPLICATION NUMBER: 60/306,809

; PRIOR FILING DATE: 2001-07-20

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 27

; LENGTH: 151

; TYPE: PRT

; ORGANISM: Human papillomavirus type 16

US-10-484-063-27

Query Match 100.0%; Score 56; DB 17; Length 151;

Best Local Similarity 100.0%; Pred. No. 0.078;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFHNRGRW 9

Db 124 RFHNRGRW 132

RESULT 9

US-10-858-384-2

; Sequence 2, Application US/10858384

; Publication No. US20050033025A1

; GENERAL INFORMATION:

; APPLICANT: CHOPPIN, JEANNINE

; APPLICANT: BOURGAULT VILLADA, ISABELLE

; APPLICANT: GUILLET, JEAN-GERARD

; APPLICANT: CONNAN, FRANCINE

; APPLICANT: FERRIES, ESTELLE

; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN

; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE

; FILE REFERENCE: 0508-1037-1

; CURRENT APPLICATION NUMBER: US/10/858,384

; CURRENT FILING DATE: 2004-06-02

; PRIOR APPLICATION NUMBER: FR 9907012

; PRIOR FILING DATE: 1999-06-03

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 2

; LENGTH: 158

; TYPE: PRT

; ORGANISM: Human Papillomavirus

US-10-858-384-2

Query Match 100.0%; Score 56; DB 17; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.082;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFHNRGRW 9

Db 131 RFHNRGRW 139

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RESULT 10
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match      100.0%; Score 56; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RFHNRGRW 9
Db      131 RFHNRGRW 139

RESULT 11
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match      100.0%; Score 56; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RFHNRGRW 9
Db      136 RFHNRGRW 144

RESULT 12
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM

```

```

; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match      100.0%; Score 56; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RFHNRGRW 9
Db      131 RFHNRGRW 139

RESULT 13
US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4

Query Match      100.0%; Score 56; DB 13; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RFHNRGRW 9
Db      237 RFHNRGRW 245

RESULT 14
US-10-899-771-4
; Sequence 4, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CPG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976

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; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeraic protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and B6 from Human papilloma virus type
US-10-899-771-4

Query Match      100.0%; Score 56; DB 17; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RHNIRGRW 9
Db      237 RHNIRGRW 245

RESULT 15
US-10-000-903-10
; Sequence 10, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-10

Query Match      100.0%; Score 56; DB 13; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RHNIRGRW 9
Db      256 RHNIRGRW 264
```

Search completed: June 29, 2005, 05:48:15
Job time : 53.8517 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:32:21 ; Search time 11.2747 Seconds
(without alignments)
76.805 Million cell updates/sec

Title: US-08-170-344-72

Perfect score: 51

Sequence: 1 CYSLYGTTL 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	158	1 W6WLHS	protein B6 - human
2	39	76.5	149	1 W6WL31	E6 protein - human
3	38	74.5	232	2 H95900	probable L-fuculos
4	38	74.5	473	2 S51256	probable membrane
5	38	74.5	1013	2 G82450	probable exonuclea
6	38	74.5	1160	2 T31688	Ca2+-transporting
7	37	72.5	323	2 T24836	hypothetical prote
8	36	70.6	91	2 E86512	hypothetical prote
9	36	70.6	91	2 D72109	hypothetical prote
10	36	70.6	148	2 A61237	E6 protein - human
11	36	70.6	148	2 S36573	E6 protein - human
12	36	70.6	149	1 W6WL58	E6 protein - human
13	36	70.6	255	2 S41690	cytochrome-c oxida
14	36	70.6	1068	2 S64015	pleiotropic drug r
15	35	68.6	262	2 T24439	hypothetical prote
16	35	68.6	429	2 D82181	GGDEF family prote
17	35	68.6	444	2 S35783	glycoprotein gx -
18	34	66.7	149	1 W6WL33	E6 protein - human
19	34	66.7	151	2 D83290	probable transcrip
20	34	66.7	155	1 W6WL56	E6 protein - human
21	34	66.7	155	2 A44890	E6 protein - human
22	34	66.7	191	1 W6WL81	E6 protein - rhesu
23	34	66.7	345	2 T22399	hypothetical prote
24	34	66.7	348	1 PABY	fructose-bisphosph
25	34	66.7	354	2 B55733	G protein-coupled
26	34	66.7	421	2 S40819	probable transport
27	34	66.7	421	2 C86075	probable resistanc
28	34	66.7	421	2 D91228	probable resistanc
29	34	66.7	604	2 H89914	hypothetical prote

ALIGNMENTS

RESULT 1

W6WLHS

protein B6 - human papillomavirus type 16

C;Species: human papillomavirus type 16

C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C;Accession: A03682; T10427

R;Sedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virology 145, 181-185, 1985

A;Title: Human papillomavirus type 16 DNA sequence.

A;Reference number: A22355; MUID:85246220; PMID:2990099

A;Accession: A03682

A;Molecule type: DNA

A;Residues: 1-158 <SEE>

A;Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G3330303

R;Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A;Title: A negative element in the human poapillomavirus type 16 genome acts at the lev

A;Reference number: Z17014; MUID:91162763; PMID:1848319

A;Accession: T10427

A;Status: preliminary; translated from GB/EMBL/DBD

A;Molecule type: DNA

A;Residues: 1-158 <KEN>

A;Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G33303032

C;Genetics: E6

C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; zinc finger

F;37-73/Region: zinc finger CCCC motif

F;110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 51; DB 1; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.024;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9

Db 87 CYSLYGTTL 95

RESULT 2

W6WL31

E6 protein - human papillomavirus type 31

C;Species: human papillomavirus type 31

A;Note: host Homo sapiens (man)

C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004

C;Accession: A32444

R;Goldsbrough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.

Virology 171, 306-311, 1989

A;Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-assoc

A;Reference number: A94398; MUID:89299478; PMID:2545036

A;Accession: A32444

A;Status: translation not shown

A;Molecule type: DNA
 A;Residues: 1-149 <GOL>
 A;Cross-references: UNIPROT:P17386; GB:J04353; NID:G333048; PIDN:AAA4950.1; PID:G459918
 C;Comment: This protein may be involved in the oncogenic potential of this virus.

C;Superfamily: papillomavirus E6 protein
 C;Keywords: DNA binding; early protein; zinc finger
 F;30-66/Region: zinc finger CCCC motif
 F;103-139/Region: zinc finger CCCC motif

Query Match 76.5%; Score 39; DB 1; Length 149;
 Best Local Similarity 87.5%; Pred. No. 4.3;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YSLYGTTL 9
 ||:||||
 Db 81 YSVYGTTL 88

RESULT 3

H95900
 probable L-fucose phosphate aldolase protein [imported] - *Sinorhizobium meliloti* (stra
 C;Species: *Sinorhizobium meliloti*
 C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C;Accession: H95900
 R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
 A;Reference number: A95842; MUID:21396508; PMID:11481431

A;Accession: H95900
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-232 <KUR>
 A;Cross-references: UNIPROT:Q9W73; GB:AL591985; PIDN:CAC48872.1; PID:G15140345; GSPDB:Q
 A;Experimental source: strain 1021, megaplasmid pSymB
 R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A;Title: The composite genome of the legume symbiont *Sinorhizobium meliloti*.
 A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation
 C;Genetics:
 A;Gene: fucA2; SMD20490
 A;Genome: plasmid

Query Match 74.5%; Score 38; DB 2; Length 232;
 Best Local Similarity 66.7%; Pred. No. 10;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9
 |:|:|
 Db 97 CHSIYATTL 105

RESULT 4

S51256
 probable membrane protein YDR105c - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: probable membrane protein YD8557.14c; probable membrane protein YD972
 C;Species: *Saccharomyces cerevisiae*
 C;Date: 23-Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004

C;Accession: S51256; S52671
 R;Murphy, L.; Harris, D.
 submitted to the EMBL Data Library, January 1995

A;Reference number: S51243
 A;Accession: S51256
 A;Molecule type: DNA

A;Residues: 1-473 <MUR>
 A;Cross-references: UNIPROT:Q12116; EMBL:Z47746; NID:G633627; PID:G633641; MIPS:YDR105c
 R;Murphy, L.; Shore, L.; Harris, D.
 submitted to the EMBL Data Library, March 1995
 A;Reference number: S52671

A;Accession: S52671
 A;Molecule type: DNA
 A;Residues: 1-473 <MUR>
 A;Cross-references: EMBL:Z48758; NID:G747879; PID:G747880; MIPS:YDR105c
 C;Genetics:

A;Cross-references: SGD:S0002512
 A;Map position: 4R

C;Keywords: transmembrane protein

F;4-20/Domain: transmembrane #status predicted <TM1>
 F;44-60/Domain: transmembrane #status predicted <TM2>
 F;90-106/Domain: transmembrane #status predicted <TM3>
 F;122-138/Domain: transmembrane #status predicted <TM4>
 F;150-166/Domain: transmembrane #status predicted <TM5>
 F;202-218/Domain: transmembrane #status predicted <TM6>
 F;228-244/Domain: transmembrane #status predicted <TM7>
 F;296-312/Domain: transmembrane #status predicted <TM8>
 F;401-417/Domain: transmembrane #status predicted <TM9>
 F;443-459/Domain: transmembrane #status predicted <TM10>

Query Match 74.5%; Score 38; DB 2; Length 473;
 Best Local Similarity 66.7%; Pred. No. 20;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9
 |:|:|
 Db 449 CYALYGTW 457

RESULT 5

G82450

probable exonuclease SbcC VCA0521 [imported] - *Vibrio cholerae* (strain N16961 serogroup

C;Species: *Vibrio cholerae*

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C;Accession: G82450

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
 chardson, D.; Ermlaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers,
 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000
 A;Title: DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: G82450

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1013 <HEI>

A;Cross-references: UNIPROT:Q9KMG7; GB:AE004382; GB:AE003853; NID:G9657917; PIDN:AAF964

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VCA0521

A;Map position: 2

Query Match 74.5%; Score 38; DB 2; Length 1013;
 Best Local Similarity 75.0%; Pred. No. 40;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 8
 |:|:|
 Db 49 CYALYGET 56

RESULT 6

T31688

Ca2+-transporting ATPase (EC 3.6.3.8), plasma membrane - *Paramecium tetraurelia*

C;Species: *Paramecium tetraurelia*

C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004

C;Accession: T31688

R;Elwess, N.L.; van Houten, J.L.

J. Eukaryot Microbiol. 44, 250-257, 1997

A;Title: Cloning and molecular analysis of the plasma membrane Ca(2+)-ATPase gene in *Pa*

A;Reference number: Z21062; MUID:97326901; PMID:9183714

A;Accession: T31688

A;Status: preliminary; translated from GB/EMBL/DBD

A;Molecule type: DNA

A;Residues: 1-1160 <ELW>

A;Cross-references: UNIPROT:Q27829; EMBL:U05880; NID:g505622; PID:g505623; PIDN:AAB81284
 C;Genetics:
 A;Genetic code: SGC5
 C;Superfamily: Nax/Kx-transporting ATPase alpha chain; ATPase nucleotide-binding domain
 C;Keywords: hydrolase

Query Match 74.5%; Score 38; DB 2; Length 1160;
 Best Local Similarity 66.7%; Pred. No. 46;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CYSLYGTTL 9
 |||||
 Db 1085 CYSYGLTI 1093

RESULT 7
 T24836
 hypothetical protein T11F9.3 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T24836
 R;Lennard, N.
 submitted to the EMBL Data Library, June 1996
 A;Reference number: Z19941
 A;Accession: T24836
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-323 <WIL>
 A;Cross-references: UNIPROT:Q22396; EMBL:Z74042; PIDN:CAA98528.1; GSPDB:GN00023; CESP:T11F9
 A;Experimental source: clone T11F9
 C;Genetics:
 A;Gene: CESP:T11F9.3
 A;Map position: 5
 A;Introns: 115/2; 229/3

Query Match 72.5%; Score 37; DB 2; Length 323;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYSLYG 6
 |||||
 Db 35 CYSLYG 40

RESULT 8
 E86512
 hypothetical protein CPj0173 [imported] - Chlamydophila pneumoniae (strain J138)
 C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: E86512
 R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ie
 Nucleic Acids Res. 28, 2311-2314, 2000
 A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
 A;Reference number: A86491; MUID:20330349; PMID:108711362
 A;Accession: E86512
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-91 <STO>
 A;Cross-references: UNIPROT:Q2911; GB:BA000008; NID:g9978546; PIDN:BAA98383.1; GSPDB:GN
 A;Experimental source: strain J138
 C;Genetics:
 A;Gene: CPj0173

Query Match 70.6%; Score 36; DB 2; Length 91;
 Best Local Similarity 62.5%; Pred. No. 10;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYSLYGTT 8
 |:|:|:|
 Db 51 CFSYVGTS 58

RESULT 9

D72109
 hypothetical protein CP0597 [imported] - Chlamydophila pneumoniae (strains CWL029 and A
 C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
 C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C;Accession: D72109; D81558
 R;Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.
 Nature Genet. 21, 385-389, 1999
 A;Title: Comparative Genomes of Chlamydia pneumoniae and C. trachomatis.
 A;Reference number: A72000; MUID:99206606; PMID:10192388
 A;Accession: D72109
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-91 <ARN>
 A;Cross-references: UNIPROT:Q2911; GB:AE001604; GB:AE001363; NID:g4376438; PIDN:AAD183
 A;Experimental source: strain CWL029
 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
 C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg
 Nucleic Acids Res. 28, 1397-1406, 2000
 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
 A;Reference number: A81500; MUID:20150255; PMID:10684935
 A;Accession: D81558
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-91 <REA>
 A;Cross-references: GB:AE002218; GB:AE002161; NID:g7189509; PIDN:AAF38414.1; PID:g71895
 A;Experimental source: strain AR39, HL cells
 C;Genetics:
 A;Gene: CPn0173; CP0597

Query Match 70.6%; Score 36; DB 2; Length 91;
 Best Local Similarity 62.5%; Pred. No. 10;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYSLYGTT 8
 |:|:|:|
 Db 51 CFSYVGTS 58

RESULT 10
 A61237
 E6 protein - human papillomavirus type 52
 C;Species: human papillomavirus type 52
 C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 03-May-1996
 C;Accession: A61237
 R;Takami, Y.; Kondoh, G.; Saito, J.; Noda, K.; Sudiro, T.M.; Sjahrurachman, A.; Warsa,
 Int. J. Cancer 48, 516-522, 1991
 A;Title: Cloning and characterization of human papillomavirus type 52 from cervical car
 A;Reference number: A61237; MUID:91258022; PMID:1646174
 A;Accession: A61237
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-148 <TAK>
 C;Superfamily: papillomavirus E6 protein

Query Match 70.6%; Score 36; DB 2; Length 148;
 Best Local Similarity 87.5%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 YSLYGTTL 9
 |||||
 Db 81 YSLYGTTL 88

RESULT 11
 S36573
 E6 protein - human papillomavirus type 52
 C;Species: human papillomavirus type 52
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C;Accession: S36573
 R;Delius, H.; Hofmann, B.
 submitted to the EMBL Data Library, August 1993
 A;Description: Primer-directed sequencing of human papillomavirus types.
 A;Reference number: S36469

```

A;Accession: S36573
A;Molecule type: DNA
A;Residues: 1-148 <DEL>
A;Cross-references: UNIPROT:P36814; EMBL:X74481; NID:G397038; PIDN:CAA52585.1; PID:G3970
C;Species: papillomavirus B6 protein
C;Superfamily: papillomavirus B6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match      70.6%; Score 36; DB 2; Length 148;
Best Local Similarity 87.5%; Pred. No. 16;
Matches      7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 YSLYGTTL 9
      |||||
Db      81 YSLYGDTL 88

RESULT 12
W6WL58
E6 protein - human papillomavirus type 58
C;Species: human papillomavirus type 58
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: E36779
R;Kirii, Y.; Iwamoto, S.; Matsukura, T.
Virology 185, 424-427, 1991
A;Title: Human papillomavirus type 58 DNA sequence.
A;Reference number: A36779; MUID:92024102; PMID:1656594
A;Accession: E36779
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-149 <KIR>
A;Cross-references: UNIPROT:P25555; GB:D90400; NID:G222386; PIDN:BA431845.1; PID:G333709
C;Superfamily: papillomavirus B6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif

Query Match      70.6%; Score 36; DB 1; Length 149;
Best Local Similarity 87.5%; Pred. No. 16;
Matches      7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 YSLYGTTL 9
      |||||
Db      81 YSLYGDTL 88

RESULT 13
S41690
Cytochrome-c oxidase (EC 1.9.3.1) chain III - Theileria parva mitochondrion
C;Species: mitochondrion Theileria parva
C;Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: S41690; S40155
R;Kairo, A.; Fairlamb, A.H.; Gobright, E.; Nene, V.
EMBO J. 13, 898-905, 1994
A;Title: A 7.1 kb linear DNA molecule of Theileria parva has scrambled rDNA sequences an
A;Reference number: S41689; MUID:94155854; PMID:8112303
A;Accession: S41690
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-255 <KAI>
A;Cross-references: UNIPROT:Q36098; EMBL:Z23263; NID:G437862; PIDN:CAA80799.1; PID:G4378
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1993
C;Genetics:
A;Genome: mitochondrion
A;Genetic code: SGC6
C;Superfamily: cytochrome-c oxidase chain III
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match      70.6%; Score 36; DB 2; Length 255;
Best Local Similarity 87.5%; Pred. No. 26;
Matches      7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 YSLYGTTL 9

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Db      50 YLLYGTTL 57
      |||||

RESULT 14
S64015
pleiotropic drug resistance control protein PDR1 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein G3722; protein YGL013c
C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 16-Aug-2004
C;Accession: S64015; S31560; A28466
R;Hebling, U.; Hofmann, B.; Delius, H.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64003
A;Accession: S64015
A;Molecule type: DNA
A;Residues: 1-1068 <HEB>
A;Cross-references: UNIPROT:P12383; EMBL:Z72535; NID:G1322470; PIDN:CAA96713.1; PID:e24
A;Experimental source: strain S288C
R;Chen, W.; Balzi, E.; Capiteaux, E.; Choder, M.; Goffeau, A.
Yeast 7, 287-299, 1991
A;Title: The DNA sequencing of the 17 kb HindIII fragment spanning the LEU1 and ATE1 lo
ntrolling pleiotropic drug resistance.
A;Reference number: S15040; MUID:91353083; PMID:1882553
A;Accession: S31560
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-410,'K',412-529,'R',531-819,'A',821-920,'I',922-980,'S',982-1009,1015-106
A;Cross-references: GB:S58126
R;Balzi, E.; Chen, W.; Ulaszewski, S.; Capiteaux, E.; Goffeau, A.
J. Biol. Chem. 262, 16871-16879, 1987
A;Title: The multidrug resistance gene PDR1 from Saccharomyces cerevisiae.
A;Reference number: A28466; MUID:88059084; PMID:3316228
A;Accession: A28466
A;Molecule type: DNA
A;Residues: 1-410,'K',412-819,'A',821-920,'I',922-980,'S',982-1009,1015-1068 <BAL>
A;Cross-references: EMBL:J03487; NID:G17211; PIDN:AAA34849.1; PID:G172112
C;Genetics:
A;Gene: SGD:PDR1
A;Cross-references: SGD:S0002981; MIPS:YGL013c
A;Map position: 7L
C;Superfamily: GAL4 zinc binuclear cluster homology
C;Keywords: transmembrane protein
F;41-77/Domain: GAL4 zinc binuclear cluster homology <GAL4>
F;754-770/Domain: transmembrane #status predicted <TM1>
F;812-828/Domain: transmembrane #status predicted <TM2>

Query Match      70.6%; Score 36; DB 2; Length 1068;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches      6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CYSLYGTTL 9
      |||||
Db      450 CYSVYNSTL 458

RESULT 15
T24439
hypothetical protein T04B2.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24439
R;Coles, L.
submitted to the EMBL Data Library, December 1995
A;Reference number: Z19890
A;Accession: T24439
A;Status: preliminary; translated from GB/EMBL/DBDB
A;Molecule type: DNA
A;Residues: 1-262 <WIL>
A;Cross-references: UNIPROT:Q22149; EMBL:Z69299; PIDN:CAA92612.1; GSPDB:GN000022; CESP:T
A;Experimental source: clone T04B2
C;Genetics:
A;Gene: CESP:T04B2.6

```


A:Map position: 4
A:Introns: 43/3; 124/3; 221/3; 243/1
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 68.6%; Score 35; DB 2; Length 262;
Best Local Similarity 75.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CYSLYGTT 8
|||
Db 93 CYELYETT 100

Search completed: June 29, 2005, 01:38:48
Job time : 12.2747 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:28:22 ; Search time 54.2473 Seconds
(without alignments)
84.958 Million cell updates/sec

Title: US-08-170-344-72

Perfect score: 51

Sequence: 1 CYSLYGTTL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	90	2 Q80883	Q80883 human papil
2	51	100.0	90	2 Q80884	Q80884 human papil
3	51	100.0	90	2 Q80885	Q80885 human papil
4	51	100.0	99	2 Q91982	Q91982 human papil
5	51	100.0	103	2 Q91986	Q91986 human papil
6	51	100.0	130	2 Q91984	Q91984 human papil
7	51	100.0	130	2 Q919D0	Q919D0 human papil
8	51	100.0	151	2 Q12336	Q12336 human papil
9	51	100.0	151	2 Q76TS0	Q76TS0 human papil
10	51	100.0	151	2 Q77816	Q77816 human papil
11	51	100.0	151	2 Q77E16	Q77E16 human papil
12	51	100.0	151	2 Q80966	Q80966 human papil
13	51	100.0	151	2 Q89640	Q89640 human papil
14	51	100.0	151	2 Q89708	Q89708 human papil
15	51	100.0	151	2 Q89755	Q89755 human papil
16	51	100.0	151	2 Q8B564	Q8B564 human papil
17	51	100.0	151	2 Q9W8C3	Q9W8C3 human papil
18	51	100.0	151	2 Q9W931	Q9W931 human papil
19	51	100.0	151	2 Q9WMP2	Q9WMP2 human papil
20	51	100.0	151	2 Q9WMP4	Q9WMP4 human papil
21	51	100.0	158	1 V86.HPV16	V86.HPV16 human papil
22	51	100.0	158	2 Q8JMU8	Q8JMU8 human papil
23	51	100.0	158	2 Q8QHN0	Q8QHN0 human papil
24	51	100.0	158	2 Q8QHP5	Q8QHP5 human papil
25	51	100.0	158	2 Q8QHT0	Q8QHT0 human papil
26	51	100.0	158	2 Q8QRD6	Q8QRD6 human papil
27	51	100.0	158	2 Q8QRD7	Q8QRD7 human papil
28	51	100.0	158	2 Q8QRD8	Q8QRD8 human papil
29	51	100.0	158	2 Q8QRD9	Q8QRD9 human papil
30	51	100.0	158	2 Q8QRE0	Q8QRE0 human papil
31	51	100.0	158	2 Q8QRE1	Q8QRE1 human papil

32 51 100.0 158 2 Q9QDH3 Q9qdh3 human papil
33 51 100.0 158 2 Q9QDH5 Q9qdh5 human papil
34 51 100.0 158 2 Q9QDH7 Q9qdh7 human papil
35 51 100.0 158 2 Q9QDH9 Q9qdh9 human papil
36 51 100.0 161 2 Q919B1 Q919b1 human papil
37 51 100.0 161 2 Q919C6 Q919c6 human papil
38 51 100.0 161 2 Q919D4 Q919d4 human papil
39 48 94.1 81 2 Q80886 Q80886 human papil
40 48 94.1 84 2 Q80882 Q80882 human papil
41 48 94.1 91 2 Q80887 Q80887 human papil
42 48 94.1 130 2 Q919B8 Q919b8 human papil
43 48 94.1 130 2 Q919C0 Q919c0 human papil
44 48 94.1 130 2 Q919C2 Q919c2 human papil
45 48 94.1 130 2 Q919C8 Q919c8 human papil

ALIGNMENTS

RESULT 1

Q80883 ID Q80883 PRELIMINARY; PRT; 90 AA.
AC Q80883; 1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14512; AAB60566.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR NON TER 1 1
FT NON TER 90 90
SQ SEQUENCE 90 AA; 10904 MW; 5D3ADF843AD6060B CRC64;

Query Match 100.0%; Score 51; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYSLYGTTL 9
|||
DB 39 CYSLYGTTL 47

RESULT 2

Q80884 ID Q80884 PRELIMINARY; PRT; 90 AA.
AC Q80884; 1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14513; AAB60567.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.

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DR GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1 1
SQ SEQUENCE 90 AA; 11021 MW; 47F42BBEFAACCC01 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9
| | | | |
Db 39 CYSLYGTTL 47

RESULT 3
Q80885
ID Q80885 PRELIMINARY; PRT; 90 AA.
AC Q80885;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14514; AAB60568.2; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1 1
FT NON_TER 90 90
SQ SEQUENCE 90 AA; 10964 MW; BC2531643ACBA76C CRC64;

Query Match 100.0%; Score 51; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9
| | | | |
Db 39 CYSLYGTTL 47

RESULT 4
Q919B2
ID Q919B2 PRELIMINARY; PRT; 99 AA.
AC Q919B2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404704; AAL01365.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
FT NON_TER 1 1
FT NON_TER 99 99
SQ SEQUENCE 99 AA; 12005 MW; C2B96025EC370E38 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9
| | | | |
Db 56 CYSLYGTTL 64

RESULT 5
Q919D6
ID Q919D6 PRELIMINARY; PRT; 103 AA.
AC Q919D6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404692; AAL01342.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1 1
FT NON_TER 103 103
SQ SEQUENCE 103 AA; 12422 MW; 6F90CBAPF25449B CRC64;

Query Match 100.0%; Score 51; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9
| | | | |
Db 32 CYSLYGTTL 40

RESULT 6
Q919B4
ID Q919B4 PRELIMINARY; PRT; 130 AA.
AC Q919B4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404703; AAL01363.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1 1
FT NON_TER 130 130
SQ SEQUENCE 130 AA; 14422 MW; 6F90CBAPF25449B CRC64;
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SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227BEDDC CRC64;

Query Match 100.0%; Score 51; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.086;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9
Db 59 CYSLYGTTL 67
|||||

RESULT 7

Q919D0 ID Q919D0 PRELIMINARY; PRT; 130 AA.
AC Q919D0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart V.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF04695; AAL01347.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15735 MW; 98FB30EDCA21AF3 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.086;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9
Db 59 CYSLYGTTL 67
|||||

RESULT 8

O12336 ID O12336 PRELIMINARY; PRT; 151 AA.
AC O12336;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003016; AAB70733.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;

Query Match 100.0%; Score 51; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9
Db 80 CYSLYGTTL 88
|||||

RESULT 9

Q76TS0 ID Q76TS0 PRELIMINARY; PRT; 151 AA.
AC Q76TS0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34114; AAA91661.1; -;
DR EMBL; U34125; AAA91672.1; -;
DR EMBL; U34130; AAA91677.1; -;
DR EMBL; U34131; AAA91678.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9
Db 80 CYSLYGTTL 88
|||||

RESULT 10

Q77816 ID Q77816 PRELIMINARY; PRT; 151 AA.
AC Q77816;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheljen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).

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DR EMBL; AJ388056; CAB45104.1; -.
DR EMBL; AJ388061; CAB45114.1; -.
DR EMBL; AJ388066; CAB45124.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18334 MW; FF8F2A2FCEBA6C02 CRC64;

Query Match      100.0%; Score 51; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTTL 9
Db 80 CYSLYGTTTL 88

RESULT 11
Q77E16 PRELIMINARY; PRT; 151 AA.
AC Q77E16;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 oncoprotein (E6 protein).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AF003014; AAB70731.1; -.
DR EMBL; AF003017; AAB70734.1; -.
DR EMBL; AF472508; AAO15697.1; -.
DR EMBL; AJ388068; CAB45128.1; -.
DR EMBL; AF003013; AAB70730.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;

Query Match      100.0%; Score 51; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTTL 9
Db 80 CYSLYGTTTL 88

RESULT 13
Q89640 PRELIMINARY; PRT; 151 AA.
ID Q89640;
AC Q89640;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RA "Human papillomavirus type 16 variant lineages in United States
RA populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RX SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34129; AAA91676.1; -.
DR EMBL; AF469198; AAO15693.1; -.
DR EMBL; U34115; AAA91662.1; -.
DR EMBL; U34120; AAA91667.1; -.
DR EMBL; U34124; AAA91671.1; -.
DR
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DR EMBL; AJ388056; CAB45104.1; -.
DR EMBL; AJ388061; CAB45114.1; -.
DR EMBL; AJ388066; CAB45124.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18334 MW; FF8F2A2FCEBA6C02 CRC64;

Query Match      100.0%; Score 51; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTTL 9
Db 80 CYSLYGTTTL 88

RESULT 11
Q77E16 PRELIMINARY; PRT; 151 AA.
AC Q77E16;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 oncoprotein (E6 protein).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AF469197; AAO15691.1; -.
DR EMBL; AJ388063; CAB45118.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CF1F CRC64;

Query Match      100.0%; Score 51; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTTL 9
Db 80 CYSLYGTTTL 88

RESULT 12
Q80966 PRELIMINARY; PRT; 151 AA.
ID Q80966;
AC Q80966; Q12650; Q12651; Q12652; Q12925; Q12926; Q12927; Q80962;
AC Q80964; Q80965;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10581;
RN [1]
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DR GO:0042025; C:host cell nucleus; IEA.
 DR GO:0003677; F:DNA binding; IEA.
 DR InterPro: IPR001334; E6.
 DR Pfam: PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18348 MW; FF3F2A2FCF0A6CB2 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9
 |||||
 Db 80 CYSLYGTTL 88

RESULT 14

Q89708 PRELIMINARY; PRT; 151 AA.
 ID Q89708
 AC Q89708;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Early transforming protein E6.
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OC NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96079021; PubMed=7494284;
 RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
 RA Jenison S.A.;
 RT "Human papillomavirus type 16 variant lineages in United States
 RT populations characterized by nucleotide sequence analysis of the E6,
 RT L2, and L1 coding segments.";
 RL J. Virol. 69:7743-7753(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Farmer A.D.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U34128; AAA91675.1; -.
 DR EMBL; U34128; AAA91664.1; -.
 DR EMBL; U34118; AAA91665.1; -.
 DR GO:0042025; C:host cell nucleus; IEA.
 DR GO:0003677; F:DNA binding; IEA.
 DR InterPro: IPR001334; E6.
 DR Pfam: PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CF1F CRC64;

Query Match 100.0%; Score 51; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9
 |||||
 Db 80 CYSLYGTTL 88

RESULT 15

Q89755 PRELIMINARY; PRT; 151 AA.
 ID Q89755
 AC Q89755;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Early transforming protein E6.
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OC NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96079021; PubMed=7494284;

RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
 RA Jenison S.A.;
 RT "Human papillomavirus type 16 variant lineages in United States
 RT populations characterized by nucleotide sequence analysis of the E6,
 RT L2, and L1 coding segments.";
 RL J. Virol. 69:7743-7753(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Farmer A.D.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U34126; AAA91673.1; -.
 DR EMBL; U34111; AAA91658.1; -.
 DR EMBL; U34121; AAA91668.1; -.
 DR EMBL; U34123; AAA91670.1; -.
 DR GO:0042025; C:host cell nucleus; IEA.
 DR GO:0003677; F:DNA binding; IEA.
 DR InterPro: IPR001334; E6.
 DR Pfam: PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18334 MW; FF8F2A2FCFBA6C02 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9
 |||||
 Db 80 CYSLYGTTL 88

Search completed: June 29, 2005, 01:34:49
 Job time : 54.2473 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:37:59 ; Search time 16.8626 Seconds
(without alignments)
39.842 Million cell updates/sec

Title: US-08-170-344-73
Perfect score: 56
Sequence: 1 RFNIRGRW 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	9	3	US-08-159-339A-245 Sequence 245, App
2	56	100.0	20	4	US-09-601-729-278 Sequence 278, App
3	56	100.0	21	2	US-08-934-915-166 Sequence 166, App
4	56	100.0	22	4	US-09-980-523A-10 Sequence 10, Appl
5	56	100.0	158	4	US-09-980-523A-2 Sequence 2, Appli
6	56	100.0	162	1	US-08-316-239B-3 Sequence 3, Appli
7	56	100.0	162	1	US-08-316-239B-4 Sequence 4, Appli
8	56	100.0	172	3	US-08-860-165-12 Sequence 12, Appl
9	56	100.0	172	3	US-09-359-382-12 Sequence 12, Appl
10	56	100.0	182	1	US-08-117-083-10 Sequence 10, Appl
11	56	100.0	266	3	US-08-860-165-10 Sequence 10, Appl
12	56	100.0	266	3	US-09-359-382-10 Sequence 10, Appl
13	56	100.0	266	4	US-09-367-309A-1 Sequence 1, Appli
14	56	100.0	273	3	US-09-485-885-4 Sequence 4, Appli
15	56	100.0	292	3	US-09-485-885-10 Sequence 10, Appl
16	56	100.0	371	3	US-09-485-885-6 Sequence 6, Appli
17	56	100.0	390	3	US-09-485-885-14 Sequence 14, Appl
18	37	66.1	203	4	US-09-270-767-44358 Sequence 44358, A
19	36	64.3	85	4	US-09-489-039A-9554 Sequence 9554, Ap
20	36	64.3	158	2	US-08-247-904B-10 Sequence 10, Appl
21	36	64.3	158	3	US-08-767-942A-19 Sequence 19, Appl
22	36	64.3	211	3	US-09-105-567A-7 Sequence 7, Appli
23	36	64.3	211	3	US-09-511-720-7 Sequence 7, Appli
24	36	64.3	211	4	US-09-844-036A-7 Sequence 7, Appli
25	36	64.3	271	1	US-08-117-083-14 Sequence 14, Appl
26	36	64.3	278	3	US-09-485-885-21 Sequence 21, Appl
27	36	64.3	383	3	US-09-485-885-23 Sequence 23, Appl

28	65	62.5	4	US-09-107-532A-4549	Sequence 4549, A
29	105	62.5	4	US-09-489-039A-13486	Sequence 13486, A
30	130	62.5	4	US-09-732-210-1457	Sequence 1457, Ap
31	149	62.5	4	US-09-252-991A-19603	Sequence 19603, A
32	165	62.5	4	US-09-252-991A-24061	Sequence 24061, A
33	193	62.5	4	US-09-489-039A-9244	Sequence 9244, Ap
34	215	62.5	4	US-09-252-991A-19156	Sequence 19156, A
35	383	62.5	4	US-09-107-532A-5773	Sequence 5773, Ap
36	391	62.5	4	US-09-489-039A-13161	Sequence 13161, A
37	511	62.5	4	US-09-492-709A-259	Sequence 259, App
38	627	62.5	3	US-09-468-578-4	Sequence 4, Appli
39	627	62.5	4	US-09-868-839-4	Sequence 4, Appli
40	654	62.5	4	US-09-270-767-45252	Sequence 45252, A
41	10	60.7	1	US-07-909-122-5	Sequence 5, Appli
42	114	60.7	4	US-09-252-991A-25775	Sequence 25775, A
43	181	60.7	4	US-09-252-991A-26910	Sequence 26910, A
44	191	60.7	1	US-08-531-525-28	Sequence 28, Appl
45	191	60.7	2	US-08-718-270A-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-08-159-339A-245
; Sequence 245, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 245:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-245

Query Match 100.0%; Score 56; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFNIRGRW 9
| | | | |
Db 1 RFNIRGRW 9

RESULT 2

US-09-601-729-278
; Sequence 278, Application US/09601729
; Patent No. 6683052
; GENERAL INFORMATION:
; APPLICANT: THIAM, KADER
; APPLICANT: AUBIAULT, CLAUDE
; APPLICANT: GRAS-MASSE, HELENE
; APPLICANT: LOING, ESTELLE
; APPLICANT: VERWAERDE, CLAUDIE
; APPLICANT: GUILLET, JEAN GERARD
; TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES
; TITLE OF INVENTION: THEREOF IN PHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: USB-97-AU-IN
; CURRENT APPLICATION NUMBER: US/09/601.729
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: PCT/FR99/00259
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 98 01439
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 278
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-601-729-278

Query Match 100.0%; Score 56; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFNIRGRW 9
| | | | |
Db 11 RFNIRGRW 19

RESULT 3

US-08-934-915-166
; Sequence 166, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 166:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-166

Query Match 100.0%; Score 56; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFNIRGRW 9
| | | | |
Db 10 RFNIRGRW 18

RESULT 4

US-09-980-523A-10
; Sequence 10, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAILT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO81 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 10
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-10

Query Match 100.0%; Score 56; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFNIRGRW 9
| | | | |
Db 14 RFNIRGRW 22

RESULT 5

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US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCES
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO/91 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2
Query Match 100.0%; Score 56; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFNIRGRW 9
Db 131 RFNIRGRW 139

RESULT 6
US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 817-9453
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3
Query Match 100.0%; Score 56; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFNIRGRW 9
Db 131 RFNIRGRW 139

RESULT 7
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 817-9453
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4
Query Match 100.0%; Score 56; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFNIRGRW 9
Db 131 RFNIRGRW 139

RESULT 8
US-08-860-165-12
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; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3
Query Match 100.0%; Score 56; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFNIRGRW 9
Db 131 RFNIRGRW 139

RESULT 7
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 817-9453
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4
Query Match 100.0%; Score 56; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFNIRGRW 9
Db 131 RFNIRGRW 139

RESULT 8
US-08-860-165-12
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; Sequence 12, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12

Query Match      100.0%; Score 56; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RFHNRGRW 9
Db      69 RFHNRGRW 77

RESULT 9
US-09-359-382-12
; Sequence 12, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-12

Query Match      100.0%; Score 56; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RFHNRGRW 9
Db      69 RFHNRGRW 77

RESULT 10
US-08-117-083-10
; Sequence 10, Application US/08117083
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; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Boursnell, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
; OTHER INFORMATION: /note= "Xaa refers to stop codon in
; the open reading frame."
US-08-117-083-10

Query Match      100.0%; Score 56; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RFHNRGRW 9
Db      92 RFHNRGRW 100

RESULT 11
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match          100.0%; Score 56; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFHNRGRW 9
Db 131 RFHNRGRW 139

RESULT 12
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match          100.0%; Score 56; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFHNRGRW 9
Db 131 RFHNRGRW 139

RESULT 13
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
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; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match          100.0%; Score 56; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFHNRGRW 9
Db 131 RFHNRGRW 139

RESULT 14
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match          100.0%; Score 56; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RFHNRGRW 9
Db 237 RFHNRGRW 245

RESULT 15
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10
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Query Match 100.0%; Score 56; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RFHNIRGW 9
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Db 256 RFHNIRGW 264

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Job time : 17.9126 secs

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OM protein - protein search, using sw model

Run on: June 29, 2005, 05:18:25 ; Search time 53.8517 Seconds
(without alignments)
64.268 Million cell updates/sec

Title: US-08-170-344-72
Perfect score: 51
Sequence: 1 CYSLYGTTL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	9	17 US-10-751-845-85	Sequence 85, Appl
2	51	100.0	15	16 US-10-476-570-33	Sequence 33, Appl
3	51	100.0	15	16 US-10-476-570-33	Sequence 33, Appl
4	51	100.0	20	16 US-10-476-570-12	Sequence 12, Appl
5	51	100.0	23	17 US-10-751-845-66	Sequence 66, Appl
6	51	100.0	29	16 US-10-476-570-55	Sequence 55, Appl
7	51	100.0	29	17 US-10-858-384-8	Sequence 8, Appl
8	51	100.0	117	17 US-10-751-845-126	Sequence 126, Appl
9	51	100.0	158	17 US-10-858-384-2	Sequence 2, Appl
10	51	100.0	158	17 US-10-367-057-16	Sequence 16, Appl
11	51	100.0	171	16 US-10-472-724-2	Sequence 2, Appl

12	51	100.0	236	17 US-10-751-845-157	Sequence 157, App
13	51	100.0	237	17 US-10-751-845-158	Sequence 158, App
14	51	100.0	261	17 US-10-751-845-160	Sequence 160, App
15	51	100.0	266	9 US-09-367-309A-1	Sequence 1, Appli
16	51	100.0	273	13 US-10-000-903-4	Sequence 4, Appli
17	51	100.0	273	17 US-10-899-771-4	Sequence 4, Appli
18	51	100.0	292	13 US-10-000-903-10	Sequence 10, Appl
19	51	100.0	292	17 US-10-899-771-10	Sequence 10, Appl
20	51	100.0	371	13 US-10-000-903-6	Sequence 6, Appli
21	51	100.0	371	17 US-10-899-771-6	Sequence 6, Appli
22	51	100.0	390	13 US-10-000-903-14	Sequence 14, Appl
23	51	100.0	390	17 US-10-899-771-14	Sequence 14, Appl
24	49	96.1	10	17 US-10-751-845-79	Sequence 79, Appl
25	48	94.1	151	14 US-10-177-390-6	Sequence 6, Appli
26	48	94.1	151	17 US-10-484-063-20	Sequence 20, Appl
27	48	94.1	151	17 US-10-484-063-27	Sequence 27, Appl
28	47	92.2	10	17 US-10-751-845-91	Sequence 91, Appl
29	42	82.4	9	17 US-10-751-845-88	Sequence 88, Appl
30	38	74.5	88	16 US-10-425-115-334474	Sequence 334474,
31	38	74.5	1013	15 US-10-282-122A-77615	Sequence 77615, A
32	37	72.5	9	US-09-832-723-103	Sequence 103, App
33	37	72.5	9	14 US-10-303-331-103	Sequence 103, App
34	37	72.5	9	17 US-10-968-732-103	Sequence 103, App
35	37	72.5	15	16 US-10-476-570-32	Sequence 32, Appl
36	37	72.5	61	13 US-10-044-359-4	Sequence 4, Appli
37	37	72.5	71	16 US-10-425-115-349387	Sequence 349387,
38	37	72.5	82	16 US-10-425-115-219864	Sequence 219864,
39	36	70.6	27	16 US-10-425-115-366746	Sequence 366746,
40	36	70.6	91	15 US-10-289-762-1162	Sequence 1162, App
41	36	70.6	1063	15 US-10-149-310-294	Sequence 294, App
42	36	70.6	1068	9 US-09-801-368-242	Sequence 242, App
43	36	70.6	1068	15 US-10-149-310-292	Sequence 292, App
44	36	70.6	1618	10 US-09-742-153-4	Sequence 4, Appli
45	36	70.6	2887	10 US-09-742-153-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-751-845-85
; Sequence 85, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicx, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-85

Query Match 100.0%; Score 51; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9
|||
Db 1 CYSLYGTTL 9

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RESULT 2
US-10-476-570-33
; Sequence 33, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from B6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 81-95
US-10-476-570-33

Query Match          100.0%; Score 51; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYSLYGTTL 9
Db 7 CYSLYGTTL 15

RESULT 3
US-10-476-570-34
; Sequence 34, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 84-98
US-10-476-570-34

Query Match          100.0%; Score 51; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CYSLYGTTL 9
Db 4 CYSLYGTTL 12

RESULT 4
US-10-476-570-12
; Sequence 12, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 20
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 76-95
US-10-476-570-12

Query Match          100.0%; Score 51; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYSLYGTTL 9
Db 12 CYSLYGTTL 20

RESULT 5
US-10-751-845-66
; Sequence 66, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-66

Query Match          100.0%; Score 51; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.023;
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9
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Db 9 CYSLYGTTL 17

RESULT 6

US-10-476-570-55
; Sequence 55, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476.570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 29
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 80-108
US-10-476-570-55

Query Match 100.0%; Score 51; DB 16; Length 29;

Best Local Similarity 100.0%; Pred. No. 0.029;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9
| | | | | | | |
Db 8 CYSLYGTTL 16

RESULT 7

US-10-858-384-8
; Sequence 8, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858.384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
; OTHER INFORMATION: for E6 of HPV

US-10-858-384-8

Query Match 100.0%; Score 51; DB 17; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9
| | | | | | | |
Db 8 CYSLYGTTL 16

RESULT 8

US-10-751-845-126
; Sequence 126, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicx, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751.845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664.225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-126

Query Match 100.0%; Score 51; DB 17; Length 117;

Best Local Similarity 100.0%; Pred. No. 0.12;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9
| | | | | | | |
Db 53 CYSLYGTTL 61

RESULT 9

US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858.384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

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Query Match      100.0%; Score 51; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYSLYGTTL 9
    |||||
Db 87 CYSLYGTTL 95

RESULT 10
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match      100.0%; Score 51; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYSLYGTTL 9
    |||||
Db 87 CYSLYGTTL 95

RESULT 11
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match      100.0%; Score 51; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYSLYGTTL 9
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Db 92 CYSLYGTTL 100

RESULT 12
US-10-751-845-157
; Sequence 157, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-157

Query Match      100.0%; Score 51; DB 17; Length 236;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYSLYGTTL 9
    |||||
Db 53 CYSLYGTTL 61

RESULT 13
US-10-751-845-158
; Sequence 158, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-158

Query Match      100.0%; Score 51; DB 17; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYSLYGTTL 9
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Search completed: June 29, 2005, 05:48:15
Job time : 54.8517 secs

Db 54 CYSLYGTTL 62
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RESULT 14
US-10-751-845-160
; Sequence 160, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-160

Query Match 100.0%; Score 51; DB 17; Length 261;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9
|||||
Db 78 CYSLYGTTL 86

RESULT 15
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 51; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9
|||||
Db 87 CYSLYGTTL 95

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:37:59 ; Search time 16.8626 Seconds
(without alignments)
39.842 Million cell updates/sec

Title: US-08-170-344-72
Perfect score: 51
Sequence: 1 CYSLYGTTL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	9	3 US-08-159-339A-563	Sequence 563, Appl
2	51	100.0	11	3 US-08-159-339A-1171	Sequence 1171, Ap
3	51	100.0	20	2 US-08-934-915-44	Sequence 44, Appl
4	51	100.0	20	2 US-08-934-915-163	Sequence 163, Appl
5	51	100.0	29	4 US-09-980-523A-8	Sequence 8, Appli
6	51	100.0	158	4 US-09-980-523A-2	Sequence 2, Appli
7	51	100.0	172	1 US-08-316-239B-3	Sequence 3, Appli
8	51	100.0	172	3 US-08-860-165-12	Sequence 12, Appl
9	51	100.0	172	3 US-08-860-165-14	Sequence 14, Appl
10	51	100.0	172	3 US-09-359-382-12	Sequence 12, Appl
11	51	100.0	172	3 US-09-359-382-14	Sequence 14, Appl
12	51	100.0	182	1 US-08-117-083-10	Sequence 10, Appl
13	51	100.0	266	3 US-08-860-165-10	Sequence 10, Appl
14	51	100.0	266	3 US-09-359-382-10	Sequence 10, Appl
15	51	100.0	266	4 US-09-367-309A-1	Sequence 1, Appli
16	51	100.0	273	3 US-09-485-885-4	Sequence 4, Appli
17	51	100.0	292	3 US-09-485-885-10	Sequence 10, Appl
18	51	100.0	371	3 US-09-485-885-6	Sequence 6, Appli
19	51	100.0	390	3 US-09-485-885-14	Sequence 14, Appl
20	48	94.1	162	1 US-08-316-239B-4	Sequence 4, Appli
21	42	82.4	9	3 US-08-159-339A-244	Sequence 244, Appl
22	37	72.5	61	4 US-10-044-359-4	Sequence 4, Appli
23	36	70.6	91	4 US-09-198-452A-1162	Sequence 1162, Ap
24	36	70.6	109	4 US-09-438-185A-175	Sequence 175, Appl
25	36	70.6	1618	3 US-08-462-467B-4	Sequence 4, Appli
26	36	70.6	2584	3 US-08-936-135-4	Sequence 4, Appli
27	36	70.6	2588	3 US-08-936-135-2	Sequence 2, Appli

28	36	70.6	2887	3	US-08-462-467B-2	Sequence 2, Appli
29	36	70.6	2887	3	US-08-462-467B-8	Sequence 8, Appli
30	35	68.6	9	3	US-08-159-339A-230	Sequence 230, Appl
31	35	68.6	364	4	US-09-134-000C-4275	Sequence 4275, Ap
32	35	68.6	441	1	US-08-191-866B-21	Sequence 21, Appl
33	35	68.6	441	2	US-08-185-949B-21	Sequence 21, Appl
34	35	68.6	712	4	US-09-270-767-46235	Sequence 46235, A
35	35	68.6	3218	1	US-08-764-100-27	Sequence 27, Appl
36	34	66.7	100	3	US-08-869-733-1	Sequence 1, Appli
37	34	66.7	100	3	US-09-215-063-1	Sequence 1, Appli
38	34	66.7	100	4	US-10-096-703-1	Sequence 1, Appli
39	34	66.7	115	4	US-09-107-532A-6191	Sequence 6191, Ap
40	34	66.7	325	4	US-08-887-534A-53	Sequence 53, Appl
41	34	66.7	325	4	US-09-527-431-53	Sequence 53, Appl
42	34	66.7	325	4	US-09-446-861-53	Sequence 53, Appl
43	34	66.7	325	4	US-09-902-540-12868	Sequence 12868, A
44	34	66.7	361	4	US-09-931-381A-20	Sequence 20, Appl
45	34	66.7	362	4	US-09-931-381A-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-08-159-339A-563
; Sequence 563, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 563:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-563

Query Match 100.0%; Score 51; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9
|||
Db 1 CYSLYGTTL 9

RESULT 2

US-08-159-339A-1171

; Sequence 1171, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esceban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1171:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-1171

Query Match 100.0%; Score 51; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9
|||
Db 3 CYSLYGTTL 11

RESULT 3

US-08-934-915-44

; Sequence 44, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-44

Query Match 100.0%; Score 51; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.0069;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9
|||
Db 11 CYSLYGTTL 19

RESULT 4

US-08-934-915-163
; Sequence 163, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500

CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 163:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-163

Query Match 100.0%; Score 51; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0069;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYSLYGTTL 9
DB 11 CYSLYGTTL 19

RESULT 5
US-09-980-523A-8
; Sequence 8, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: WO81 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-8

Query Match 100.0%; Score 51; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYSLYGTTL 9

DB 8 CYSLYGTTL 16

RESULT 6
US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: WO81 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 51; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.066;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYSLYGTTL 9
DB 87 CYSLYGTTL 95

RESULT 7
US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 100.0%; Score 51; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYSLYGTTT 9
| | | | | | | |
Db 87 CYSLYGTTT 95

RESULT 8
US-08-860-165-12
; Sequence 12, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12

Query Match 100.0%; Score 51; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYSLYGTTT 9
| | | | | | | |
Db 25 CYSLYGTTT 33

RESULT 9
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20

; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14

Query Match 100.0%; Score 51; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYSLYGTTT 9
| | | | | | | |
Db 156 CYSLYGTTT 164

RESULT 10
US-09-359-382-12
; Sequence 12, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-09-359-382-12

Query Match 100.0%; Score 51; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CYSLYGTTT 9
| | | | | | | |
Db 25 CYSLYGTTT 33

RESULT 11
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868

;; EARLIER FILING DATE: 1995-12-20
;; EARLIER APPLICATION NUMBER: AU PN0157/94
;; EARLIER FILING DATE: 1994-12-20
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 14
;; LENGTH: 172
;; TYPE: PRT
;; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match 100.0%; Score 51; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9
Db 156 CYSLYGTTL 164

RESULT 12
US-08-117-083-10
; Sequence 10, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Boursnell, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
; OTHER INFORMATION: /note= "Xaa refers to stop codon in
; OTHER INFORMATION: the open reading frame."
US-08-117-083-10

Query Match 100.0%; Score 51; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9
Db 68 CYSLYGTTL 76

RESULT 13
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 51; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9
Db 87 CYSLYGTTL 95

RESULT 14
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 51; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9

Db 87 CYSLYGTTL 95
|||||

RESULT 15
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 51; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CYSLYGTTL 9
|||||
Db 87 CYSLYGTTL 95

Search completed: June 29, 2005, 01:44:27
Job time : 16.9126 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2005, 23:28:22 ; Search time 54.2473 Seconds
(without alignments)
84.958 Million cell updates/sec

Title: US-08-170-344-71
Perfect score: 57
Sequence: 1 HVCYSLYGT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	90	2	Q80883
2	57	100.0	90	2	Q80884
3	57	100.0	99	2	Q919B2
4	57	100.0	103	2	Q919D6
5	57	100.0	130	2	Q919B4
6	57	100.0	130	2	Q919D0
7	57	100.0	143	2	Q919B6
8	57	100.0	151	2	Q12336
9	57	100.0	151	2	Q77816
10	57	100.0	151	2	Q89640
11	57	100.0	151	2	Q89755
12	57	100.0	151	2	Q8B564
13	57	100.0	151	2	Q9W931
14	57	100.0	151	2	Q9WMP4
15	57	100.0	158	1	V56 HPV16
16	57	100.0	158	2	Q8QH25
17	57	100.0	158	2	Q8QHT0
18	57	100.0	158	2	Q8QRD6
19	57	100.0	158	2	Q8QRD7
20	57	100.0	158	2	Q8QRD8
21	57	100.0	158	2	Q8QRD9
22	57	100.0	158	2	Q8QRE0
23	57	100.0	158	2	Q8QRE1
24	57	100.0	158	2	Q9QDH3
25	57	100.0	158	2	Q9QDH5
26	57	100.0	158	2	Q9QDH7
27	57	100.0	158	2	Q9QDH9
28	57	100.0	161	2	Q919B1
29	57	100.0	161	2	Q919C6
30	57	100.0	161	2	Q919D4
31	54	94.7	84	2	Q80882

32	54	94.7	130	2	Q919B8
33	54	94.7	130	2	Q919C0
34	54	94.7	130	2	Q919C2
35	54	94.7	130	2	Q919C8
36	54	94.7	138	2	Q919D2
37	54	94.7	143	2	Q919C4
38	54	94.7	151	2	O12335
39	54	94.7	151	2	O77JC7
40	54	94.7	151	2	O77ZJ5
41	54	94.7	151	2	O80963
42	54	94.7	151	2	O89648
43	54	94.7	151	2	O89852
44	54	94.7	151	2	O8BB19
45	54	94.7	151	2	O8BB20

Q919b8 human papil
Q919c0 human papil
Q919c2 human papil
Q919c8 human papil
Q919d2 human papil
Q919c4 human papil
O12335 human papil
Q77jc7 human papil
Q77zj5 human papil
O80963 human papil
O89648 human papil
O89852 human papil
Q8bb19 human papil
Q8bb20 human papil

ALIGNMENTS

RESULT 1

Q80883 PRELIMINARY; PRT; 90 AA.
AC Q80883; 1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
RN NCBI_TaxID=10566;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G.; Galucira D.F.; Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14512; AAB60566.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
FT NON TER 90
SQ SEQUENCE 90 AA; 10904 MW; 5D3ADF843AD6060B CRC64;

Query Match 100.0%; Score 57; DB 2; Length 90;

Best Local Similarity 100.0%; Pred. No. 0.04;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVCYSLYGT 9

DB 37 HVCYSLYGT 45

RESULT 2

Q80884 PRELIMINARY; PRT; 90 AA.
AC Q80884; 1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
RN NCBI_TaxID=10566;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G.; Galucira D.F.; Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14513; AAB60567.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.

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DR GO: 0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 11021 MW; 47P42BBEFACCC01 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVCYSLYGT 9
|
Db 37 HVCYSLYGT 45

RESULT 3
Q919B2 ID Q919B2 PRELIMINARY; PRT; 99 AA.
AC Q919B2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF04704; AAL01365.1; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 99
SQ SEQUENCE 99 AA; 12005 MW; C2B96025EC370E38 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVCYSLYGT 9
|
Db 54 HVCYSLYGT 62

RESULT 4
Q919D6 ID Q919D6 PRELIMINARY; PRT; 103 AA.
AC Q919D6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF04692; AAL01342.1; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 103
SQ SEQUENCE 103 AA; 12422 MW; 6F90CBAF1F25449B CRC64;

Query Match 100.0%; Score 57; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVCYSLYGT 9
|
Db 30 HVCYSLYGT 38

RESULT 5
Q919B4 ID Q919B4 PRELIMINARY; PRT; 130 AA.
AC Q919B4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF04703; AAL01363.1; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 130
SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227EEDDC CRC64;

Query Match 100.0%; Score 57; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVCYSLYGT 9
|
Db 57 HVCYSLYGT 65

RESULT 6
Q919D0 ID Q919D0 PRELIMINARY; PRT; 130 AA.
AC Q919D0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF04695; AAL01347.1; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 130
SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227EEDDC CRC64;

Query Match 100.0%; Score 57; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVCYSLYGT 9
|
Db 57 HVCYSLYGT 65
```

SQ SEQUENCE 130 AA; 15735 MW; 9EFB30EEDCA21AF3 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVCYSLYGT 9
| | | | |
Db 57 HVCYSLYGT 65

RESULT 7

Q919B6 PRELIMINARY; PRT; 143 AA.
ID Q919B6
AC Q919B6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF04702; AAL01361.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;

Query Match 100.0%; Score 57; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVCYSLYGT 9
| | | | |
Db 70 HVCYSLYGT 78

RESULT 8

O12336 PRELIMINARY; PRT; 151 AA.
ID O12336
AC O12336;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonauro F.M., Meglio A., Buonauro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003016; AAB70733.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;

Query Match 100.0%; Score 57; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVCYSLYGT 9
| | | | |
Db 78 HVCYSLYGT 86

RESULT 9

Q778I6 PRELIMINARY; PRT; 151 AA.
ID Q778I6
AC Q778I6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388056; CAB45104.1; -.
DR EMBL; AJ388061; CAB45114.1; -.
DR EMBL; AJ388066; CAB45124.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18334 MW; FF8F2A2FCEBA6C02 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVCYSLYGT 9
| | | | |
Db 78 HVCYSLYGT 86

RESULT 10

Q89640 PRELIMINARY; PRT; 151 AA.
ID Q89640
AC Q89640;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [3]

RP SEQUENCE FROM N.A.
 RA Ponglikitmongkol M., Vaeteewoottacharn K.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U34129; AA91676.1; -.
 DR EMBL; AF469198; AA015693.1; -.
 DR EMBL; U34115; AA91662.1; -.
 DR EMBL; U34120; AA91667.1; -.
 DR EMBL; U34124; AA91671.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18348 MW; F83F2A2FCF0A6CB2 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.064;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVCYSLYGT 9
 |||||
 Db 78 HVCYSLYGT 86

RESULT 11

Q89755 ID Q89755 PRELIMINARY; PRT; 151 AA.
 AC Q89755;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Early transforming protein E6.
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OC NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96079021; PubMed=7494284;
 RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
 RA Jenison S.A.;
 RT "Human papillomavirus type 16 variant lineages in United States
 RT populations characterized by nucleotide sequence analysis of the E6,
 RT L2, and L1 coding segments.";
 RL J. Virol. 69:7743-7753(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Farmer A.D.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U34126; AA91673.1; -.
 DR EMBL; U34111; AA91658.1; -.
 DR EMBL; U34121; AA91668.1; -.
 DR EMBL; U34123; AA91670.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18334 MW; F8F82A2FCF8A6C02 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.064;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVCYSLYGT 9
 |||||
 Db 78 HVCYSLYGT 86

RESULT 12

Q8B564 ID Q8B564 PRELIMINARY; PRT; 151 AA.
 AC Q8B564;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein.
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OC NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ponglikitmongkol M., Vaeteewoottacharn K.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF548023; AA016239.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18348 MW; FE3F2D5FCD7A69B2 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.064;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVCYSLYGT 9
 |||||
 Db 78 HVCYSLYGT 86

RESULT 13

Q9W931 ID Q9W931 PRELIMINARY; PRT; 151 AA.
 AC Q9W931;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE E6 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OC NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20112892; PubMed=10644829;
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
 RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
 RT "Analysis of human papillomavirus type 16 E6 variants in relation to
 RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
 RL J. Gen. Virol. 81:317-325(2000).
 DR EMBL; AJ388059; CAB45110.1; -.
 DR EMBL; AJ388058; CAB45108.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18306 MW; 6FB3D9E0F24A5300 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.064;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVCYSLYGT 9
 |||||
 Db 78 HVCYSLYGT 86

RESULT 14

Q9WMP4 ID Q9WMP4 PRELIMINARY; PRT; 151 AA.
 AC Q9WMP4;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

```
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388060; CAB45112.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18387 MW; E2244784BBA6C02 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVCYSLYGT 9
Db 78 HVCYSLYGT 86

RESULT 15
ID VE6 HPV16 STANDARD; PRT; 158 AA.
AC P03126;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E6 protein.
GN Name=E6;
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85246220; PubMed=2990099;
RA Seedorf K., Krammer G., Durst M., Suhai S., Rowekamp W.G.;
RT "Human papillomavirus type 16 DNA sequence.";
RL Virology 145:181-185(1985).
RN [2]
RP SEQUENCE OF 31-50 FROM N.A.
RX MEDLINE=90218027; PubMed=2157796;
RA Schneider-Maunoury S., Pehau-Arnauudet G., Breitburd F., Orth G.;
RT "Expression of the human papillomavirus type 16 genome in SK-v cells,
RT a line derived from a vulvar intraepithelial neoplasia.";
RL J. Gen. Virol. 71:809-817(1990).
RN [3]
RP INTERACTION WITH FBLN1, AND INHIBITION OF E6-MEDIATED TRANSFORMATION.
RX MEDLINE=22188366; PubMed=12200142; DOI=10.1016/S0006-291X(02)02041-7;
RA Du M., Fan X., Hong E., Chen J.J.;
RT "Interaction of oncogenic papillomavirus E6 proteins with fibulin-1.";
RL Biochem. Biophys. Res. Commun. 296:962-969(2002).
CC -!- FUNCTION: This protein has transforming activity in vitro.
CC -!- FUNCTION: Exhibits a strong, but non specific affinity for double
CC stranded DNA (in vitro).
CC -!- SUBUNIT: Interacts with FBLN1.
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC -!- MISCELLANEOUS: HPV16, in comparison to HPV types 6 and 11, is more
CC often associated with malignant genital cancers in humans.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@ebi.ac.uk).
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CC EMBL; K02718; AAA46939.1; -.
DR EMBL; D00735; BAA00632.1; -.
DR PIR; A03682; W6WLHS.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
KW DNA-binding; Early protein; Nuclear protein; Oncogene; Zinc-finger.
FT ZN_FING 37 73
FT ZN_FING 110 146
SQ SEQUENCE 158 AA; 19187 MW; 01FEF5ADCFDB37EB CRC64;

Query Match 100.0%; Score 57; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVCYSLYGT 9
Db 85 HVCYSLYGT 93

Search completed: June 29, 2005, 01:34:49
Job time : 55.2473 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:32:21 ; Search time 11.2747 Seconds
(without alignments)
76.805 Million cell updates/sec

Title: US-08-170-344-71
Perfect score: 57
Sequence: 1 HYCVSLYGT 9
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	158	1 W6WLHS	protein E6 - human
2	40	70.2	148	2 A61237	E6 protein - human
3	40	70.2	148	2 S36573	E6 protein - human
4	40	70.2	149	1 W6WL58	E6 protein - human
5	40	70.2	153	2 S36503	E6 protein - human
6	39	68.4	646	2 S37165	dnak-type molecula
7	38	66.7	216	2 JX0265	platelet aggregati
8	38	66.7	795	2 D64343	hypothetical prote
9	38	66.7	2573	2 D71614	hypothetical prote
10	37	64.9	97	2 S59427	hypothetical prote
11	37	64.9	109	2 PH1668	Ig heavy chain v r
12	37	64.9	149	1 W6WL33	E6 protein - human
13	37	64.9	152	1 VGBEV9	early glycoprotein
14	37	64.9	323	2 T24836	hypothetical prote
15	37	64.9	383	2 D88633	protein F56H3.2 [i
16	37	64.9	419	2 S41607	atrolysin A (EC 3.
17	37	64.9	571	2 S24789	jararhagin C precu
18	37	64.9	759	2 S76989	sensory transducti
19	37	64.9	944	2 AC2073	two-component sens
20	37	64.9	1715	2 T14103	probable DNA-direc
21	37	64.9	1717	2 T13961	DNA-directed RNA p
22	36.5	64.0	307	2 D75143	udp-glucose 4-epim
23	36	63.2	209	2 JX0266	platelet aggregati
24	36	63.2	350	2 B39364	GpI-1 embryonic gr
25	36	63.2	406	2 F70632	probable metZ prot
26	36	63.2	419	2 A59414	metalloproteinase
27	36	63.2	421	2 S40819	probable transport
28	36	63.2	421	2 C86075	probable resistanc
29	36	63.2	421	2 D91228	probable resistanc

30 36 63.2 489 2 S76768
31 36 63.2 493 2 A32454
32 36 63.2 493 2 S72196
33 36 63.2 551 2 T44635
34 36 63.2 609 2 S55270
35 36 63.2 664 2 T28852
36 36 63.2 706 2 D82452
37 36 63.2 921 1 A40981
38 36 63.2 928 1 J02486
39 36 63.2 1541 2 T02831
40 35 61.4 91 2 E86512
41 35 61.4 91 2 D72109
42 35 61.4 101 2 S20810
43 35 61.4 108 2 F86669
44 35 61.4 187 2 S32968
45 35 61.4 246 2 T28166

ALIGNMENTS

RESULT 1
W6WLHS
protein E6 - human papillomavirus type 16
C;Species: human papillomavirus type 16
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C;Accession: A03682; T10427
R;Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
Virology 145, 181-185, 1985
A;Title: Human papillomavirus type 16 DNA sequence.
A;Reference number: A22355; MUID:85246220; PMID:2990099
A;Accession: A03682
A;Molecule type: DNA
A;Residues: 1-158 <SEE>
A;Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333033
R;Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A;Title: A negative element in the human poapillomavirus type 16 genome acts at the lev
A;Reference number: Z17014; MUID:91162763; PMID:1848319
A;Accession: T10427
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-158 <KEN>
A;Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
C;Genetics:
A;Gene: E6
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;37-73/Region: zinc finger CCCC motif
F;110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 57; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYCVSLYGT 9
Db 85 HYCVSLYGT 93

RESULT 2
A61237
E6 protein - human papillomavirus type 52
C;Species: human papillomavirus type 52
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 03-May-1996
C;Accession: A61237
R;Takami, Y.; Kondoh, G.; Saito, K.; Noda, K.; Sudiro, T.M.; Sjahrurachman, A.; Warsa,
Int. J. Cancer 48, 516-522, 1991
A;Title: Cloning and characterization of human papillomavirus type 52 from cervical car
A;Reference number: A61237; MUID:91258022; PMID:1646174
A;Accession: A61237
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-148 <TAK>
C;Superfamily: papillomavirus E6 protein

Query Match 70.2%; Score 40; DB 2; Length 148;
Best Local Similarity 87.5%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HVCYSLYG 8
|||
Db 78 HYQYSLYG 85

RESULT 3
S36573
E6 protein - human papillomavirus type 52
C;Species: human papillomavirus type 52
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36573

R;Deilus, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.

A;Reference number: S36469
A;Accession: S36573
A;Molecule type: DNA

A;Residues: 1-148
A;Cross-references: UNIPROT:P36814; EMBL:X74481; NID:G397038; PIDN:CAA52585.1; PID:G3970
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 70.2%; Score 40; DB 2; Length 148;
Best Local Similarity 87.5%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HVCYSLYG 8
|||
Db 78 HYQYSLYG 85

RESULT 4
W6WL58
E6 protein - human papillomavirus type 58
C;Species: human papillomavirus type 58
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: E36779

R;Kirii, Y.; Iwamoto, S.; Matsukura, T.
Virology 185, 424-427, 1991

A;Title: Human papillomavirus type 58 DNA sequence.

A;Reference number: A36779; MUID:92024102; PMID:1656594

A;Accession: E36779

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-149 <KIR>

A;Cross-references: UNIPROT:P26555; GB:D90400; NID:G222386; PIDN:BAA31845.1; PID:G333709

C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; zinc finger

F;30-66/Region: zinc finger CCCC motif

F;103-139/Region: zinc finger CCCC motif

Query Match 70.2%; Score 40; DB 1; Length 149;
Best Local Similarity 87.5%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HVCYSLYG 8
|||
Db 78 HYNYSLYG 85

RESULT 5
S36503
E6 protein - human papillomavirus type 30
C;Species: human papillomavirus type 30
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C;Accession: S36503

R;Deilus, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A;Description: Primer-directed sequencing of human papillomavirus types.

A;Reference number: S36469

A;Accession: S36503

A;Molecule type: DNA

A;Residues: 1-153

A;Cross-references: UNIPROT:P36809; EMBL:X74474; NID:G396973; PIDN:CAA52543.1; PID:G396

C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 70.2%; Score 40; DB 2; Length 153;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HVCYSLYG 8
|||
Db 81 HYNYSLYG 88

RESULT 6

S37165

dnak-type molecular chaperone - Bimeria acervulina

N;Alternate names: heat shock protein

C;Species: Eimeria acervulina

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C;Accession: S37165

R;laurent, F.; Bourdieu, C.; Yvor, P.; Pry, P.

submitted to the EMBL Data Library, September 1993

A;Description: Cloning of a 70 kDa protein of E.acervulina sporozoite which is related

A;Reference number: S37165

A;Accession: S37165

A;Molecule type: mRNA

A;Residues: 1-646 <LAU>

A;Cross-references: UNIPROT:Q24768; EMBL:Z26134; NID:G401828; PIDN:CAA81135.1; PID:G401

C;Function:

A;Description: Involved in protein folding and assembling/disassembling of protein comp

A;Superfamily: heat shock protein 70

C;Keywords: ATP; molecular chaperone

Query Match 68.4%; Score 39; DB 2; Length 646;
Best Local Similarity 66.7%; Pred. No. 52;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HVCYSLYGT 9
:||||: ||
Db 546 NYCYSMRGT 554

RESULT 7

JX0265

platelet aggregation inhibitor - red diamond rattlesnake (fragment)

N;Alternate names: disintegrin

C;Species: Crotalus ruber ruber (red diamond rattlesnake)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C;Accession: JX0265

R;Takeya, H.; Nishida, S.; Nishino, N.; Makinose, Y.; Omori-Satoh, T.; Sugih

J. Biochem. 113, 473-483, 1993

A;Title: Primary structures of platelet aggregation inhibitors (disintegrins) autoprote

hese enzymes.

A;Reference number: JX0265; MUID:93293798; PMID:8514736

A;Accession: JX0265

A;Molecule type: protein

A;Residues: 1-216 <TAK>

A;Cross-references: UNIPROT:Q9PSN7

A;Experimental source: venom

C;Superfamily: mouse meltrin alpha; disintegrin homology

F;7-89/Domain: disintegrin homology <DIS>

Query Match 66.7%; Score 38; DB 2; Length 216;
Best Local Similarity 55.6%; Pred. No. 31;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```

Qy      1 HVCYSLYGT 9
Db      115 HQCVALFGS 123

RESULT 8
D64343
hypothetical protein MJ0348 - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 24-Nov-1999
C:Accession: D64343
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.
; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8686087
A:Accession: D64343
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-795 <BUL>
A:Cross-references: GB:U67488; GB:L77117; NID:G1591055; PID:G1591062; TIGR:MJ0348; PID:G
C:Genetics:
A:Map position: FOR319611-321998
A:Start codon: GTG
C:Superfamily: Methanococcus jannaschii hypothetical protein MJ0348

Query Match      66.7%; Score 38; DB 2; Length 795;
Best Local Similarity 62.5%; Pred. No. 92;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      2 YCYSLYGT 9
Db      695 YCYRIYGS 702

RESULT 9
D71614
hypothetical protein PFB0460c - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C>Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C:Accession: D71614
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
; Perlea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.
Science 282, 1126-1132, 1998
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A:Reference number: A71600; MUID:99021743; PMID:9804551
A:Accession: D71614
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-2573 <GAR>
A:Cross-references: UNIPROT:O96185; GB:AE001396; GB:AE001362; NID:G3845188; PIDN:AACT188
C:Experimental source: clone 3D7
C:Genetics:
A:Gene: PFB0460c

Query Match      66.7%; Score 38; DB 2; Length 2573;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 HVCYSLY 7
Db      2508 HVCYDLF 2514

RESULT 10
S59427
hypothetical protein YDR220c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein YD9934.05c
C:Species: Saccharomyces cerevisiae
C>Date: 30-Nov-1995 #sequence_revision 16-Feb-1996 #text_change 09-Jul-2004

C:Accession: S59427
R;Murphy, L.; Harris, D.
submitted to the EMBL Data Library, March 1995
A:Reference number: S59423
A:Accession: S59427
A:Molecule type: DNA
A:Residues: 1-97 <MUR>
A:Cross-references: UNIPROT:Q04923; EMBL:Z48612; NID:G728671; PID:G728676; GSPDB:GN0000
A:Experimental source: strain AB972
C:Genetics:
A:Gene: MIPS:YDR220C
A:Cross-references: SGD:S0002628
A:Map position: 4R

Query Match      64.9%; Score 37; DB 2; Length 97;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 HVCYSLYG 8
Db      23 HYYYSFYG 30

RESULT 11
PH1668
IG heavy chain V region (clone 3G5) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C:Accession: PH1668
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphyl
A:Reference number: PH1642; MUID:93301610; PMID:8315388
A:Accession: PH1668
A:Molecule type: mRNA
A:Residues: 1-109 <HIL>
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match      64.9%; Score 37; DB 2; Length 109;
Best Local Similarity 75.0%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 HVCYSLYG 8
Db      86 YYCASLYG 93

RESULT 12
W6WL33
E6 protein - human papillomavirus type 33
C:Species: human papillomavirus type 33
C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: A03683
R;Cole, S.T.; Strebeck, R.E.
J. Virol. 58, 991-995, 1986
A:Title: Genome organization and nucleotide sequence of human papillomavirus type 33, w
A:Reference number: A93020; MUID:86200464; PMID:3009902
A:Accession: A03683
A:Molecule type: DNA
A:Residues: 1-149 <COL>
A:Cross-references: UNIPROT:P06427; GB:M12732; NID:G333049; PIDN:AAA46958.1; PID:G463117
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif

Query Match      64.9%; Score 37; DB 1; Length 149;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

Qy 1 HVCYSLYG 8
||| :|||
Db 78 HYNYSVYG 85

RESULT 13

VGBEY9
early glycoprotein gp48 precursor - human cytomegalovirus (strain AD169)
N;Alternate names: early glycoprotein UL4
C;Species: human cytomegalovirus, human herpesvirus 5
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S09767
R;Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.; Brown, C.M.; Cerny, R.; Horsnell, T.; M.; Barrrell, B.G.

Curr. Top. Microbiol. Immunol. 154, 125-169, 1990
A;Title: Analysis of the protein-coding content of the sequence of human cytomegalovirus
A;Reference number: S09749; MUID:90269039; PMID:2161319
A;Accession: S09767
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-152 <CHE>
A;Cross-references: UNIPROT:P17146; EMBL:X17403; NID:g59591; PIDN:CAA35437.1; PID:g59609
A;Note: possible protein-coding frames are given
A;Note: the DNA sequence was submitted to the EMBL Data Library, December 1989, in compu
C;Superfamily: cytomegalovirus early glycoprotein gp48
C;Keywords: early protein; glycoprotein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-152/Product: early glycoprotein gp48 #status predicted <MAT>
F;48,53,61,69,108,112,122,139,148/Binding site: carbohydrate (Asn) (covalent) #status pr

Query Match 64.9%; Score 37; DB 1; Length 152;
Best Local Similarity 62.5%; Pred. No. 34;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YCYSLYGT 9
||| :|||
Db 19 YCYCVFGT 26

RESULT 14

T24836
hypothetical protein T11F9.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24836
R;Lennard, N.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19941
A;Accession: T24836
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-323 <WIL>
A;Cross-references: UNIPROT:Q22396; EMBL:Z74042; PIDN:CAA98528.1; GSPDB:GN000023; CESP:TI
A;Experimental source: clone T11F9
C;Genetics:
A;Gene: CESP:T11F9.3
A;Map position: 5
A;Introns: 115/2; 229/3

Query Match 64.9%; Score 37; DB 2; Length 323;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CYSLYG 8
||| :|||
Db 35 CYSLYG 40

RESULT 15

D88633
protein F56B3.2 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: D88633
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_el
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an
A;Accession: D88633
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-383 <STO>
A;Cross-references: GB:chr_IV; PIDN:AAC02613.1; PID:g2854199; GSPDB:GN000022; CESP:F56B3
A;Note: contains similarity to tenascins
C;Genetics:
A;Gene: F56B3.2
A;Map position: 4

Query Match 64.9%; Score 37; DB 2; Length 383;
Best Local Similarity 75.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HVCYSLYG 8
||| :|||
Db 177 HCYFLSG 184

Search completed: June 29, 2005, 01:38:47
Job time : 12.2747 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 05:18:25 ; Search time 53.8517 Seconds
(without alignments)
64.268 Million cell updates/sec

Title: US-08-170-344-71
Perfect score: 57
Sequence: 1 HCYSLYGT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	9	17	US-10-751-845-88
2	57	100.0	10	17	US-10-751-845-91
3	57	100.0	15	16	US-10-476-570-33
4	57	100.0	15	16	US-10-476-570-34
5	57	100.0	20	16	US-10-476-570-12
6	57	100.0	23	17	US-10-751-845-66
7	57	100.0	23	17	US-10-476-570-55
8	57	100.0	29	16	US-10-858-384-8
9	57	100.0	117	17	US-10-751-845-126
10	57	100.0	158	17	US-10-858-384-2
11	57	100.0	158	17	US-10-367-057-16

12	57	100.0	171	16	US-10-472-724-2	Sequence 2, Appli
13	57	100.0	236	17	US-10-751-845-157	Sequence 157, App
14	57	100.0	237	17	US-10-751-845-158	Sequence 158, App
15	57	100.0	261	17	US-10-751-845-160	Sequence 160, App
16	57	100.0	266	9	US-09-367-309A-1	Sequence 1, Appli
17	57	100.0	273	13	US-10-000-903-4	Sequence 4, Appli
18	57	100.0	273	17	US-10-899-771-4	Sequence 4, Appli
19	57	100.0	292	13	US-10-000-903-10	Sequence 10, Appli
20	57	100.0	292	17	US-10-899-771-10	Sequence 10, Appli
21	57	100.0	371	13	US-10-000-903-6	Sequence 6, Appli
22	57	100.0	371	17	US-10-899-771-6	Sequence 6, Appli
23	57	100.0	390	13	US-10-000-903-14	Sequence 14, Appli
24	57	100.0	390	17	US-10-899-771-14	Sequence 14, Appli
25	54	94.7	151	14	US-10-177-390-6	Sequence 6, Appli
26	54	94.7	151	17	US-10-484-063-20	Sequence 20, Appli
27	54	94.7	151	17	US-10-484-063-27	Sequence 27, Appli
28	52	91.2	15	16	US-10-476-570-32	Sequence 32, Appli
29	47	82.5	10	17	US-10-751-845-79	Sequence 79, Appli
30	46	80.7	10	17	US-10-751-845-93	Sequence 93, Appli
31	42	73.7	9	17	US-10-751-845-85	Sequence 85, Appli
32	40	70.2	438	17	US-10-732-923-23922	Sequence 23922, A
33	39	68.4	9	14	US-10-239-313A-313	Sequence 313, App
34	39	68.4	9	17	US-10-751-845-86	Sequence 86, Appli
35	39	68.4	10	17	US-10-751-845-80	Sequence 80, Appli
36	39	68.4	15	16	US-10-476-570-31	Sequence 31, Appli
37	39	68.4	226	16	US-10-128-520-106	Sequence 106, App
38	39	68.4	226	16	US-10-425-115-209019	Sequence 209019,
39	39	68.4	263	16	US-10-437-963-193431	Sequence 193431,
40	39	68.4	1233	15	US-10-343-710-85	Sequence 85, Appli
41	39	68.4	1234	15	US-10-343-710-83	Sequence 83, Appli
42	38	66.7	838	15	US-10-343-710-110	Sequence 110, App
43	38	66.7	838	15	US-10-343-710-112	Sequence 112, App
44	38	66.7	1226	16	US-10-437-963-129996	Sequence 129996,
45	38	66.7	1965	15	US-10-359-012-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-10-751-845-88
; Sequence 88, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-88

Query Match 100.0%; Score 57; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HCYSLYGT 9
Db 1 HCYSLYGT 9

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RESULT 2
US-10-751-845-91
; Sequence 91, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-91

Query Match      100.0%; Score 57; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVCVSLYGT 9
Db 1 HVCVSLYGT 9

RESULT 3
US-10-476-570-33
; Sequence 33, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from B6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 81-95
US-10-476-570-33

Query Match      100.0%; Score 57; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVCVSLYGT 9
Db 5 HVCVSLYGT 13
```

```
RESULT 4
US-10-476-570-34
; Sequence 34, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from B6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 84-98
US-10-476-570-34

Query Match      100.0%; Score 57; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVCVSLYGT 9
Db 2 HVCVSLYGT 10

RESULT 5
US-10-476-570-12
; Sequence 12, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from B6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 20
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 76-95
US-10-476-570-12

Query Match      100.0%; Score 57; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.015;
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HCYCSLYGT 9
| | | | |
Db 10 HCYCSLYGT 18

RESULT 6

US-10-751-845-66
; Sequence 66, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-66

Query Match 100.0%; Score 57; DB 17; Length 23;

Best Local Similarity 100.0%; Pred. No. 0.017; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HCYCSLYGT 9
| | | | |
Db 7 HCYCSLYGT 15

RESULT 7

US-10-476-570-55
; Sequence 55, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUEVILLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 29
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 80-108
US-10-476-570-55

Query Match 100.0%; Score 57; DB 16; Length 29;

Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HCYCSLYGT 9
| | | | |
Db 6 HCYCSLYGT 14

RESULT 8

US-10-858-384-8
; Sequence 8, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
; OTHER INFORMATION: for E6 of HPV
US-10-858-384-8

Query Match 100.0%; Score 57; DB 17; Length 29;

Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HCYCSLYGT 9
| | | | |
Db 6 HCYCSLYGT 14

RESULT 9

US-10-751-845-126
; Sequence 126, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-126

Query Match 100.0%; Score 57; DB 17; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.08; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 HCYCSLYGT 9
Db 51 HCYCSLYGT 59
|||||

RESULT 10
US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match 100.0%; Score 57; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.11; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 HCYCSLYGT 9
Db 85 HCYCSLYGT 93
|||||

RESULT 11
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: Curaseq1ist version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match 100.0%; Score 57; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.11; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 HCYCSLYGT 9

Db 85 HCYCSLYGT 93
|||||

RESULT 12
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match 100.0%; Score 57; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.12; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 HCYCSLYGT 9
Db 90 HCYCSLYGT 98
|||||

RESULT 13
US-10-751-845-157
; Sequence 157, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-157

Query Match 100.0%; Score 57; DB 17; Length 236;
Best Local Similarity 100.0%; Pred. No. 0.16; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 HCYCSLYGT 9
Db 51 HCYCSLYGT 59
|||||

Db 76 HCYSLYGT 84

Search completed: June 29, 2005, 05:48:14
Job time : 53.8517 secs

RESULT 14
US-10-751-845-158
; Sequence 158, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-158

Query Match 100.0%; Score 57; DB 17; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HCYSLYGT 9
|||
Db 52 HCYSLYGT 60

RESULT 15
US-10-751-845-160
; Sequence 160, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-160

Query Match 100.0%; Score 57; DB 17; Length 261;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HCYSLYGT 9
|||

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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:37:59 ; Search time 16.8626 Seconds
(without alignments)
39.842 Million cell updates/sec

Title: US-08-170-344-71
Perfect score: 57
Sequence: 1 HVCYSLYGT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA.*
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	11	3	US-08-159-339A-1171
2	57	100.0	20	2	US-08-934-915-44
3	57	100.0	20	2	US-08-934-915-163
4	57	100.0	29	4	US-09-980-523A-8
5	57	100.0	158	4	US-09-980-523A-2
6	57	100.0	162	1	US-08-316-239B-3
7	57	100.0	172	3	US-08-860-165-12
8	57	100.0	172	3	US-08-860-165-14
9	57	100.0	172	3	US-09-359-382-12
10	57	100.0	172	3	US-09-359-382-14
11	57	100.0	182	1	US-08-117-083-10
12	57	100.0	266	3	US-08-860-165-10
13	57	100.0	266	3	US-09-359-382-10
14	57	100.0	266	4	US-09-367-309A-1
15	57	100.0	273	3	US-09-485-885-4
16	57	100.0	292	3	US-09-485-885-10
17	57	100.0	371	3	US-09-485-885-6
18	57	100.0	390	3	US-09-485-885-14
19	54	94.7	162	1	US-08-316-239B-4
20	48	84.2	9	3	US-08-159-339A-251
21	43	75.4	9	3	US-08-159-339A-235
22	42	73.7	9	3	US-08-159-339A-563
23	42	71.9	99	4	US-09-248-796A-563
24	41	70.9	115	4	US-09-107-532A-6191
25	40	70.2	457	4	US-09-270-767-45501
26	39	68.4	63	4	US-09-248-796A-24718
27	38	66.7	950	4	US-09-409-604-2

28	38	66.7	2584	3	US-08-936-135-4	Sequence 4, Appli
29	38	66.7	2588	3	US-08-936-135-2	Sequence 2, Appli
30	37	64.9	295	4	US-09-893-737-324	Sequence 324, App
31	37	64.9	571	4	US-09-460-295B-13	Sequence 13, Appl
32	37	64.9	1380	4	US-09-949-016-11688	Sequence 11688, A
33	36	63.2	141	4	US-08-755-100A-12	Sequence 12, Appl
34	36	63.2	493	4	US-09-949-016-5911	Sequence 5911, Ap
35	36	63.2	499	4	US-09-949-016-7409	Sequence 7409, Ap
36	36	63.2	606	4	US-09-460-295B-12	Sequence 12, Appl
37	36	63.2	802	4	US-09-949-016-7922	Sequence 7922, Ap
38	36	63.2	905	3	US-09-754-250-4	Sequence 4, Appli
39	36	63.2	920	3	US-09-754-250-2	Sequence 2, Appli
40	36	63.2	921	1	US-07-872-644-39	Sequence 39, Appl
41	36	63.2	921	1	US-08-297-494-39	Sequence 39, Appl
42	36	63.2	921	1	US-08-297-510-39	Sequence 39, Appl
43	36	63.2	921	1	US-08-479-532-39	Sequence 39, Appl
44	36	63.2	921	1	US-08-455-526-39	Sequence 39, Appl
45	36	63.2	921	1	US-08-455-525-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-08-159-339A-1171
; Sequence 1171, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Cellis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1171:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-1171

Query Match 100.0%; Score 57; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVCYSLYGT 9
| | | | | | | | | |
Db 1 HVCYSLYGT 9

RESULT 2

US-08-934-915-44
; Sequence 44, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-44

Query Match 100.0%; Score 57; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVCYSLYGT 9
| | | | | | | | | |
Db 9 HVCYSLYGT 17

RESULT 3

US-08-934-915-163
; Sequence 163, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:

; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 163:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-163

Query Match 100.0%; Score 57; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVCYSLYGT 9
| | | | | | | | | |
Db 9 HVCYSLYGT 17

US-08-934-915-523A

RESULT 4
US-09-980-523A-8
; Sequence 8, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO/91 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24

Query Match 100.0%; Score 57; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVCYSLYGT 9
| | | | | | | | | |
Db 9 HVCYSLYGT 17

RESULT 3

US-08-934-915-163
; Sequence 163, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-8

Query Match      100.0%; Score 57; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVCYSLYGT 9
Db 6 HVCYSLYGT 14

RESULT 5
US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO/01 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match      100.0%; Score 57; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVCYSLYGT 9
Db 85 HVCYSLYGT 93

RESULT 6
US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3
```

```
Query Match      100.0%; Score 57; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 HVCYSLYGT 9
Db 85 HVCYSLYGT 93
```

```
RESULT 7
US-08-860-165-12
; Sequence 12, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12
```

```
Query Match      100.0%; Score 57; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 HVCYSLYGT 9
Db 23 HVCYSLYGT 31
```

```
RESULT 8
US-08-860-165-14
; Sequence 14, Application US/08860165A
```

```
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14

Query Match          100.0%; Score 57; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HCYCSLYGT 9
Db      154 HCYCSLYGT 162

RESULT 9
US-09-359-382-12
; Sequence 12, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-12

Query Match          100.0%; Score 57; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HCYCSLYGT 9
Db      23 HCYCSLYGT 31

RESULT 10
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
```

```
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match          100.0%; Score 57; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HCYCSLYGT 9
Db      154 HCYCSLYGT 162

RESULT 11
US-08-117-083-10
; Sequence 10, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Bournsnel, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
; OTHER INFORMATION: /note= "Xaa refers to stop codon in
; OTHER INFORMATION: the open reading frame."
US-08-117-083-10

Query Match 100.0%; Score 57; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVCYSLYGT 9
Db 66 HVCYSLYGT 74
|||||

RESULT 12
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian

; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860.165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 57; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVCYSLYGT 9
Db 85 HVCYSLYGT 93
|||||

RESULT 13
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359.382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860.165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 57; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVCYSLYGT 9
Db 85 HVCYSLYGT 93
|||||

RESULT 14
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367.309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 57; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.062;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HVCYSLYGT 9
Db 85 HVCYSLYGT 93
|||||

RESULT 15
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485.885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match 100.0%; Score 57; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVCYSLYGT 9
|||
Db 191 HVCYSLYGT 199
|||

Search completed: June 29, 2005, 01:44:27
Job time : 17.9126 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:28:22 ; Search time 54.2473 Seconds
(without alignments)
84.958 Million cell updates/sec

Title: US-08-170-344-70
Perfect score: 56
Sequence: 1 EYRHYCYSL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	90	2 Q80883	Q80883 human papil
2	56	100.0	90	2 Q80884	Q80884 human papil
3	56	100.0	99	2 Q91982	Q91982 human papil
4	56	100.0	103	2 Q919D6	Q919D6 human papil
5	56	100.0	130	2 Q919B4	Q919B4 human papil
6	56	100.0	130	2 Q919D0	Q919D0 human papil
7	56	100.0	143	2 Q919B6	Q919B6 human papil
8	56	100.0	151	2 Q12336	Q12336 human papil
9	56	100.0	151	2 Q77816	Q77816 human papil
10	56	100.0	151	2 Q89640	Q89640 human papil
11	56	100.0	151	2 Q89755	Q89755 human papil
12	56	100.0	151	2 Q8B564	Q8B564 human papil
13	56	100.0	151	2 Q9W931	Q9W931 human papil
14	56	100.0	151	2 Q9WMP4	Q9WMP4 human papil
15	56	100.0	158	1 V56 HPV16	V56 HPV16 human papil
16	56	100.0	158	2 Q8QH5	Q8QH5 human papil
17	56	100.0	158	2 Q8QHT0	Q8QHT0 human papil
18	56	100.0	158	2 Q8QRD6	Q8QRD6 human papil
19	56	100.0	158	2 Q8QRD7	Q8QRD7 human papil
20	56	100.0	158	2 Q8QRD8	Q8QRD8 human papil
21	56	100.0	158	2 Q8QRD9	Q8QRD9 human papil
22	56	100.0	158	2 Q8QRD0	Q8QRD0 human papil
23	56	100.0	158	2 Q8QRE1	Q8QRE1 human papil
24	56	100.0	158	2 Q9QDH3	Q9QDH3 human papil
25	56	100.0	158	2 Q9QDH5	Q9QDH5 human papil
26	56	100.0	158	2 Q9QDH7	Q9QDH7 human papil
27	56	100.0	158	2 Q9QDH9	Q9QDH9 human papil
28	56	100.0	161	2 Q919B1	Q919B1 human papil
29	56	100.0	161	2 Q919C6	Q919C6 human papil
30	56	100.0	161	2 Q919D4	Q919D4 human papil
31	53	94.6	84	2 Q80882	Q80882 human papil

32	53	94.6	130	2	Q919B8	Q919B8 human papil
33	53	94.6	130	2	Q919C0	Q919C0 human papil
34	53	94.6	130	2	Q919C2	Q919C2 human papil
35	53	94.6	130	2	Q919C8	Q919C8 human papil
36	53	94.6	138	2	Q919D2	Q919D2 human papil
37	53	94.6	143	2	Q919C4	Q919C4 human papil
38	53	94.6	151	2	O12335	O12335 human papil
39	53	94.6	151	2	Q77JC7	Q77JC7 human papil
40	53	94.6	151	2	Q77ZJ5	Q77ZJ5 human papil
41	53	94.6	151	2	Q80963	Q80963 human papil
42	53	94.6	151	2	Q89648	Q89648 human papil
43	53	94.6	151	2	Q89852	Q89852 human papil
44	53	94.6	151	2	Q8BB19	Q8BB19 human papil
45	53	94.6	151	2	Q8BB20	Q8BB20 human papil

ALIGNMENTS

RESULT 1
Q80883 ID Q80883 PRELIMINARY; PRT; 90 AA.
AC Q80883; 100.0%; Score 56; DB 2; Length 90;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14513; AAB60566.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1 1
FT NON_TER 90 90
SQ SEQUENCE 90 AA; 10904 MW; 5D3ADF843AD6060B CRC64;

Query Match 100.0%; Score 56; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYRHYCYSL 9
| | | | | | | | | |
DB 34 EYRHYCYSL 42

RESULT 2
Q80884 ID Q80884 PRELIMINARY; PRT; 90 AA.
AC Q80884; 100.0%; Score 56; DB 2; Length 90;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14513; AAB60567.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.

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DR GO: 0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 90 AA; 11021 MW; 47F42BBEFACCC01 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
| | | | |
Db 34 EYRHYCYSL 42

RESULT 3
Q919B2 ID Q919B2 PRELIMINARY; PRT; 99 AA.
AC Q919B2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404704; AAL01365.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 99 AA; 12005 MW; C2B96025EC370E38 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
| | | | |
Db 51 EYRHYCYSL 59

RESULT 4
Q919D6 ID Q919D6 PRELIMINARY; PRT; 103 AA.
AC Q919D6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404692; AAL01342.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.

DR GO: 0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 103 AA; 12422 MW; 6F90CBAP1F25449B CRC64;

Query Match 100.0%; Score 56; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
| | | | |
Db 27 EYRHYCYSL 35

RESULT 5
Q919B4 ID Q919B4 PRELIMINARY; PRT; 130 AA.
AC Q919B4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404703; AAL01363.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227EEDDC CRC64;

Query Match 100.0%; Score 56; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
| | | | |
Db 54 EYRHYCYSL 62

RESULT 6
Q919D0 ID Q919D0 PRELIMINARY; PRT; 130 AA.
AC Q919D0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404695; AAL01347.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1

```

SQ SEQUENCE 130 AA; 15735 MW; 9EPB30EEDCA21AF3 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 130;

Best Local Similarity 100.0%; Pred. No. 0.25;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYRHYCYSL 9

Db 54 EYRHYCYSL 62

RESULT 7

Q919B6 PRELIMINARY; PRT; 143 AA.

AC Q919B6; (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE E6 protein (Fragment).

OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI_TaxID=10581;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21846229; PubMed=11857370;

RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

RT "Sequence variation and physical state of human papillomavirus type 16

cervical cancer isolates from Australia and New Caledonia.";

RL Int. J. Cancer 97:868-874(2002).

DR EMBL; AF04702; AAL01361.1; -.

DR GO; GO:0042025; C:host cell nucleus; IEA.

DR GO; GO:0003677; F:DNA binding; IEA.

DR Pfam; PF00518; E6; 1.

FT NON TER 1

SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;

Query Match

Best Local Similarity 100.0%; Score 56; DB 2; Length 143;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYRHYCYSL 9

Db 67 EYRHYCYSL 75

RESULT 8

O12336 PRELIMINARY; PRT; 151 AA.

AC O12336; (TREMBLrel. 04, Created)

DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)

DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

DE E6 protein.

OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI_TaxID=10581;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97437474; PubMed=9292007;

RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.;

RA Beth-Girardo E., Giraldo G.;

RT "Sequence variations and viral genomic state of human papillomavirus

type 16 in penile carcinomas from Ugandan patients.";

RL J. Gen. Virol. 78:2199-2208(1997).

DR EMBL; AF003016; AAB70733.1; -.

DR GO; GO:0042025; C:host cell nucleus; IEA.

DR GO; GO:0003677; F:DNA binding; IEA.

DR InterPro; IPR001334; E6.

DR Pfam; PF00518; E6; 1.

SQ SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;

Query Match 100.0%; Score 56; DB 2; Length 151;

Best Local Similarity 100.0%; Pred. No. 0.28;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYRHYCYSL 9

Db 75 EYRHYCYSL 83

RESULT 9

Q77816 PRELIMINARY; PRT; 151 AA.

AC Q77816;

DT 05-JUL-2004 (TREMBLrel. 27, Created)

DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE E6 protein.

OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI_TaxID=10581;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20112892; PubMed=10644829;

RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.;

RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;

RT "Analysis of human papillomavirus type 16 E6 variants in relation to

p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";

RL J. Gen. Virol. 81:317-325(2000).

DR EMBL; AJ388056; CAB45104.1; -.

DR EMBL; AJ388061; CAB45114.1; -.

DR EMBL; AJ388066; CAB45124.1; -.

DR GO; GO:0042025; C:host cell nucleus; IEA.

DR GO; GO:0003677; F:DNA binding; IEA.

DR InterPro; IPR001334; E6.

DR Pfam; PF00518; E6; 1.

SQ SEQUENCE 151 AA; 18334 MW; FF8F2A2FCEBA6C02 CRC64;

Query Match

Best Local Similarity 100.0%; Score 56; DB 2; Length 151;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYRHYCYSL 9

Db 75 EYRHYCYSL 83

RESULT 10

Q89640 PRELIMINARY; PRT; 151 AA.

AC Q89640;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE Early transforming protein E6.

OS Human papillomavirus.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI_TaxID=10566;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=96079021; PubMed=7494284;

RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.;

RA Jenison S.A.;

RT "Human papillomavirus type 16 variant lineages in United States

populations characterized by nucleotide sequence analysis of the E6,

L2, and L1 coding segments.";

RL J. Virol. 69:7743-7753(1995).

RN [2]

RP SEQUENCE FROM N.A.

RA Farmer A.D.;

RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34129; AA91676.1; -.
DR EMBL; AF469198; AA015693.1; -.
DR EMBL; U34115; AA91662.1; -.
DR EMBL; U34120; AA91667.1; -.
DR EMBL; U34124; AA91671.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18348 MW; FE3F2A2FCF0A6CB2 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
| | | | | | | |
Db 75 EYRHYCYSL 83

RESULT 11
Q89755 PRELIMINARY; PRT; 151 AA.
AC Q89755;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RT J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34126; AA91673.1; -.
DR EMBL; U34111; AA91658.1; -.
DR EMBL; U34121; AA91668.1; -.
DR EMBL; U34123; AA91670.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18334 MW; FF8F2A2FCFEBAC02 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
| | | | | | | |
Db 75 EYRHYCYSL 83

RESULT 12
QB564 PRELIMINARY; PRT; 151 AA.
AC QB564;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF548023; AA016239.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18348 MW; FE3F2D5FCD7A69B2 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
| | | | | | | |
Db 75 EYRHYCYSL 83

RESULT 13
Q9W931 PRELIMINARY; PRT; 151 AA.
AC Q9W931;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388059; CAB45110.1; -.
DR EMBL; AJ388058; CAB45108.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18306 MW; 6FB3D9E0F24A5300 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
| | | | | | | |
Db 75 EYRHYCYSL 83

RESULT 14
Q9WMP4 PRELIMINARY; PRT; 151 AA.
AC Q9WMP4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

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OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL: AJ388060; CAB45112.1; -;
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18387 MW; E2244784BBA6C02 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYRHYCYSL 9
Db 75 EYRHYCYSL 83

RESULT 15
V06 HPV16
ID V06 HPV16 STANDARD; PRT; 158 AA.
AC P03126;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E6 protein.
GN Name=E6;
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RX SEQUENCE FROM N.A.
RX MEDLINE=85246220; PubMed=2990099;
RA Seedorf K., Krammer G., Durst M., Suhai S., Rowekamp W.G.;
RT "Human papillomavirus type 16 DNA sequence.";
RL Virology 145:181-185(1985).
RN [2]
RX SEQUENCE OF 31-50 FROM N.A.
RX MEDLINE=90218027; PubMed=2157796;
RA Schneider-Maunoury S., Pehau-Arnauudet G., Breitburd F., Orth G.;
RT "Expression of the human papillomavirus type 16 genome in SK-v cells,
RT a line derived from a vulvar intraepithelial neoplasia.";
RL J. Gen. Virol. 71:809-817(1990).
RN [3]
RX INTERACTION WITH FBLN1, AND INHIBITION OF E6-MEDIATED TRANSFORMATION.
RX MEDLINE=22188366; PubMed=12200142; DOI=10.1016/S0006-291X(02)02041-7;
RA Du M., Fan X., Hong E., Chen J.J.;
RT "Interaction of oncogenic papillomavirus E6 proteins with fibulin-1.";
RL Biochem. Biophys. Res. Commun. 296:962-969(2002).
CC -!- FUNCTION: This protein has transforming activity in vitro.
CC -!- FUNCTION: Exhibits a strong, but non specific affinity for double
CC stranded DNA (in vitro).
CC -!- SUBUNIT: Interacts with FBLN1.
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC -!- MISCELLANEOUS: HPV16, in comparison to HPV types 6 and 11, is more
CC often associated with malignant genital cancers in humans.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).

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CC EMBL: K02718; AAA46939.1; -;
DR EMBL: D00735; BAA00632.1; -;
DR PIR: A03682; W6WLHS.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
KW DNA-binding; Early protein; Nuclear protein; Oncogene; Zinc-finger.
FT ZN_FING 37 73 Potential.
FT ZN_FING 110 146 Potential.
SQ SEQUENCE 158 AA; 19187 MW; 01FEF5ADCDFDB37EB CRC64;

Query Match 100.0%; Score 56; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EYRHYCYSL 9
Db 82 EYRHYCYSL 90

Search completed: June 29, 2005, 01:34:48
Job time : 54.2473 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 05:18:25 ; Search time 53.8517 Seconds
(without alignments)
64.268 Million cell updates/sec

Title: US-08-170-344-70
Perfect score: 56
Sequence: 1 EYRHYCYSL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 394547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*
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20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	9	14	US-10-239-313A-313
2	56	100.0	9	17	US-10-751-845-86
3	56	100.0	10	17	US-10-751-845-80
4	56	100.0	10	17	US-10-751-845-93
5	56	100.0	15	16	US-10-751-845-31
6	56	100.0	15	16	US-10-476-570-31
7	56	100.0	15	16	US-10-476-570-32
8	56	100.0	20	16	US-10-476-570-33
9	56	100.0	23	17	US-10-476-570-12
10	56	100.0	23	17	US-10-751-845-66
11	56	100.0	29	17	US-10-476-570-55
					Sequence 8, Appli
					Sequence 313, App
					Sequence 86, Appl
					Sequence 80, Appl
					Sequence 93, Appl
					Sequence 31, Appl
					Sequence 32, Appl
					Sequence 33, Appl
					Sequence 12, Appl
					Sequence 66, Appl
					Sequence 55, Appl
					Sequence 8, Appli

12	56	100.0	117	17	US-10-751-845-126	Sequence 126, App
13	56	100.0	158	17	US-10-858-384-2	Sequence 2, Appli
14	56	100.0	158	17	US-10-367-057-16	Sequence 16, Appl
15	56	100.0	171	16	US-10-472-724-2	Sequence 2, Appli
16	56	100.0	236	17	US-10-751-845-157	Sequence 157, App
17	56	100.0	237	17	US-10-751-845-158	Sequence 158, App
18	56	100.0	261	17	US-10-751-845-160	Sequence 160, App
19	56	100.0	266	9	US-09-367-309A-1	Sequence 1, Appli
20	56	100.0	273	13	US-10-000-903-4	Sequence 4, Appli
21	56	100.0	273	17	US-10-899-771-4	Sequence 4, Appli
22	56	100.0	292	13	US-10-000-903-10	Sequence 10, Appl
23	56	100.0	292	17	US-10-899-771-10	Sequence 10, Appl
24	56	100.0	371	13	US-10-000-903-6	Sequence 6, Appli
25	56	100.0	371	17	US-10-899-771-6	Sequence 6, Appli
26	56	100.0	390	13	US-10-000-903-14	Sequence 14, Appl
27	56	100.0	390	17	US-10-899-771-14	Sequence 14, Appl
28	53	94.6	151	14	US-10-177-390-6	Sequence 6, Appli
29	53	94.6	151	17	US-10-484-063-20	Sequence 20, Appl
30	53	94.6	151	17	US-10-484-063-27	Sequence 27, Appl
31	52	92.9	10	17	US-10-751-845-75	Sequence 75, Appl
32	48	85.7	9	17	US-10-751-845-70	Sequence 70, Appl
33	48	85.7	10	17	US-10-751-845-76	Sequence 76, Appl
34	44	78.6	15	16	US-10-476-570-34	Sequence 34, Appl
35	43	76.8	98	16	US-10-425-115-217471	Sequence 217471,
36	41	73.2	9	17	US-10-751-845-78	Sequence 78, Appl
37	39	69.6	9	17	US-10-751-845-88	Sequence 88, Appl
38	39	69.6	10	17	US-10-751-845-91	Sequence 91, Appl
39	38	67.9	227	15	US-10-425-114-38060	Sequence 38060, A
40	38	67.9	375	15	US-10-424-599-274361	Sequence 274361,
41	38	67.9	387	15	US-10-425-114-49909	Sequence 49909, A
42	38	67.9	392	15	US-10-406-686A-65	Sequence 65, Appl
43	38	67.9	415	16	US-10-425-115-191132	Sequence 191132,
44	38	67.9	416	16	US-10-437-963-139343	Sequence 139343,
45	38	67.9	432	16	US-10-425-115-266645	Sequence 266645,

ALIGNMENTS

RESULT 1

US-10-239-313A-313
; Sequence 313, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 313
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-239-313A-313

Query Match 100.0%; Score 56; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EYRHYCYSL 9
Db 1 EYRHYCYSL 9

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US-10-751-845-86
; Sequence 86, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10751,845
; PRIOR FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-86

Query Match      100.0%; Score 56; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
Db 1 EYRHYCYSL 9

RESULT 3
US-10-751-845-80
; Sequence 80, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10751,845
; PRIOR FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 80
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-80

Query Match      100.0%; Score 56; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
Db 2 EYRHYCYSL 10

RESULT 4
US-10-751-845-93
; Sequence 93, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10751,845
; PRIOR FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-93

Query Match      100.0%; Score 56; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
Db 1 EYRHYCYSL 9

RESULT 5
US-10-476-570-31
; Sequence 31, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from B6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; PRIOR FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 76-90
US-10-476-570-31

Query Match      100.0%; Score 56; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
Db 7 EYRHYCYSL 15

```


RESULT 6
US-10-476-570-32
; Sequence 32, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 78-92
US-10-476-570-32

Query Match 100.0%; Score 56; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
Db 5 EYRHYCYSL 13

RESULT 7
US-10-476-570-33
; Sequence 33, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 81-95
US-10-476-570-33

Query Match 100.0%; Score 56; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
Db 2 EYRHYCYSL 10

RESULT 8
US-10-476-570-12
; Sequence 12, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 20
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 76-95
US-10-476-570-12

Query Match 100.0%; Score 56; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
Db 7 EYRHYCYSL 15

RESULT 9
US-10-751-845-66
; Sequence 66, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-66

Query Match 100.0%; Score 56; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
| | | | | | | |
Db 4 EYRHYCYSL 12

RESULT 10

US-10-476-570-55
; Sequence 55, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 29
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 80-108
US-10-476-570-55

Query Match 100.0%; Score 56; DB 16; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
| | | | | | | |
Db 3 EYRHYCYSL 11

RESULT 11

US-10-858-384-8
; Sequence 8, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
; OTHER INFORMATION: for E6 of HPV
US-10-858-384-8

Query Match 100.0%; Score 56; DB 17; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
| | | | | | | |
Db 3 EYRHYCYSL 11

RESULT 12

US-10-751-845-126
; Sequence 126, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicx, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-126

Query Match 100.0%; Score 56; DB 17; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
| | | | | | | |
Db 48 EYRHYCYSL 56

RESULT 13

US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match 100.0%; Score 56; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Search completed: June 29, 2005, 05:48:14
Job time : 53.8517 secs

Qy 1 EYRHYCYSL 9
Db 82 EYRHYCYSL 90

RESULT 14

US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match 100.0%; Score 56; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
Db 82 EYRHYCYSL 90

RESULT 15

US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match 100.0%; Score 56; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
Db 87 EYRHYCYSL 95

Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:37:59 ; Search time 16.8626 Seconds
(without alignments)
39.842 Million cell updates/sec

Title: US-08-170-344-70
Perfect score: 56
Sequence: 1 EYRHYCYSL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	56	100.0	20	US-08-934-915-44	Sequence 44, Appl
2	56	100.0	20	US-08-934-915-163	Sequence 163, App
3	56	100.0	29	US-09-980-523A-8	Sequence 8, Appl
4	56	100.0	158	US-09-980-523A-2	Sequence 2, Appli
5	56	100.0	162	US-08-316-239B-3	Sequence 3, Appli
6	56	100.0	172	US-08-860-165-12	Sequence 12, Appl
7	56	100.0	172	US-08-860-165-14	Sequence 14, Appl
8	56	100.0	172	US-09-359-382-12	Sequence 12, Appl
9	56	100.0	172	US-09-359-382-14	Sequence 14, Appl
10	56	100.0	182	US-08-117-083-10	Sequence 10, Appl
11	56	100.0	266	US-08-860-165-10	Sequence 10, Appl
12	56	100.0	266	US-09-359-382-10	Sequence 10, Appl
13	56	100.0	266	US-09-367-309A-1	Sequence 1, Appli
14	56	100.0	273	US-09-485-885-4	Sequence 4, Appli
15	56	100.0	292	US-09-485-885-10	Sequence 10, Appl
16	56	100.0	371	US-09-485-885-6	Sequence 6, Appli
17	56	100.0	390	US-09-485-885-14	Sequence 14, Appl
18	53	94.6	162	US-08-316-239B-4	Sequence 4, Appli
19	48	85.7	9	US-08-159-339A-76	Sequence 76, Appl
20	48	85.7	9	US-09-601-729-277	Sequence 277, App
21	47	83.9	9	US-08-159-339A-247	Sequence 247, App
22	44	78.6	63	US-09-248-796A-24718	Sequence 24718, A
23	42	75.0	128	US-09-107-532A-4132	Sequence 4132, Ap
24	41	73.2	370	US-09-454-071-6	Sequence 6, Appli
25	39	69.6	11	US-08-159-339A-134	Sequence 134, App
26	39	69.6	11	US-08-159-339A-1171	Sequence 1171, Ap
27	39	69.6	174	US-08-401-530A-6	Sequence 6, Appli

Sequence 6, Appli
Sequence 13995, A
Sequence 5911, Ap
Sequence 7409, Ap
Sequence 22612, A
Sequence 21392, A
Sequence 18861, A
Sequence 2, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 14, Appl
Sequence 4, Appli
Sequence 6, Appli
Sequence 14, Appl
Sequence 2, Appli
Sequence 12, Appl
Sequence 6, Appli
Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-934-915-44
; Sequence 44, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; TITLE OF INVENTION: CHEUNG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-934-915-44
Query Match 100.0%; Score 56; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.017;

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
Db 6 EYRHYCYSL 14

RESULT 2
US-08-934-915-163
; Sequence 163, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Fouch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 163:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-163

Query Match 100.0%; Score 56; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
Db 6 EYRHYCYSL 14

RESULT 3
US-09-980-523A-8
; Sequence 8, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
Db 82 EYRHYCYSL 90

RESULT 5
US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
```

```
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: WO/91/01111
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-8

Query Match 100.0%; Score 56; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
Db 3 EYRHYCYSL 11

RESULT 4
US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: WO/91/01111
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 56; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
Db 82 EYRHYCYSL 90

RESULT 5
US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
```

;; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
;; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
;; TITLE OF INVENTION: Cervical Cancer
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Jagtiani & Associates
;; STREET: 6126 Rocky Way Court
;; CITY: Centreville
;; STATE: VA
;; COUNTRY: USA
;; ZIP: 20120-3400
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/316.239B
;; FILING DATE: 30-SEP-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jagtiani, Ajay A.
;; REGISTRATION NUMBER: 35,205
;; REFERENCE/DOCKET NUMBER: UNWE-0001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 817-9453
;; TELEFAX: (703) 803-9387
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 162 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: protein
;; HYPOTHEICAL: NO
US-08-316-239B-3

Query Match 100.0%; Score 56; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
Db 82 EYRHYCYSL 90

RESULT 6
US-08-860-165-12
; Sequence 12, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12

Query Match 100.0%; Score 56; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EYRHYCYSL 9
Db 20 EYRHYCYSL 28
RESULT 7
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14

Query Match 100.0%; Score 56; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
Db 151 EYRHYCYSL 159

RESULT 8
US-09-359-382-12
; Sequence 12, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-09-359-382-12

Query Match 100.0%; Score 56; DB 3; Length 172;

Best Local Similarity 100.0%; Pred. No. 0.13; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 EYRHYCYSL 9
Db 20 EYRHYCYSL 28

RESULT 9

US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match 100.0%; Score 56; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.13; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 EYRHYCYSL 9
Db 151 EYRHYCYSL 159

RESULT 10

US-08-117-083-10
; Sequence 10, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Boursnell, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.

; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
; OTHER INFORMATION: /note= "Xaa refers to stop codon in
; the open reading frame."
US-08-117-083-10

Query Match 100.0%; Score 56; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.13; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 EYRHYCYSL 9
Db 63 EYRHYCYSL 71

RESULT 11

US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 56; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.19; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 EYRHYCYSL 9
Db 82 EYRHYCYSL 90

RESULT 12

US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann

; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359.382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860.165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU P0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 56; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
Db 82 EYRHYCYSL 90
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RESULT 13
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367.309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 56; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
Db 82 EYRHYCYSL 90
|||||

RESULT 14
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485.885

; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match 100.0%; Score 56; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
Db 188 EYRHYCYSL 196
|||||

RESULT 15
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485.885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10

Query Match 100.0%; Score 56; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EYRHYCYSL 9
Db 207 EYRHYCYSL 215
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Search completed: June 29, 2005, 01:44:26
Job time : 16.9126 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 17:44:26 ; Search time 55.3 Seconds
(without alignments)
83.340 Million cell updates/sec

Title: US-08-170-344-7
Perfect score: 49
Sequence: 1 TIHDIILEC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03: +
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	26	Q81956	Q81956 human papil
2	49	100.0	130	Q919C0	Q919C0 human papil
3	49	100.0	130	Q919C2	Q919C2 human papil
4	49	100.0	130	Q919D0	Q919D0 human papil
5	49	100.0	138	Q919D2	Q919D2 human papil
6	49	100.0	143	Q919B6	Q919B6 human papil
7	49	100.0	143	Q919C4	Q919C4 human papil
8	49	100.0	151	Q12335	Q12335 human papil
9	49	100.0	151	Q12336	Q12336 human papil
10	49	100.0	151	Q76TS0	Q76TS0 human papil
11	49	100.0	151	Q77816	Q77816 human papil
12	49	100.0	151	Q77816	Q77816 human papil
13	49	100.0	151	Q77JC7	Q77JC7 human papil
14	49	100.0	151	Q77ZJ5	Q77ZJ5 human papil
15	49	100.0	151	Q80963	Q80963 human papil
16	49	100.0	151	Q80966	Q80966 human papil
17	49	100.0	151	Q89648	Q89648 human papil
18	49	100.0	151	Q89708	Q89708 human papil
19	49	100.0	151	Q89755	Q89755 human papil
20	49	100.0	151	Q89852	Q89852 human papil
21	49	100.0	151	Q89887	Q89887 human papil
22	49	100.0	151	Q9W8C3	Q9W8C3 human papil
23	49	100.0	151	Q9W931	Q9W931 human papil
24	49	100.0	151	Q9WMP2	Q9WMP2 human papil
25	49	100.0	151	Q9WMP4	Q9WMP4 human papil
26	49	100.0	158	1 VE6 Hpv16	P03126 human papil
27	49	100.0	158	2 Q8JMU8	Q8JMU8 human papil
28	49	100.0	158	2 Q8QHN0	Q8QHN0 human papil
29	49	100.0	158	2 Q8QHP5	Q8QHP5 human papil
30	49	100.0	158	2 Q8QRD5	Q8QRD5 human papil
31	49	100.0	158	2 Q8QRD6	Q8QRD6 human papil

RESULT 1

Q81956 PRELIMINARY; PRT; 26 AA.
AC Q81956; 1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6E7 (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC SHIPPI R., Siwkowski A., Hampel A.;
RA Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U59900; AAB03505.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1 1
SQ SEQUENCE 26 AA; 3208 MW; F06EBBE995EB67D5 CRC64;
Query Match 100.0%; Score 49; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9

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Db 5 TIHDIILEC 13

RESULT 2

Q919C0 PRELIMINARY; PRT; 130 AA.
ID Q919C0
AC Q919C0; 2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE-21846229; PubMed-11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404700; AAL01357.1; -.

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DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
Db 1 TIHDIILEC 9

RESULT 3
Q919C2 PRELIMINARY; PRT; 130 AA.
AC Q919C2,
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF04699; AAL01345.1; -.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
Db 1 TIHDIILEC 9

RESULT 4
Q919D0 PRELIMINARY; PRT; 130 AA.
AC Q919D0,
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF04699; AAL01347.1; -.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
Db 1 TIHDIILEC 9

RESULT 5
Q919D2 PRELIMINARY; PRT; 138 AA.
AC Q919D2,
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF04694; AAL01345.1; -.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 138 AA; 16696 MW; 481B5AEA90895FC2 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
Db 9 TIHDIILEC 17

RESULT 6
Q919B6 PRELIMINARY; PRT; 143 AA.
AC Q919B6,
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF04702; AAL01361.1; -.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;

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FT NON TER 1
SQ SEQUENCE 130 AA; 15735 MW; 9EFB30EEDCA21AF3 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.085;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
Db 1 TIHDIILEC 9

RESULT 5
Q919D2 PRELIMINARY; PRT; 138 AA.
AC Q919D2,
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF04694; AAL01345.1; -.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 138 AA; 16696 MW; 481B5AEA90895FC2 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
Db 9 TIHDIILEC 17

RESULT 6
Q919B6 PRELIMINARY; PRT; 143 AA.
AC Q919B6,
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF04702; AAL01361.1; -.
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;

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Query Match 100.0%; Score 49; DB 2; Length 143;
 Best Local Similarity 100.0%; Pred. No. 0.094;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIHDIILEC 9
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 DB 14 TIHDIILEC 22

RESULT 7

ID Q919C4 PRELIMINARY; PRT; 143 AA.
 AC Q919C4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF040698; AAL01353.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 143;
 Best Local Similarity 100.0%; Pred. No. 0.094;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIHDIILEC 9
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 DB 14 TIHDIILEC 22

RESULT 8

ID Q12335 PRELIMINARY; PRT; 151 AA.
 AC Q12335;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97437474; PubMed=9292007;
 RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
 RA Beth-Giraldo E., Giraldo G.;
 RT "Sequence variations and viral genomic state of human papillomavirus
 RT type 16 in penile carcinomas from Ugandan patients.";
 RL J. Gen. Virol. 78:2199-2208(1997).
 DR EMBL; AF003015; AAB70732.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18238 MW; BFF32A8B016CC88B CRC64;
 Query Match 100.0%; Score 49; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.1;

QY 1 TIHDIILEC 9
 |||||
 DB 14 TIHDIILEC 22

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TIHDIILEC 9
 |||||
 DB 22 TIHDIILEC 30

RESULT 9

ID Q12336 PRELIMINARY; PRT; 151 AA.
 AC Q12336;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97437474; PubMed=9292007;
 RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
 RA Beth-Giraldo E., Giraldo G.;
 RT "Sequence variations and viral genomic state of human papillomavirus
 RT type 16 in penile carcinomas from Ugandan patients.";
 RL J. Gen. Virol. 78:2199-2208(1997).
 DR EMBL; AF003016; AAB70733.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;

Query Match 100.0%; Score 49; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIHDIILEC 9
 |||||
 DB 22 TIHDIILEC 30

RESULT 10

ID Q76TS0 PRELIMINARY; PRT; 151 AA.
 AC Q76TS0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Early transforming protein E6.
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96079021; PubMed=7494284;
 RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
 RA Jenison S.A.;
 RT "Human papillomavirus type 16 variant lineages in United States
 RT populations characterized by nucleotide sequence analysis of the E6,
 RT L2, and L1 coding segments.";
 RL J. Virol. 69:7743-7753(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Farmer A.D.;
 RL Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U34114; AAA91661.1; -;
 DR EMBL; U34125; AAA91672.1; -;
 DR EMBL; U34130; AAA91677.1; -;
 DR EMBL; U34131; AAA91678.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.

DR GO: 0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C3S CRC64;
 Query Match 100.0%; Score 49; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TIHDIILEC 9
 Db 22 TIHDIILEC 30
 RESULT 11
 Q77816 PRELIMINARY; PRT; 151 AA.
 ID Q77816;
 AC Q77816;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE E6 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20112892; PubMed=10644829;
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
 RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
 RT "Analysis of human papillomavirus type 16 E6 variants in relation to
 RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
 RL J. Gen. Virol. 81:317-325(2000).
 DR EMBL; AJ388056; CAB45104.1; -;
 DR EMBL; AJ388061; CAB45114.1; -;
 DR EMBL; AJ388066; CAB45124.1; -;
 DR GO: 00042025; C:host cell nucleus; IEA.
 DR GO: 0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18334 MW; FF8F2A2FCEBA6C02 CRC64;
 Query Match 100.0%; Score 49; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TIHDIILEC 9
 Db 22 TIHDIILEC 30
 RESULT 12
 Q77E16 PRELIMINARY; PRT; 151 AA.
 ID Q77E16;
 AC Q77E16;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE E6 oncoprotein (E6 protein).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX Ponglikitmongkol M., Vaeteswootacharn K.;
 RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20112892; PubMed=10644829;
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
 RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;

RT "Analysis of human papillomavirus type 16 E6 variants in relation to
 RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
 RL J. Gen. Virol. 81:317-325(2000).
 DR EMBL; AF469197; AA015691.1; -;
 DR EMBL; AJ388063; CAB45118.1; -;
 DR GO: 00042025; C:host cell nucleus; IEA.
 DR GO: 0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CF1F CRC64;
 Query Match 100.0%; Score 49; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TIHDIILEC 9
 Db 22 TIHDIILEC 30
 RESULT 13
 Q77JC7 PRELIMINARY; PRT; 151 AA.
 ID Q77JC7;
 AC Q77JC7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Early transforming protein E6 variant (Transforming protein E6).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Xinjiang;
 RC Ma Z., Qian D., Ma J., Lin R., Ming W., Zhong Z., Zhang Q., Zhang F.;
 RA "Cloning and Sequencing of HPV16 E6 gene from Cervical Carcinoma
 RA Biopsies in Xinjiang";
 RT Sheng Wu Hua Xue Yu Sheng Wu Wu Li Jin Zhan 0:0-0(2001).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=20112892; PubMed=10644829;
 RX van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
 RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
 RT "Analysis of human papillomavirus type 16 E6 variance in relation to
 RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
 RL J. Gen. Virol. 81:317-325(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2242222; PubMed=12355268; DOI=10.1007/s00239-002-2344-Y;
 RA Defilippis V.R., Ayala F.J., Villarreal L.P.;
 RT "Evidence of diversifying selection in human papillomavirus type 16 E6
 RT but not E7 oncogenes.";
 RL J. Mol. Evol. 55:491-499(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Cruz Mr., Cerqueira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,
 RA Martins C.R.F.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Cruz M.R., Martins C.R.F.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF327851; AAG45940.1; -;
 DR EMBL; AJ388057; CAB45106.1; -;
 DR EMBL; AJ388069; CAB45130.1; -;
 DR EMBL; AY089951; AAM11875.1; -;
 DR EMBL; AY089954; AAM11881.1; -;
 DR EMBL; AY112663; AAM51854.1; -;
 DR GO: 00042025; C:host cell nucleus; IEA.
 DR GO: 0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.

SQ SEQUENCE 151 AA; 18320 MW; 617D2A2FDB4F9C17 CRC64;
 Query Match 100.0%; Score 49; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
 |||||
 Db 22 TIHDIILEC 30

RESULT 14

Q77ZJ5 PRELIMINARY; PRT; 151 AA.
 AC Q77ZJ5;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE E6 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97437474; PubMed=9292007;
 RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
 RA Beth-Giraldo E., Giraldo G.;
 RT "Sequence variations and viral genomic state of human papillomavirus
 RT type 16 in penile carcinomas from Ugandan patients.";
 RL J. Gen. Virol. 78:2199-2208(1997).
 DR EMBL; AF003019; AAB70736.1; -.
 DR EMBL; AF003018; AAB70735.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18221 MW; 60CD2A34DAF48CB7 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
 |||||
 Db 22 TIHDIILEC 30

RESULT 15

Q80963 PRELIMINARY; PRT; 151 AA.
 AC Q80963;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Early transforming protein E6.
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10566;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96079021; PubMed=7494284;
 RA Yanada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
 RA Jenison S.A.;
 RT "Human papillomavirus type 16 variant lineages in United States
 RT populations characterized by nucleotide sequence analysis of the E6,
 RT L2, and L1 coding segments.";
 RL J. Virol. 69:7743-7753(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Farmer A.D.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.

DR EMBL; U34122; AAA91669.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18291 MW; 97C7028D5169382D CRC64;

Query Match 100.0%; Score 49; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
 |||||
 Db 22 TIHDIILEC 30

Search completed: June 28, 2005, 19:19:21
 Job time : 55.3 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:23:48 ; Search time 11.2 Seconds
(without alignments)
77.317 Million cell updates/sec

Title: US-08-170-344-7

Perfect score: 49

Sequence: 1 TIHDIILEC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : FIR_79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	158	1	W6LHS
2	37	75.5	145	2	small heat shock p
3	37	75.5	681	1	transferrin precu
4	36	73.5	75	2	hypothetical prote
5	36	73.5	158	1	E6 protein - human
6	36	73.5	324	2	gag-related protei
7	36	73.5	519	2	hypothetical prote
8	36	73.5	1164	2	tumor suppressor p
9	35	71.4	321	1	ATP adenylitransf
10	35	71.4	1140	2	protein F15B4.7 [i
11	35	71.4	1140	2	hypothetical prote
12	35	71.4	1496	2	hypothetical prote
13	34	69.4	32	2	E6-II protein - hu
14	34	69.4	35	2	E6-III protein - h
15	34	69.4	47	2	E6-I protein - hum
16	34	69.4	149	1	E6 protein - rhesu
17	34	69.4	191	1	E6 protein - rhesu
18	34	69.4	217	2	hypothetical prote
19	34	69.4	249	2	molybdopterin bios
20	34	69.4	303	2	hypothetical prote
21	34	69.4	342	2	hypothetical prote
22	34	69.4	358	2	transcription regu
23	34	69.4	359	2	conserved hypotet
24	34	69.4	437	2	chromosome 6 open
25	34	69.4	465	2	dnaK-type molecula
26	34	69.4	505	1	protein-tyrosine k
27	34	69.4	516	2	cytochrome P450 (C
28	34	69.4	523	2	hypothetical prote
29	33.5	68.4	924	1	DNA-directed DNA p

30	33	67.3	218	2	AI2215	RNA polymerase sig
31	33	67.3	221	2	A87284	hydrolase, haloaci
32	33	67.3	306	2	T45586	hypothetical prote
33	33	67.3	326	2	B85344	hypothetical prote
34	33	67.3	326	2	T00421	probable phospholi
35	33	67.3	447	2	E96008	probable glycosylt
36	33	67.3	473	2	I49283	ADAM 4 protein pre
37	33	67.3	536	2	S33569	protein-tyrosine k
38	33	67.3	700	2	S23052	long-chain-fatty-a
39	33	67.3	1276	2	T27859	hypothetical prote
40	33	67.3	1297	2	T39287	hypothetical prote
41	33	67.3	1428	2	S62419	hypothetical prote
42	32.5	66.3	1208	2	T34469	hypothetical prote
43	32	65.3	142	2	S46445	YMF46 protein - Ac
44	32	65.3	171	2	B83815	hypothetical prote
45	32	65.3	210	2	S48023	dnaK-type molecula

ALIGNMENTS

RESULT 1

W6LHS

Protein E6 - human papillomavirus type 16

C:Species: human papillomavirus type 16

C>Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03682; T10427

R:Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virology 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A2355; MUID:85246220; PMID:2990099

A:Accession: A03682

A:Molecule type: DNA

A:Residues: 1-158 <SEE>

A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333033

R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human poapillomavirus type 16 genome acts at the lev

A:Reference number: Z17014; MUID:91162763; PMID:1848319

A:Accession: T10427

A>Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: DNA

A:Residues: 1-158 <REN>

A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G3330332

C:Genetics: E6

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:37-73/Region: zinc finger CCCC motif

F:110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 49; DB 1; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.032;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TIHDIILEC 9

|||||||

Db 29 TIHDIILEC 37

RESULT 2

H83709

small heat shock protein BH0480 [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C:Accession: H83709

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, N.; Fujii, F.; Hir

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: H83709

A>Status: preliminary

A:Molecule type: DNA

```

A;Residues: 1-145 <STO>
A;Cross-references: UNIPROT:Q9KFJ9; GB:AP001508; GB:BA000004; NID:gl0172890; PIDN:BA041
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH0480
C;Superfamily: alpha-crystallin-related small heat shock protein

Query Match      75.5%; Score 37; DB 2; Length 145;
Best Local Similarity 66.7%; Pred. No. 6.6;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
|:|:|:|:|
Db 46 TDEHILEC 54

RESULT 3
A36500
transferin precursor - tobacco hornworm
C;Species: Manduca sexta (tobacco hornworm)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A36500
R;Bartfeld, N.S.; Law, J.H.
J. Biol. Chem. 265, 21684-21691, 1990
A;Title: Isolation and molecular cloning of transferrin from the tobacco hornworm, Manduca sexta
A;Reference number: A36500; MUID:91072368; PMID:2254322
A;Accession: A36500
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-681 <BAR>
A;Cross-references: UNIPROT:P22297; GB:M62802; GB:M36296; NID:gl59543; PIDN:AAA29338.1;
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication

Query Match      75.5%; Score 37; DB 1; Length 681;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
|:|:|:|:|
Db 670 TIHDIILEC 678

RESULT 4
A3163
hypothetical protein Atu5034 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: A3163
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.;
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan,
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: A3163
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-75 <KUR>
A;Cross-references: UNIPROT:Q8UKR5; GB:AE008687; PIDN:AAL45727.1; PID:gl7743458; GSPDB:C
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu5034
A;Genome: plasmid

Query Match      73.5%; Score 36; DB 2; Length 75;
Best Local Similarity 71.4%; Pred. No. 5.3;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HDIILEC 9
|:|:|:|:|

```

Db 22 HDLLEEC 28

RESULT 5

W6MLPR

E6 protein - human papillomavirus type ME180 (provirus)

C;Species: human papillomavirus type ME180

A;Note: Host Homo sapiens (man)

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C;Accession: C40509

R;Reuter, S.; Delius, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.

J. Virol. 65, 5564-5568, 1991

A;Title: Characterization of a novel human papillomavirus DNA in the cervical carcinoma

A;Reference number: A40509; MUID:91374616; PMID:1716694

A;Accession: C40509

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-158 <REU>

A;Cross-references: UNIPROT:P27962; GB:M73258

C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; zinc finger

F;32-68/Region: zinc finger CCCC motif

F;105-141/Region: zinc finger CCCC motif

Query Match 73.5%; Score 36; DB 1; Length 158;

Best Local Similarity 44.4%; Pred. No. 11;

Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9

|:|:|:|:|

Db 24 TLHDVTIDC 32

RESULT 6

S54361

gag-related protein - Trypanosoma cruzi

C;Species: Trypanosoma cruzi

C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004

C;Accession: S54361

R;Martin, F.; Maranon, C.; Olivares, M.; Alonso, C.; Lopez, M.C.

J. Mol. Biol. 247, 49-59, 1995

A;Title: Characterization of a non-long terminal repeat retrotransposon cDNA (LITc) fro

A;Reference number: S54359; MUID:95205412; PMID:7534829

A;Accession: S54361

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-324 <MAR>

A;Cross-references: UNIPROT:Q9Y028; EMBL:X83098

C;Genetics:

A;Start codon: GTG

Query Match 73.5%; Score 36; DB 2; Length 324;

Best Local Similarity 55.6%; Pred. No. 23;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9

|:|:|:|:|

Db 268 TLHLLLEEC 276

RESULT 7

T24772

hypothetical protein T10B10.7 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T24772

R;Sims, M.

submitted to the EMBL Data Library, May 1996

A;Reference number: Z19934

A;Accession: T24772

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-519 <WIL>

R;Plateau, P.; Fromant, M.; Schmitter, J.M.; Buhler, J.M.; Blanquet, S.
J. Bacteriol. 171, 6437-6445, 1989
A;Title: Isolation, characterization, and inactivation of the APA1 gene encoding yeast
A;Reference number: S07847; MUID:90078083; PMID:2556364
A;Accession: S07847
A;Molecule type: DNA
A;Residues: 1-99, 'E', 101-321 <PLA>
A;Cross-references: GB:M31791; NID:G171063; PIDN:AAA34427.1; PID:G171064
A;Accession: A37535
A;Molecule type: protein
A;Residues: 15-33;39-99, 'E', 101-260;263-321 <PLA2>
C;Genetics:
A;Gene: SGD:APAL; DTP1; MIPS:YCL050c
A;Cross-references: SGD:S0000555; MIPS:YCL050c
A;Map position: 3L
C;Superfamily: ATP adenyllyltransferase
C;Keywords: acetylated amino end; blocked amino end; nucleotidyltransferase
E;2-321/Product: ATP adenyllyltransferase I #status predicted <MAT>
F;2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted

Query Match	71.4%	Score 35;	DB 1;	Length 321;
Best Local Similarity	75.0%;	Pred. No. 36;		
Matches	6;	Conservative	2;	Mismatches 0; Indels 0; Gaps 0;

Qy 2 IHDIILEC 9
|:|:|:|
Db 299 INDILLEC 306

RESULT 10
F88349
protein F15D4.7 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: F88349
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biol
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_e
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; a
A;Accession: F88349
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1140 <STO>
A;Cross-references: UNIPROT:Q93515; GB:chr_11; PIDN:CAB02490.1; PID:G3875970; GSPDB:GN
C;Genetics:
A;Gene: F15D4.7
A;Map position: 2

Query Match	71.4%	Score 35;	DB 2;	Length 1140;
Best Local Similarity	62.5%;	Pred. No. 1.3e+02;		
Matches	5;	Conservative	2;	Mismatches 1; Indels 0; Gaps 0;

Qy 2 IHDIILEC 9
|:|:|:|
Db 551 IHDMVAEC 558

RESULT 11
T20984
hypothetical protein F15D4.7 - Caenorhabditis elegans (fragment)
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20984
R;Smyle, R.
submitted to the EMBL Data Library, September 1996
A;Reference number: Z19354
A;Accession: T20984
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1140 <MIL>
A;Cross-references: UNIPROT:Q93515; EMBL:Z80344; PIDN:CAB02490.1; GSPDB:GN00020; CESP:

A;Experimental source: clone F15D4

C;Genetics:

A;Gene: CESP:F15D4.7

A;Map position: 2

A;Introns: 747/3

Query Match 71.4%; Score 35; DB 2; Length 1140;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IHDIIIEC 9

||||:|

Db 551 IHDNVAEC 558

RESULT 12

T19833

hypothetical protein C38D9.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T19833

R;Ainscough, R.

submitted to the EMBL Data Library, November 1996

A;Reference number: Z19184

A;Accession: T19833

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1496 <WIL>

A;Cross-references: UNIPROT:Q9XVC3; EMBL:Z81481; PIDN:CAB03949.1; GSPDB:GN00023; CESP:C38D9

C;Genetics:

A;Gene: CESP:C38D9.3

A;Map position: 5

A;Introns: 786/3

Query Match 71.4%; Score 35; DB 2; Length 1496;

Best Local Similarity 62.5%; Pred. No. 1.7e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IHDIIIEC 9

||||:|

Db 590 IHDNVAEC 597

RESULT 13

S19906

E6-II protein - human papillomavirus type 33 (fragment)

C;Species: human papillomavirus type 33

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C;Accession: S19906

R;Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; Me

submitted to the EMBL Data Library, January 1992

A;Description: HPV type 33 in a tonsillar carcinoma generates its putative E7 mRNA via t

A;Reference number: S19906

A;Accession: S19906

A;Molecule type: mRNA

A;Residues: 1-32 <SNI>

A;Cross-references: UNIPROT:Q81885; EMBL:X64086; NID:g60282; PIDN:CAA45435.1; PID:g60283

C;Superfamily: papillomavirus E6 protein

C;Keywords: early protein

Query Match 69.4%; Score 34; DB 2; Length 32;

Best Local Similarity 66.7%; Pred. No. 5.5;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TIHDIIEC 9

||||:|

Db 10 TIHNIELQC 18

RESULT 14

S19909

E6-III protein - human papillomavirus type 33 (fragment)

C;Species: human papillomavirus type 33

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C;Accession: S19909

R;Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; M

submitted to the EMBL Data Library, January 1992

A;Description: HPV type 33 in a tonsillar carcinoma generates its putative E7 mRNA via

A;Reference number: S19906

A;Accession: S19909

A;Molecule type: mRNA

A;Residues: 1-35 <SNI>

A;Cross-references: UNIPROT:Q81887; EMBL:X64087; NID:g60286; PIDN:CAA45438.1; PID:g6028

C;Superfamily: papillomavirus E6 protein

C;Keywords: early protein

Query Match 69.4%; Score 34; DB 2; Length 35;

Best Local Similarity 66.7%; Pred. No. 6;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TIHDIIEC 9

||||:|

Db 10 TIHNIELQC 18

RESULT 15

S23825

E6-I protein - human papillomavirus type 33 (fragment)

C;Species: human papillomavirus type 33

C;Date: 20-Feb-1995 #sequence_revision 30-Jan-1998 #text_change 09-Jul-2004

C;Accession: S23825; S23829

R;Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; M

submitted to the EMBL Data Library, January 1992

A;Description: HPV type 33 in a tonsillar carcinoma generates its putative E7 mRNA via

A;Reference number: S19906

A;Accession: S23825

A;Molecule type: mRNA

A;Residues: 1-47 <SNI>

A;Cross-references: UNIPROT:Q81883; UNIPROT:Q81884; EMBL:X64084; NID:g60273; PIDN:CAA45

C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; zinc finger

Query Match 69.4%; Score 34; DB 2; Length 47;

Best Local Similarity 66.7%; Pred. No. 8.1;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TIHDIIEC 9

||||:|

Db 10 TIHNIELQC 18

Search completed: June 28, 2005, 19:23:21

Job time : 13.2 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 01:35:30 ; Search time 57.55 Seconds
(without alignments)
60.138 Million cell updates/sec

Title: US-08-170-344-7
Perfect score: 49
Sequence: 1 TIHDIILEC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	9	16	US-10-777-053-547
2	49	100.0	9	16	US-10-837-217-547
3	49	100.0	10	14	US-10-128-711-72
4	49	100.0	10	14	US-10-133-210-280
5	49	100.0	15	16	US-10-476-570-22
6	49	100.0	15	16	US-10-476-570-23
7	49	100.0	30	16	US-10-476-570-53
8	49	100.0	30	17	US-10-858-384-4
9	49	100.0	32	16	US-10-476-570-9
10	49	100.0	33	16	US-10-476-570-19
11	49	100.0	151	14	US-10-177-390-6
					Sequence 547, App
					Sequence 547, App
					Sequence 72, App
					Sequence 280, App
					Sequence 22, App
					Sequence 23, App
					Sequence 53, App
					Sequence 4, App
					Sequence 9, App
					Sequence 19, App
					Sequence 6, App

12	49	100.0	151	17	US-10-484-063-20	Sequence 20, Appl
13	49	100.0	151	17	US-10-484-063-27	Sequence 27, Appl
14	49	100.0	158	17	US-10-858-384-2	Sequence 2, Appl
15	49	100.0	158	17	US-10-367-057-16	Sequence 16, Appl
16	49	100.0	171	16	US-10-472-724-2	Sequence 2, Appl
17	49	100.0	266	9	US-09-367-309A-1	Sequence 1, Appl
18	49	100.0	273	13	US-10-000-903-4	Sequence 4, Appl
19	49	100.0	273	17	US-10-899-771-4	Sequence 4, Appl
20	49	100.0	292	13	US-10-000-903-10	Sequence 10, Appl
21	49	100.0	292	17	US-10-899-771-10	Sequence 10, Appl
22	49	100.0	371	13	US-10-000-903-6	Sequence 6, Appl
23	49	100.0	371	17	US-10-899-771-6	Sequence 6, Appl
24	49	100.0	390	13	US-10-000-903-14	Sequence 14, Appl
25	49	100.0	390	17	US-10-899-771-14	Sequence 14, Appl
26	49	100.0	536	15	US-10-367-095-10	Sequence 10, Appl
27	49	100.0	536	15	US-10-368-046-10	Sequence 10, Appl
28	49	100.0	536	16	US-10-367-367-10	Sequence 10, Appl
29	49	100.0	536	17	US-10-918-337-10	Sequence 10, Appl
30	44	89.8	21	16	US-10-476-570-10	Sequence 10, Appl
31	41	83.7	306	16	US-10-437-963-149433	Sequence 149433, Appl
32	40	81.6	15	16	US-10-476-570-24	Sequence 24, Appl
33	40	81.6	150	16	US-10-437-963-153797	Sequence 153797, Appl
34	39	79.6	297	15	US-10-424-599-275411	Sequence 275411, Appl
35	39	79.6	298	15	US-10-424-599-168507	Sequence 168507, Appl
36	37	75.5	145	17	US-10-732-923-21847	Sequence 21847, A
37	37	75.5	554	16	US-10-739-930-10846	Sequence 10846, A
38	36	73.5	70	14	US-10-029-386-33593	Sequence 33593, A
39	36	73.5	83	16	US-10-425-115-205547	Sequence 205547, Appl
40	36	73.5	117	16	US-10-425-115-194068	Sequence 194068, Appl
41	36	73.5	164	16	US-10-425-115-358720	Sequence 358720, Appl
42	36	73.5	173	16	US-10-425-115-358724	Sequence 358724, Appl
43	36	73.5	174	17	US-10-947-979-18	Sequence 18, Appl
44	36	73.5	176	16	US-10-425-115-236213	Sequence 236213, Appl
45	36	73.5	176	17	US-10-947-979-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-10-777-053-547
; Sequence 547, Application US/10777053
; Publication No. US20040132089A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANK 022C1
; CURRENT APPLICATION NUMBER: US/10777,053
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,368
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 547
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papillomavirus 16
US-10-777-053-547

Query Match 100.0%; Score 49; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TIHDIILEC 9
Db 1 TIHDIILEC 9

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RESULT 2
US-10-837-217-547
; Sequence 547, Application US/10837217
; Publication No. US20040203051A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANNK.022C2
; CURRENT APPLICATION NUMBER: US/10/837,217
; CURRENT FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 547
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papillomavirus 16
US-10-837-217-547

Query Match 100.0%; Score 49; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
Db 1 TIHDIILEC 9

RESULT 3
US-10-128-711-72
; Sequence 72, Application US/10128711
; Publication No. US20030099634A1
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Esteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend Khourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/128,711
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; APPLICATION NUMBER: US 07/827,682
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; FILING DATE: 29-JAN-1992
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 72:
US-10-128-711-72

Query Match 100.0%; Score 49; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
Db 1 TIHDIILEC 9

RESULT 4
US-10-133-210-280
; Sequence 280, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: Delisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 280
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-280

Query Match 100.0%; Score 49; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
Db 1 TIHDIILEC 9

RESULT 5
US-10-476-570-22
; Sequence 22, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
```

```

; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 24-38
US-10-476-570-22

Query Match          100.0%; Score 49; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
Db 6 TIHDIILEC 14

RESULT 6
US-10-476-570-23
; Sequence 23, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 28-42
US-10-476-570-23

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Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
Db 2 TIHDIILEC 10

RESULT 7
US-10-476-570-53
; Sequence 53, Application US/10476570
; Publication No. US20040170644A1

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; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 30
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide B6 15-44
US-10-476-570-53

Query Match          100.0%; Score 49; DB 16; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
Db 15 TIHDIILEC 23

RESULT 8
US-10-858-384-4
; Sequence 4, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
; OTHER INFORMATION: for E6 of HPV
US-10-858-384-4

Query Match          100.0%; Score 49; DB 17; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
Db 15 TIHDIILEC 23

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RESULT 9
US-10-476-570-9
; Sequence 9, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 32
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-45
US-10-476-570-9
Query Match 100.0%; Score 49; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 TIHDIILEC 9
Db 16 TIHDIILEC 24
RESULT 10
US-10-476-570-19
; Sequence 19, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 33
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-46
US-10-476-570-19
Query Match 100.0%; Score 49; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TIHDIILEC 9
Db 16 TIHDIILEC 24
RESULT 11
US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerp Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6
Query Match 100.0%; Score 49; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 TIHDIILEC 9
Db 22 TIHDIILEC 30
RESULT 12
US-10-484-063-20
; Sequence 20, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: UTS-560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-20
Query Match 100.0%; Score 49; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 TIHDIILEC 9
Db 22 TIHDIILEC 30
RESULT 13
US-10-484-063-27
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:

; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: US/10-484,063
; CURRENT APPLICATION NUMBER: US/10-484,063
; PRIOR FILING DATE: 2004-01-16
; PRIOR FILING DATE: 2002-07-19
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-484-063-27

Query Match 100.0%; Score 49; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.19; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
Db 22 TIHDIILEC 30

RESULT 14
US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match 100.0%; Score 49; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.2; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
Db 29 TIHDIILEC 37

RESULT 15
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng

; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match 100.0%; Score 49; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.2; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
Db 29 TIHDIILEC 37

Search completed: June 29, 2005, 03:24:07
Job time : 58.55 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:32:21 ; Search time 11.2747 Seconds
(without alignments)
76.805 Million cell updates/sec

Title: US-08-170-344-64

Perfect score: 54

Sequence: 1 VCPICSOXP 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	98	1 W7LHS	E7 protein - human
2	45	83.3	98	1 W7L11	E7 protein - human
3	43	79.6	1496	1 CGH2V	collagen alpha 2(V
4	41	75.9	74	2 C7L17	hypothetical prote
5	41	75.9	95	2 D75036	hypothetical prote
6	41	75.9	166	2 A40783	18.2K protein - ph
7	41	75.9	1295	2 S60179	pol polyprotein ho
8	40	74.1	283	2 C70390	formate dehydrogen
9	40	74.1	565	2 H86477	protein F1504.19 [
10	40	74.1	729	2 C89038	transcription regu
11	39	72.2	181	2 C71349	probable anti-gigm
12	39	72.2	200	2 E36604	unknown protein F1
13	39	72.2	206	2 S51478	drought-induced pr
14	39	72.2	210	2 T45654	zinc-finger-like p
15	39	72.2	261	2 AF1939	hypothetical prote
16	39	72.2	506	2 F85016	probable RING zinc
17	39	72.2	506	2 T01716	hypothetical prote
18	39	72.2	587	2 S63176	probable membrane
19	39	72.2	644	2 S39356	transcription fact
20	39	72.2	695	2 T13648	mitosis initiation
21	39	72.2	708	2 A38436	mitosis initiation
22	39	72.2	1042	2 T16169	hypothetical prote
23	39	72.2	1955	1 AGCH	agrin precursor -
24	38	70.4	98	1 W7L6	E7 protein - human
25	38	70.4	211	2 E70428	recombination prot
26	38	70.4	214	2 T01522	drought-induced pr
27	38	70.4	273	2 S39200	formamidopyrimidin
28	38	70.4	331	2 B40951	Tif1 protein - mou
29	38	70.4	435	2 T30114	hypothetical prote

RESULT 1

W7LHS

E7 protein - human papillomavirus type 16

C;Species: human papillomavirus type 16

C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C;Accession: A03688; S12367; T10428

R;Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virolgy 145, 181-185, 1985

A;Title: Human papillomavirus type 16 DNA sequence.

A;Reference number: A22355; MUID:85246220; PMID:2990099

A;Accession: A03688

A;Molecule type: DNA

A;Residues: 1-98 <SE>

A;Cross-references: UNIPROT:P03129; GB:K02718; NID:G333031; PIDN:AAA46940.1; PID:G33303

R;Barbosa, W.S.; Edmonds, C.; Fisher, C.; Schiller, J.T.; Lowy, D.R.; Vonsden, K.H.

EMBO J. 9, 153-160, 1990

A;Title: The region of the HPV E7 oncoprotein homologous to adenovirus Ela and SV40 la

A;Reference number: S12367; MUID:90107938; PMID:2153075

A;Accession: S12367

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-98 <BAR>

R;Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A;Title: A negative element in the human poapillomavirus type 16 genome acts at the lev

A;Reference number: Z17014; MUID:91162763; PMID:1848319

A;Accession: T10428

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-98 <KEN>

A;Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46940.1; PID:G333033

C;Genetics:

A;Gene: E7

C;Superfamily: papillomavirus E7 protein

C;Keywords: DNA binding; early protein; transcription regulation; zinc finger

F;58-94/Region: zinc finger CCOC motif

Query Match 100.0%; Score 54; DB 1; Length 98;

Best Local Similarity 100.0%; Pred. No. 0.13;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VCPICSOXP 9

Db 90 VCPICSOXP 98

RESULT 2

W7L11

E7 protein - human papillomavirus type 11

C;Species: human papillomavirus type 11

C;Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 09-Jul-2004

C;Accession: A03690

R:Dartmann, K.; Schwarz, E.; Gissmann, L.; zur Hausen, H.
 Virology 151, 124-130, 1986
 A>Title: The nucleotide sequence and genome organization of human papilloma virus type 1
 A:Reference number: A94338; MUID:86181601; PMID:3008427
 A:Accession: A03690
 A:Molecule type: DNA
 A:Residues: 1-98 <DAR>
 A:Cross-references: UNIPROT:P04020; GB:M14119; NID:g333026; PIDN:AAA46928.1; PID:g496194
 C:Superfamily: papillomavirus E7 protein
 C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
 F:58-94/Region: zinc finger CCCC motif

Query Match 83.3%; Score 45; DB 1; Length 98;
 Best Local Similarity 77.8%; Pred. No. 3;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VCPICSOQK 9
 |||||: ||
 Db 90 VCPICAPKP 98

RESULT 3
 CGHU2V
 collagen alpha 2(V) chain precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 31-Jul-1989 #sequence revision 28-Jul-1995 #text_change 09-Jul-2004
 C:Accession: A31427; A54555; S43643; A25874; A25374; A30017
 R:Woodbury, D.; Benson-Chanda, V.; Ramirez, F.
 J. Biol. Chem. 264, 2735-2738, 1989
 A>Title: Amino-terminal propeptide of human pro-alpha2(V) collagen conforms to the struc
 A:Reference number: A31427; MUID:89123368; PMID:2914927
 A:Accession: A31427
 A:Molecule type: mRNA
 A:Residues: 1-463 <WOO>
 A:Cross-references: UNIPROT:P05997; GB:J04478; NID:g179697; PIDN:AAA51859.1; PID:g179698
 A:Experimental source: Placenta
 R:Greenspan, D.S.; Lee, S.T.; Lee, B.S.; Hoffman, G.G.
 Gene Expr. 1, 29-39, 1991
 A>Title: Homology between alpha2(V) and alpha1(III) collagen promoters and evidence for
 A:Reference number: A54555; MUID:92314691; PMID:1820205
 A:Accession: A54555
 A:Molecule type: DNA
 A:Residues: 1-32 <GRE>
 A:Cross-references: GB:M58529; NID:g180834; PIDN:AA41699.1; PID:g553235
 R:Moradi-Ameli, M.; Rousseau, J.C.; Kleman, J.P.; Champliand, M.F.; Boutillon, M.M.; Ben
 Eur. J. Biochem. 221, 987-995, 1994
 A>Title: Diversity in the processing events at the N-terminus of type-V collagen.
 A:Reference number: S43642; MUID:94237164; PMID:8181482
 A:Accession: S43643
 A:Molecule type: protein
 A:Residues: 288-291, 'P', 293-294, 'X', 296-297, 606, 'X', 608-617 <MOR>
 R:Weil, D.; Bernard, M.; Gargano, S.; Ramirez, F.
 Nucleic Acids Res. 15, 181-198, 1987
 A>Title: The pro alpha 2(V) collagen gene is evolutionarily related to the major fibrill
 A:Reference number: A25874; MUID:87146331; PMID:3029669
 A:Accession: A25874
 A:Molecule type: mRNA; DNA
 A:Residues: 398-1496 <WEI>
 A:Cross-references: GB:X04758; NID:g29588; PIDN:CAA28454.1; PID:g1340175
 R:Myers, J.C.; Loidl, H.R.; Stolle, C.A.; Seyer, J.M.
 J. Biol. Chem. 260, 5533-5541, 1985
 A>Title: Partial covalent structure of the human alpha 2 type V collagen chain.
 A:Reference number: I55239; MUID:85182703; PMID:2985598
 A:Accession: I55239
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1002-1226 <R22>
 A:Cross-references: GB:M10956; NID:g180427; PIDN:AAA52007.1; PID:g180428
 A>Note: part of this sequence were determined by protein sequencing
 R:Emanuel, B.S.; Cannizzaro, L.A.; Seyer, J.M.; Myers, J.C.
 Proc. Natl. Acad. Sci. U.S.A. 82, 3385-3389, 1985
 A>Title: Human alpha 1(III) and alpha 2(V) procollagen genes are located on the long arm

A:Reference number: I59025; MUID:85216505; PMID:3858826
 A:Accession: I59025
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1003-1034 <RES>
 A:Cross-references: GB:M11135; NID:g179693; PIDN:AAA51857.1; PID:g179694
 A>Note: part of this sequence were determined by protein sequencing
 R:Myers, J.C.; Loidl, H.R.; Seyer, J.M.; Dion, A.S.
 J. Biol. Chem. 260, 11216-11222, 1985
 A>Title: Complete primary structure of the human alpha-2 type V procollagen COOH-termin
 A:Reference number: A25374; MUID:85289337; PMID:2411731
 A:Accession: A25374
 A:Molecule type: mRNA
 A:Residues: 1227-1417, 'T', 1419-1437, 'S', 1439-1496 <MYE>
 A:Cross-references: GB:M11718; NID:g180912; PIDN:AAA52058.1; PID:g180913
 A:Experimental source: normal fibroblasts
 R:Tsiouras, P.; Schwartz, R.C.; Liddell, A.C.; Salkeid, C.S.; Weil, D.; Ramirez, F.
 Genomics 3, 275-277, 1988
 A>Title: Genetic distance of two fibrillar collagen loci, COL3A1 and COL5A2, located on
 A:Reference number: A30017; MUID:89138450; PMID:3224983
 A:Accession: A30017
 A:Molecule type: DNA
 A:Residues: 1449-1463, 'E', 1465-1495, 'A' <TSI>
 A:Cross-references: GB:J03051; NID:g179695; PIDN:AAA51858.1; PID:g179696
 A>Note: the authors translated the codon GAA for residue 1460 as Gln, and GAG for resid
 C:Comment: Prolines and lysines at the third position of the tripeptide repeating unit
 are 5-hydroxylated and subsequently O-glycosylated.
 C:Comment: The amino-terminal propeptide domain appears not to be completely cleaved.
 C:Genetics:
 A:Gene: GDB:COL5A2
 A:Cross-references: GDB:119064; OMIM:120190
 A:Map position: 2q31-2q31
 A:Introns: 33/1; 812/3; 830/3; 848/3; 884/3; 902/3; 922/3; 974/3; 1046/3; 1064/3; 1448/3
 C:Complex: type V collagen may be a homotrimer of alpha 1(V) chains (see PIR:CGHU1V), a
 alpha 2(V) chain and one alpha 3(V) chain, initially linked by disulfide bonds among th
 engh, is formed with desmosine cross-links made from lysine and allysine residues
 C:Function:
 A:Description: structural component of extracellular fibrous polymer associated with ce
 A>Note: may play a role in controlling the lateral growth of collagen I fibrils
 C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology
 C:Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxyprol
 F:1-26/Domain: signal sequence #status predicted <SIG>
 F:1-2650/Product: collagen alpha 2(V) chain #status predicted <MAT>
 F:27-193/Domain: amino-terminal propeptide (uncleaved) #status predicted <NPP>
 F:27-108/Region: nonhelical
 F:40-99/Domain: von Willebrand factor type C repeat homology <VMC>
 F:109-186/Region: helical
 F:187-208/Region: nonhelical
 F:209-1225/Region: helical
 F:503-505/Region: cell attachment (R-G-D) motif
 F:941-943/Region: cell attachment (R-G-D) motif
 F:1064-1066/Region: cell attachment (R-G-D) motif
 F:1067-1069/Region: cell attachment (R-G-D) motif
 F:1097-1099/Region: cell attachment (R-G-D) motif
 F:1124-1126/Region: cell attachment (R-G-D) motif
 F:1133-1135/Region: cell attachment (R-G-D) motif
 F:1225-1250/Region: carboxyl-terminal nonhelical telopeptide
 F:1251-1496/Domain: carboxyl-terminal propeptide #status predicted <CPP>
 F:1269-1496/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
 F:27/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicte
 F:193-194/Cleavage site: Ala-Gln (procollagen N-endorpeptidase) #status predicted
 F:194/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predict
 F:201/Modified site: allysine (Lys) #status predicted
 F:230,293,296,608,614,1004,1007,1013,1028,1034/Modified site: 4-hydroxyproline (Pro) #s
 F:299,1139/Modified site: 5-hydroxylysine (Lys) (covalent) #status predicted
 F:299,1139/Binding site: carbohydriate (Lys) #status predicted
 F:1025/Modified site: 5-hydroxylysine (Lys) #status experimental
 F:1250-1251/Cleavage site: Glu-Asp (procollagen C-endorpeptidase) #status predicted
 F:1259,1397/Binding site: carbohydriate (Asn) (covalent) #status predicted
 F:1293,1299,1325/Disulfide bonds: interchain #status predicted
 F:1333-1494,1402-1447/Disulfide bonds: #status predicted

Query Match 79.6%; Score 43; DB 1; Length 1496;

Best Local Similarity 75.0%; Pred. No. 45;
Matches 6; Conservative 1; Mismatches 0; Gaps 0;

Qy 2 CPICSQKP 9
|||
Db 93 CPVCSQTP 100

RESULT 4

C71127
hypothetical protein PHS025 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 16-Aug-2004
C:Accession: C71127
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohkuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: C71127
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-74 <KAW>
A:Cross-references: UNIPROT:O73989; GB:AP000003; NID:G3236130; PIDN:BA29877.1; PID:G325
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PHS025
C:Superfamily: pyrophosphohydrolase, MazG-related, AF0820 type

Query Match 75.9%; Score 41; DB 2; Length 74;
Best Local Similarity 66.7%; Pred. No. 9.9;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
|||
Db 60 VCPYCGRKP 68

RESULT 5

D75036
hypothetical protein PAB3319 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: D75036
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: D75036
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-95 <KAW>
A:Cross-references: UNIPROT:Q9U274; GB:AJ248287; GB:AL096836; NID:G5458657; PIDN:CAB5018
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB3319
C:Superfamily: pyrophosphohydrolase, MazG-related, AF0820 type

Query Match 75.9%; Score 41; DB 2; Length 95;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
|||
Db 82 VCPYCGRKP 90

RESULT 6

A40783
18.2K protein - phage Cfl1
C:Species: phage Cfl1
C>Date: 18-Nov-1992 #sequence_revision 18-Nov-1992 #text_change 09-Jul-2004

C:Accession: A40783
R:Shieh, G.J.; Charnig, Y.C.; Yang, B.C.; Tu, J.; Bau, H.J.; Kuo, T.T.
Virology 185, 316-322, 1991
A:Title: Identification and nucleotide sequence analysis of an open reading frame invol
A:Reference number: A40783; MUID:92024088; PMID:1926778
A:Accession: A40783
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-166 <SHI>
A:Cross-references: UNIPROT:Q37902

Query Match 75.9%; Score 41; DB 2; Length 166;
Best Local Similarity 62.5%; Pred. No. 18;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CPICSQKP 9
|||
Db 6 CPICQKP 13

RESULT 7

S60179
pol polyprotein homolog - fungus (Fusarium oxysporum) retrotransposon skippy
C:Species: Fusarium oxysporum
C>Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jul-2000
C:Accession: S60179
R:Anaya, N.; Roncero, M.I.G.
Mol. Gen. Genet. 249, 637-647, 1995
A:Title: Skippy, a retrotransposon from the fungal plant pathogen Fusarium oxysporum.
A:Reference number: S60178; MUID:96132549; PMID:8544829
A:Accession: S60179
A:Molecule type: DNA
A:Residues: 1-1295 <ANA>
A:Cross-references: EMBL:L34658; NID:G510695; PIDN:AA88791.1; PID:G510697
A:Experimental source: retrotransposon skippy
C:Genetics:
A:Mobile element: retrotransposon skippy
C:Superfamily: Fusarium retrotransposon skippy pol polyprotein; chromobox homology
F:1236-1273/Domain: chromobox homology <CBH>

Query Match 75.9%; Score 41; DB 2; Length 1295;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CPICSQKP 9
|||
Db 837 CPICQKP 844

RESULT 8

C70390
formate dehydrogenase formation protein FdhE - Aquifex aeolicus
C:Species: Aquifex aeolicus
C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: C70390
R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; C
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: C70390
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-283 <AQF>
A:Cross-references: UNIPROT:O67150; GB:AE000720; NID:G2983529; PIDN:AAC07106.1; PID:G29
A:Experimental source: strain VF5
C:Genetics:
A:Gene: fdhE
C:Superfamily: formate dehydrogenase accessory protein FdhE

Query Match 74.1%; Score 40; DB 2; Length 283;
Best Local Similarity 62.5%; Pred. No. 38;

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Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CPICSQKP 9
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Db 167 CPVCGSKP 174

RESULT 9
H86477
C:Species: Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: H86477
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H86477
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-565 <STO>
A:CROSS-references: UNIPROT:Q9LQG6; GB:AE005172; NID:g8778343; PIDN:AAF79351.1; GSPDB:GN
C:Genetics:
A:Gene: F1504.19
A:Map position: 1

Query Match 74.1%; Score 40; DB 2; Length 565;
Best Local Similarity 62.5%; Pred. No. 63;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CPICSQKP 9
   |||:| ||
Db 269 CPVCKQNP 276

RESULT 10
C69038
transcription regulator HypF homolog - Methanobacterium thermoautotrophicum (strain Delta
C:Species: Methanobacterium thermoautotrophicum
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 14-Apr-2003
C:Accession: C69038
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan, N.
Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A>Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: C69038
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-729 <MTH>
A:CROSS-references: GB:AE000894; GB:AE000666; NID:g2622392; PIDN:AAB85769.1; PID:g262239
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH1287
C:Superfamily: carbamoyl phosphate-converting enzyme ([NiFe]-hydrogenase maturation fac

Query Match 74.1%; Score 40; DB 2; Length 729;
Best Local Similarity 75.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CPICSQKP 9
   |||:| ||
Db 145 CPICGPKP 152

```

```

RESULT 11
C71349
Probable anti-sigma F factor antagonist - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: C71349
R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwi
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McD
rson, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A>Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876
A:Accession: C71349
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-181 <COL>
A:CROSS-references: UNIPROT:O83261; GB:AE001205; GB:AE000520; NID:g3322501; PIDN:AAAC652
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0233

Query Match 72.2%; Score 39; DB 2; Length 181;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CPICSQK 8
   |||:| ||
Db 146 CPICSRK 152

RESULT 12
E96604
unknown protein F14G9.11 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E96604
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E96604
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-200 <STO>
A:CROSS-references: UNIPROT:Q9C7K3; GB:AE005173; NID:gl1094735; PIDN:AAG29670.1; GSPDB:
C:Genetics:
A:Gene: F14G9.11
A:Map position: 1

Query Match 72.2%; Score 39; DB 2; Length 200;
Best Local Similarity 75.0%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VCPICSQK 8
   |||:| ||
Db 65 VCPVCSTK 72

RESULT 13
S51478
drought-induced protein Dil9 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: S51478; S43179
R:Gosti, F.; Bertauche, N.; Vartanian, N.; Giraudat, J.
Mol. Gen. Genet. 246, 10-18, 1995

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A:Title: Absciscic acid-dependent and -independent regulation of gene expression by prog
 A:Reference number: S51478; MUID:95124290; PMID:7823904
 A:Accession: S51478
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-206 <GOS>
 A:Cross-references: UNIPROT:Q39083; EMBL:X78584; NID:9469109; PIDN:CAAS5321.1; PID:94691
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
 C:Genetics:
 A:Gene: D19

Query Match 72.2%; Score 39; DB 2; Length 206;
 Best Local Similarity 75.0%; Pred. No. 43;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VCPICSQK 8
 :|||:
 Db 65 VCPVCSLK 72

RESULT 14

T45654
 zinc-finger-like protein - Arabidopsis thaliana
 N:Alternate names: protein F13112.230
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
 C:Accession: T45654
 R:Choisme, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa
 submitted to the Protein Sequence Database, November 1999
 A:Reference number: Z23010
 A:Accession: T45654
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-210 <CHO>
 A:Cross-references: UNIPROT:Q9SD55; EMBL:AL133292
 A:Experimental source: cultivar Columbia; BAC clone F13112
 C:Genetics:
 A:Map position: 3
 A:Note: F13112.230

Query Match 72.2%; Score 39; DB 2; Length 210;
 Best Local Similarity 55.6%; Pred. No. 43;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
 :|||:
 Db 199 ICPICCSEP 207

RESULT 15

AF1939
 hypothetical protein all1065 [imported] - Nostoc sp. (strain PCC 7120)
 C:Species: Nostoc sp. PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
 C:Accession: AF1939
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
 DNA Res. 8, 205-213, 2001
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
 A:Reference number: AB1807; MUID:21595285; PMID:11759840
 A:Accession: AF1939
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-261 <KUR>
 A:Cross-references: UNIPROT:Q8YXZ1; GB:BA000019; PIDN:BAW73022.1; PID:G17130411; GSPDB:G
 A:Experimental source: strain PCC 7120
 C:Genetics:
 A:Gene: all1065

Query Match 72.2%; Score 39; DB 2; Length 261;
 Best Local Similarity 75.0%; Pred. No. 51;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VCPICSQK 8
 :|||:
 Db 20 ICPCSQK 27

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OM protein - protein search, using sw model

Run on: June 29, 2005, 05:18:25 ; Search time 53.8517 Seconds
(without alignments)
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Title: US-08-170-344-64

Perfect score: 54

Sequence: 1 VCPICSQKP 9

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Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	15	16	US-10-476-570-52
2	54	100.0	15	16	US-10-306-541-71
3	54	100.0	17	17	US-10-751-845-69
4	54	100.0	21	15	US-10-432-465-51
5	54	100.0	21	16	US-10-476-570-18
6	54	100.0	21	16	US-10-890-526-76
7	54	100.0	98	9	US-09-728-466-1
8	54	100.0	98	9	US-09-820-785-4
9	54	100.0	98	9	US-09-824-017-4
10	54	100.0	98	10	US-09-986-118A-4
11	54	100.0	98	14	US-10-267-311-8
					Sequence 52, Appl
					Sequence 71, Appl
					Sequence 69, Appl
					Sequence 51, Appl
					Sequence 18, Appl
					Sequence 76, Appl
					Sequence 1, Appl
					Sequence 4, Appl
					Sequence 4, Appl
					Sequence 8, Appl

12	54	100.0	98	14	US-10-177-390-8	Sequence 8, Appl
13	54	100.0	98	14	US-10-201-764-19	Sequence 19, Appl
14	54	100.0	98	15	US-10-392-113-29	Sequence 29, Appl
15	54	100.0	98	15	US-10-654-129-4	Sequence 4, Appl
16	54	100.0	98	15	US-10-681-410-19	Sequence 19, Appl
17	54	100.0	98	16	US-10-772-988-3	Sequence 3, Appl
18	54	100.0	98	16	US-10-479-541-5	Sequence 5, Appl
19	54	100.0	98	17	US-10-042-526A-4	Sequence 4, Appl
20	54	100.0	98	17	US-10-657-399-1	Sequence 1, Appl
21	54	100.0	98	17	US-10-858-384-12	Sequence 12, Appl
22	54	100.0	98	17	US-10-484-063-26	Sequence 26, Appl
23	54	100.0	98	17	US-10-343-448-5	Sequence 5, Appl
24	54	100.0	98	17	US-10-679-956-8	Sequence 8, Appl
25	54	100.0	98	17	US-10-367-057-17	Sequence 17, Appl
26	54	100.0	111	16	US-10-472-724-4	Sequence 4, Appl
27	54	100.0	117	17	US-10-751-845-126	Sequence 126, App
28	54	100.0	121	14	US-10-267-311-12	Sequence 12, Appl
29	54	100.0	121	17	US-10-679-956-12	Sequence 12, Appl
30	54	100.0	198	14	US-10-267-311-35	Sequence 35, Appl
31	54	100.0	198	17	US-10-679-956-35	Sequence 35, Appl
32	54	100.0	220	13	US-10-000-903-1	Sequence 1, Appl
33	54	100.0	220	13	US-10-000-903-8	Sequence 8, Appl
34	54	100.0	220	17	US-10-899-771-1	Sequence 1, Appl
35	54	100.0	220	17	US-10-899-771-8	Sequence 8, Appl
36	54	100.0	236	17	US-10-751-845-157	Sequence 157, App
37	54	100.0	237	17	US-10-751-845-158	Sequence 158, App
38	54	100.0	239	13	US-10-000-903-12	Sequence 12, Appl
39	54	100.0	239	17	US-10-899-771-12	Sequence 12, Appl
40	54	100.0	261	17	US-10-751-845-160	Sequence 160, App
41	54	100.0	266	9	US-09-367-309A-1	Sequence 1, Appl
42	54	100.0	295	14	US-10-267-311-33	Sequence 33, Appl
43	54	100.0	295	17	US-10-679-956-33	Sequence 33, Appl
44	54	100.0	324	14	US-10-267-311-25	Sequence 25, Appl
45	54	100.0	324	17	US-10-679-956-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1

US-10-476-570-52
; Sequence 52, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E7 84-98

Query Match 100.0%; Score 54; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.094;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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US-10-890-526-76
; Sequence 76, Application US/10890526
; Publication No. US20040258708A1
; GENERAL INFORMATION:
; APPLICANT: Jochmus, Ingrid
; APPLICANT: Nieland, John
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
; TITLE OF INVENTION: Papilloma Virus Li-Protein and Use Thereof in Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/036001
; CURRENT APPLICATION NUMBER: US/10/890,526
; CURRENT FILING DATE: 2004-07-13
; PRIOR APPLICATION NUMBER: US/09/980,177
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: PCT/EP00/05006
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: DE 19925199.1
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-890-526-76

Query Match      100.0%; Score 54; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
Db 13 VCPICSQKP 21

RESULT 7
US-09-728-466-1
; Sequence 1, Application US/09728466
; Patent No. US20010029022A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Christopher
; APPLICANT: He, Wanxia
; TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
; FILE REFERENCE: 28341/6216
; CURRENT APPLICATION NUMBER: US/09/728,466
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/382,616
; PRIOR FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Papillomavirus sylvilagi
US-09-728-466-1

Query Match      100.0%; Score 54; DB 9; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
Db 90 VCPICSQKP 98

RESULT 8
US-09-820-765-4
; Sequence 4, Application US/09820765
; Publication No. US20020039584A1
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; APPLICANT: HALLEK, Michael
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE

```

```

; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/820,765
; FILING DATE: 30-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,896
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-820-765-4

Query Match      100.0%; Score 54; DB 9; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
Db 90 VCPICSQKP 98

RESULT 9
US-09-824-017-4
; Sequence 4, Application US/09824017
; Publication No. US20020197668A1
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; APPLICANT: HALLEK, Michael
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/824,017
; FILING DATE: 03-Apr-2001
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: 09/026,896
; FILING DATE: 1998-02-20
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-824-017-4

Query Match      100.0%; Score 54; DB 9; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VCPICSQKP 9
      |||||
Db      90 VCPICSQKP 98

RESULT 10
US-09-986-118A-4
; Sequence 4, Application US/09986118A
; Publication No. US20030021806A1
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; HALEK, Michael
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/986,118A
; FILING DATE: 07-NO. US20030021806A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,896
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-986-118A-4

Query Match      100.0%; Score 54; DB 10; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VCPICSQKP 9
      |||||
Db      90 VCPICSQKP 98

RESULT 11
US-10-267-311-8
; Sequence 8, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-8

Query Match      100.0%; Score 54; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VCPICSQKP 9
      |||||
Db      90 VCPICSQKP 98

RESULT 12
US-10-177-390-8
; Sequence 8, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerps Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 8
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: fragment of
; OTHER INFORMATION: human papilloma virus type 16 E7 gene
US-10-177-390-8

Query Match      100.0%; Score 54; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VCPICSQKP 9
      |||||
Db      90 VCPICSQKP 98
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RESULT 13

US-10-201-764-19
; Sequence 19, Application US/10201764
; Publication No. US20030166140A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, SI-YI AND ZHAOYANG, YOU
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTIGENS WHICH ELICIT AN
; FILE REFERENCE: IMMUNE RESPONSE
; CURRENT APPLICATION NUMBER: US/10/201,764
; PRIOR FILING DATE: 2002-07-22
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,752
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 60/132,750
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.0
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Human papillomavirus type E7
US-10-201-764-19

Query Match 100.0%; Score 54; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.51; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
Db 90 VCPICSQKP 98
|||||

RESULT 14

US-10-392-113-29
; Sequence 29, Application US/10392113
; Publication No. US20030224993A1
; GENERAL INFORMATION:
; APPLICANT: Land, Hartmut
; APPLICANT: Deleu, Laurent
; TITLE OF INVENTION: COMPOSITIONS THAT INHIBIT PROLIFERATION
; FILE REFERENCE: OF CANCER CELLS
; FILE REFERENCE: 21108.0005U3
; CURRENT APPLICATION NUMBER: US/10/392,113
; PRIOR FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: 60/365,078
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: PCT/US01/32127
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/239,705
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence./Note #
; OTHER INFORMATION: Synthetic Construct
US-10-392-113-29

Query Match 100.0%; Score 54; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
Db 90 VCPICSQKP 98
|||||

RESULT 15

US-10-654-129-4
; Sequence 4, Application US/10654129
; Publication No. US20040081661A1
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; APPLICANT: HALLEK, Michael
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/654,129
; FILING DATE: 04-Sep-2003
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/824,017
; FILING DATE: 03-Apr-2001
; APPLICATION NUMBER: 09/026,896
; FILING DATE: 1998-02-20
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-654-129-4

Query Match 100.0%; Score 54; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
Db 90 VCPICSQKP 98
|||||

Search completed: June 29, 2005, 05:48:12
Job time : 53.8517 secs

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	54	100.0	21	2	US-08-934-915-50	Sequence 50, Appl
2	54	100.0	21	2	US-08-934-915-157	Sequence 157, Appl
3	54	100.0	21	4	US-09-980-177A-76	Sequence 76, Appl
4	54	100.0	28	4	US-09-486-394-5	Sequence 5, Appl
5	54	100.0	30	2	US-08-934-915-54	Sequence 54, Appl
6	54	100.0	98	1	US-08-406-248-6	Sequence 6, Appl
7	54	100.0	98	3	US-08-075-541D-42	Sequence 42, Appl
8	54	100.0	98	3	US-09-382-616A-1	Sequence 1, Appl
9	54	100.0	98	3	US-08-944-368A-4	Sequence 4, Appl
10	54	100.0	98	3	US-09-820-764-4	Sequence 4, Appl
11	54	100.0	98	4	US-09-613-303-8	Sequence 8, Appl
12	54	100.0	98	4	US-09-566-420-19	Sequence 19, Appl
13	54	100.0	98	4	US-09-986-118A-4	Sequence 4, Appl
14	54	100.0	98	4	US-09-728-466-1	Sequence 1, Appl
15	54	100.0	98	4	US-09-824-017-4	Sequence 4, Appl
16	54	100.0	98	4	US-10-267-311-8	Sequence 8, Appl
17	54	100.0	98	4	US-10-201-764-19	Sequence 19, Appl
18	54	100.0	98	4	US-09-637-746-3	Sequence 3, Appl
19	54	100.0	98	4	US-09-501-097A-7	Sequence 7, Appl
20	54	100.0	98	4	US-09-980-523A-12	Sequence 12, Appl
21	54	100.0	121	4	US-09-613-303-12	Sequence 12, Appl
22	54	100.0	121	4	US-10-267-311-12	Sequence 12, Appl
23	54	100.0	172	3	US-08-860-165-14	Sequence 14, Appl
24	54	100.0	172	3	US-09-359-382-14	Sequence 14, Appl
25	54	100.0	198	4	US-09-613-303-35	Sequence 35, Appl
26	54	100.0	198	4	US-10-267-311-35	Sequence 35, Appl
27	54	100.0	220	3	US-09-485-885-1	Sequence 1, Appl

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
Db 13 VCPICSQKP 21

RESULT 2
US-08-934-915-157
; Sequence 157, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:

INFORMATION FOR SEQ ID NO: 157:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-157

Query Match 100.0%; Score 54; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
Db 13 VCPICSQKP 21

RESULT 3
US-09-980-177A-76
; Sequence 76, Application US/09980177A
; Patent No. 6838084
; GENERAL INFORMATION:
; APPLICANT: Jochmus, Ingrid
; APPLICANT: Nieland, John
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
; TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and

; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/036001
; CURRENT APPLICATION NUMBER: US/09/980,177A
; CURRENT FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: PCT/EP00/05006
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: DE 19925199.1
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 76
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-980-177A-76

Query Match 100.0%; Score 54; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
Db 13 VCPICSQKP 21

RESULT 4
US-09-486-394-5
; Sequence 5, Application US/09486394
; Patent No. 6478749
; GENERAL INFORMATION:
; APPLICANT: Hopfl, Reinhard
; TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method
; FILE REFERENCE: 032929-001
; CURRENT APPLICATION NUMBER: US/09/486,394
; CURRENT FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/04773
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: DE 197 37 409.3
; PRIOR FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(28)
; OTHER INFORMATION: E7 peptide.
US-09-486-394-5

Query Match 100.0%; Score 54; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
Db 20 VCPICSQKP 28

RESULT 5
US-08-934-915-54
; Sequence 54, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES

NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-54

Query Match 100.0%; Score 54; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
Db 22 VCPICSQKP 30

RESULT 6
US-08-406-248-6
Sequence 6, Application US/08406248
Patent No. 5736318
GENERAL INFORMATION:
APPLICANT: Munger, Karl
APPLICANT: Jones, D. Leanne
TITLE OF INVENTION: METHOD AND KIT FOR EVALUATING
TITLE OF INVENTION: TRANSFORMED CELLS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ann-Louise Kerner, Ph.D., Lappin & Kusmer
STREET: 200 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,248
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: McDaniels, Patricia A.
REGISTRATION NUMBER: 33,194

REFERENCE/DOCKET NUMBER: HAZ-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-330-1300
TELEFAX: 617-330-1311
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-406-248-6

Query Match 100.0%; Score 54; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
Db 90 VCPICSQKP 98

RESULT 7
US-08-075-541D-42
Sequence 42, Application US/08075541D
Patent No. 6183745
GENERAL INFORMATION:
APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERMAIN
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
CITY: PHILADELPHIA
STATE: PENNSYLVANIA
COUNTRY: USA
ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-075-541D-42

Query Match 100.0%; Score 54; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-944-368A-4

Query Match      100.0%; Score 54; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
Db 90 VCPICSQKP 98

RESULT 8
US-09-382-616A-1
; Sequence 1, Application US/09382616A
; Patent No. 6200746
; GENERAL INFORMATION:
; APPLICANT: Fisher, Christopher
; TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
; FILE REFERENCE: 28341/6216
; CURRENT APPLICATION NUMBER: US/09/382.616A
; CURRENT FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/382.616
; PRIOR FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Papillomavirus sylvilagi
US-09-382-616A-1

Query Match      100.0%; Score 54; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
Db 90 VCPICSQKP 98

RESULT 9
US-08-944-368A-4
; Sequence 4, Application US/08944368A
; Patent No. 6228368
; GENERAL INFORMATION:
; APPLICANT: Gisman, et al.
; TITLE OF INVENTION: Papilloma Virus Capsomere vaccine
; TITLE OF INVENTION: Formulations and Methods of Use
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 233 South Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944.368A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27013/34028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-944-368A-4

Query Match      100.0%; Score 54; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
Db 90 VCPICSQKP 98

RESULT 10
US-09-820-764-4
; Sequence 4, Application US/09820764
; Patent No. 6352696
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/820.764
; FILING DATE: 30-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026.896
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-820-764-4

Query Match      100.0%; Score 54; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
Db 90 VCPICSQKP 98

RESULT 11
US-09-613-303-8
; Sequence 8, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
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; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-09-613-303-8

Query Match      100.0%; Score 54; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VCPICSQKP 9
Db      90 VCPICSQKP 98

RESULT 12
US-09-566-420-19
; Sequence 19, Application US/09566420
; Patent No. 6500641
; GENERAL INFORMATION:
; APPLICANT: CHEN, SI-YI AND ZHAOYANG, YOU
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTIGENS WHICH ELICIT AN
; TITLE OF INVENTION: IMMUNE RESPONSE
; FILE REFERENCE: TEA
; CURRENT APPLICATION NUMBER: US/09/566,420
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,752
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 60/132,750
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Human papillomavirus type E7
US-09-566-420-19

Query Match      100.0%; Score 54; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VCPICSQKP 9
Db      90 VCPICSQKP 98

RESULT 13
US-09-986-118A-4
; Sequence 4, Application US/09986118A
; Patent No. 6562351
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; APPLICANT: HALLEK, Michael
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
```

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; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/986,118A
; FILING DATE: 07-No. 6562351-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,896
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-986-118A-4

Query Match      100.0%; Score 54; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VCPICSQKP 9
Db      90 VCPICSQKP 98

RESULT 14
US-09-728-466-1
; Sequence 1, Application US/09728466
; Patent No. 6641994
; GENERAL INFORMATION:
; APPLICANT: Fisher, Christopher
; APPLICANT: He, Wanxia
; TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
; FILE REFERENCE: 28341/6216
; CURRENT APPLICATION NUMBER: US/09/728,466
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/382,616
; PRIOR FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Papillomavirus sylvilagi
US-09-728-466-1

Query Match      100.0%; Score 54; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VCPICSQKP 9
Db      90 VCPICSQKP 98

RESULT 15
US-09-824-017-4
; Sequence 4, Application US/09824017
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; Patent No. 6649167
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; HALLEK, Michael
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/824,017
; FILING DATE: 03-Apr-2001
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/026,896
; FILING DATE: 1998-02-20
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-824-017-4

Query Match 100.0%; Score 54; DB 4; Length 98;
Best Local Similarity 100.0%; Pred.No. 0.11; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
Db 90 VCPICSQKP 98

Search completed: June 29, 2005, 01:44:22
Job time : 16.9126 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:27:48 ; Search time 17.15 Seconds
(without alignments)
39.174 Million cell updates/sec

Title: US-08-170-344-7
Perfect score: 49
Sequence: 1 TIRHIIIEC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pap:*
6: /cgn2_6/ptodata/1/iaa/backfiles.pap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	10	4	US-08-197-484-72
2	49	100.0	10	4	US-09-601-729-273
3	49	100.0	10	5	PCT-US95-02121-72
4	49	100.0	14	1	US-07-909-122-3
5	49	100.0	30	1	US-08-363-586-4
6	49	100.0	30	4	US-09-980-523A-4
7	49	100.0	59	3	US-09-390-027-6
8	49	100.0	158	4	US-09-980-523A-2
9	49	100.0	162	1	US-08-316-239B-3
10	49	100.0	162	1	US-08-316-239B-4
11	49	100.0	172	3	US-08-860-165-14
12	49	100.0	172	3	US-09-359-382-14
13	49	100.0	182	1	US-08-117-083-10
14	49	100.0	266	3	US-08-860-165-10
15	49	100.0	266	3	US-09-359-382-10
16	49	100.0	266	4	US-09-367-309A-1
17	49	100.0	273	3	US-09-485-885-4
18	49	100.0	292	3	US-09-485-885-10
19	49	100.0	371	3	US-09-485-885-6
20	49	100.0	390	3	US-09-485-885-14
21	44	89.8	10	3	US-08-159-339A-73
22	42	85.7	620	4	US-08-248-796A-15013
23	36	73.5	1164	3	US-09-457-708-2
24	36	73.5	1164	4	US-09-950-046A-2
25	36	73.5	1164	4	US-09-976-594-989
26	35	71.4	20	2	US-08-934-915-159
27	34	69.4	111	4	US-09-270-767-33608

28	34	69.4	111	4	US-09-270-767-48825	Sequence 48825, A
29	34	69.4	266	4	US-09-489-039A-13381	Sequence 13381, A
30	33	67.3	374	4	US-09-638-937-2	Sequence 2, Appli
31	33	67.3	536	3	US-08-426-509A-12	Sequence 12, Appl
32	33	67.3	536	4	US-08-232-545-12	Sequence 12, Appl
33	33	67.3	536	5	PCT-US95-05008-12	Sequence 12, Appl
34	32	65.3	10	3	US-08-159-339A-573	Sequence 573, App
35	32	65.3	217	4	US-09-270-767-60201	Sequence 60201, A
36	32	65.3	227	4	US-09-252-991A-29181	Sequence 29181, A
37	32	65.3	305	4	US-09-107-532A-5486	Sequence 5486, Ap
38	32	65.3	343	4	US-09-266-965-112	Sequence 112, App
39	32	65.3	343	4	US-09-248-796A-22434	Sequence 22434, A
40	32	65.3	361	4	US-09-270-767-44745	Sequence 44745, A
41	32	65.3	512	4	US-09-248-796A-15186	Sequence 15186, A
42	32	65.3	520	4	US-09-527-073-2	Sequence 2, Appli
43	32	65.3	590	1	US-08-448-196A-9	Sequence 9, Appli
44	32	65.3	780	4	US-09-785-381-11	Sequence 11, Appl
45	32	65.3	803	4	US-09-949-016-11498	Sequence 11498, A

ALIGNMENTS

RESULT 1
US-08-197-484-72
; Sequence 72, Application US/08197484
; Patent No. 6419931
; GENERAL INFORMATION:
; APPLICANT: VITIELLO, Maria A.
; APPLICANT: CHESTNUT, Robert W.
; APPLICANT: SETTE, Alessandro D.
; APPLICANT: CELIS, Esteban
; APPLICANT: GRAY, Howard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: Stewart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/197,484
; FILING DATE: 16-FEB-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (206) 623-6793
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-197-484-72

Query Match 100.0%; Score 49; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
| | | | | | | |
Db 1 TIHDIILEC 9

RESULT 2

US-09-601-729-273
; Sequence 273, Application US/09601729
; Patent No. 6683052
; GENERAL INFORMATION:
; APPLICANT: THIAM, KADER
; APPLICANT: AURIAULT, CLAUDE
; APPLICANT: GRAS-MASSE, HELENE
; APPLICANT: LOING, ESTELLE
; APPLICANT: VERWAERDE, CLAUDIE
; APPLICANT: GUILLET, JEAN GERARD
; TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES
; TITLE OF INVENTION: THEREOF IN PHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: USB-97-AU-IN
; CURRENT APPLICATION NUMBER: US/09/601,729
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: PCT/FR99/00259
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 98 01439
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 273
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-601-729-273

Query Match 100.0%; Score 49; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
| | | | | | | |
Db 1 TIHDIILEC 9

RESULT 3

PCT-US95-02121-72
; Sequence 72, Application PC/TUS9502121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
; TITLE OF INVENTION: CTL IMMUNITY
; NUMBER OF SEQUENCES: 153
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02121
; FILING DATE: 16-FEB-1995
; CLASSIFICATION:

;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/197,484
; FILING DATE: 16-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,811
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14137-26-4PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 467-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 72:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US95-02121-72

Query Match 100.0%; Score 49; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
| | | | | | | |
Db 1 TIHDIILEC 9

RESULT 4

US-07-909-122-3
; Sequence 3, Application US/07909122
; Patent No. 5415995
; GENERAL INFORMATION:
; APPLICANT: SCHOOLNIK, GARY K.
; APPLICANT: PALEFSKY, JOEL M.
; TITLE OF INVENTION: DIAGNOSTIC PEPTIDES OF HUMAN PAPILLOMA
; TITLE OF INVENTION: VIRUS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/909,122
; FILING DATE: 19920706
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: BENZ, WILLIAM H.
; REGISTRATION NUMBER: 25,952
; REFERENCE/DOCKET NUMBER: 28600-20105.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792

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; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-909-122-3

Query Match      100.0%; Score 49; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
Db 6 TIHDIILEC 14

RESULT 5
US-08-363-586-4
; Sequence 4, Application US/08363586
; Patent No. 5629161
; GENERAL INFORMATION:
; APPLICANT: Mueller, Martin
; APPLICANT: Gismann, Lutz
; TITLE OF INVENTION: Use of HPV-16 E6 and E7-Gene Derived
; TITLE OF INVENTION: Peptides for the Diagnostic Purpose
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,586
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/909,296
; FILING DATE: 09-JUL-1992
; APPLICATION NUMBER: EP 91111720.8
; FILING DATE: 13-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wadler, Linda A.
; REGISTRATION NUMBER: 33,218
; REFERENCE/DOCKET NUMBER: 02481-1195-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-363-586-4

Query Match      100.0%; Score 49; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 TIHDIILEC 9
Db 22 TIHDIILEC 30
```

```
RESULT 6
US-09-980-523A-4
; Sequence 4, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIS, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: WO/01 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-4
```

```
Query Match      100.0%; Score 49; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 TIHDIILEC 9
Db 15 TIHDIILEC 23
```

```
RESULT 7
US-09-390-027-6
; Sequence 6, Application US/09390027
; Patent No. 6235523
; GENERAL INFORMATION:
; APPLICANT: GAJEWCZYK, Diane M.
; APPLICANT: PERSSON, Roy
; APPLICANT: YAO, Fei-Long
; APPLICANT: CAO, Shi-Xian
; APPLICANT: KLEIN, Michel H.
; APPLICANT: TARTAGLIA, James
; APPLICANT: MOINGEON, Philippe
; APPLICANT: ROVINSKI, Benjamin
; TITLE OF INVENTION: TREATMENT OF CERVICAL CANCER
; FILE REFERENCE: 1038-982 MIS:jb
; CURRENT APPLICATION NUMBER: US/09/390,027
; CURRENT FILING DATE: 1999-09-03
; EARLIER APPLICATION NUMBER: 60/099,291
; EARLIER FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-390-027-6
```

```
Query Match      100.0%; Score 49; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
Db 15 TIHDIILEC 23
```

```
Db          50 TIHDIILEC 58

RESULT 8
US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO1 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match          100.0%; Score 49; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 TIHDIILEC 9
          |||||||
Db          29 TIHDIILEC 37

RESULT 9
US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match          100.0%; Score 49; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 TIHDIILEC 9
          |||||||
Db          29 TIHDIILEC 37

; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match          100.0%; Score 49; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 TIHDIILEC 9
          |||||||
Db          29 TIHDIILEC 37

RESULT 10
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match          100.0%; Score 49; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 TIHDIILEC 9
          |||||||
Db          29 TIHDIILEC 37
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RESULT 11
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PNO157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14

Query Match 100.0%; Score 49; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
|||
Db 98 TIHDIILEC 106

RESULT 12
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PNO157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match 100.0%; Score 49; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
|||
Db 98 TIHDIILEC 106

RESULT 13
US-08-117-083-10
; Sequence 10, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Boursnell, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESS: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
; OTHER INFORMATION: /note= "Xaa refers to stop codon in
; OTHER INFORMATION: the open reading frame."
US-08-117-083-10

Query Match 100.0%; Score 49; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.083;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TIHDIILEC 9
|||
Db 30 TIHDIILEC 38

RESULT 14
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868

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; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10
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```
Query Match      100.0%; Score 49; DB 3; Length 266;
Best Local Similarity 100.0%; Pred.No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 TTHDIIIEC 9
    |||||
Db 29 TTHDIIIEC 37
```

```
RESULT 15
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10
```

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Query Match      100.0%; Score 49; DB 3; Length 266;
Best Local Similarity 100.0%; Pred.No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 TTHDIIIEC 9
    |||||
Db 29 TTHDIIIEC 37
```

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Search completed: June 28, 2005, 19:29:11
Job time : 18.15 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:28:22 ; Search time 54.2473 Seconds
(without alignments)
84.958 Million cell updates/sec

Title: US-08-170-344-69
Perfect score: 49
Sequence: 1 KCLKFYSKI 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	81	2 Q80886	Q80886 human papil
2	49	100.0	84	2 Q80882	Q80882 human papil
3	49	100.0	90	2 Q80884	Q80884 human papil
4	49	100.0	90	2 Q80885	Q80885 human papil
5	49	100.0	91	2 Q80887	Q80887 human papil
6	49	100.0	99	2 Q81982	Q81982 human papil
7	49	100.0	103	2 Q81986	Q81986 human papil
8	49	100.0	130	2 Q81984	Q81984 human papil
9	49	100.0	130	2 Q81988	Q81988 human papil
10	49	100.0	130	2 Q819C0	Q819C0 human papil
11	49	100.0	130	2 Q819C2	Q819C2 human papil
12	49	100.0	130	2 Q819C8	Q819C8 human papil
13	49	100.0	130	2 Q819D0	Q819D0 human papil
14	49	100.0	138	2 Q819D2	Q819D2 human papil
15	49	100.0	143	2 Q819B6	Q819B6 human papil
16	49	100.0	143	2 Q819C4	Q819C4 human papil
17	49	100.0	149	1 V86_HPV35	P27228 human papil
18	49	100.0	149	2 Q84298	Q84298 human papil
19	49	100.0	151	2 Q12335	Q12335 human papil
20	49	100.0	151	2 Q12336	Q12336 human papil
21	49	100.0	151	2 Q76TS0	Q76TS0 human papil
22	49	100.0	151	2 Q77816	Q77816 human papil
23	49	100.0	151	2 Q77E16	Q77E16 human papil
24	49	100.0	151	2 Q77JC7	Q77JC7 human papil
25	49	100.0	151	2 Q77ZJ5	Q77ZJ5 human papil
26	49	100.0	151	2 Q80963	Q80963 human papil
27	49	100.0	151	2 Q80966	Q80966 human papil
28	49	100.0	151	2 Q89640	Q89640 human papil
29	49	100.0	151	2 Q89648	Q89648 human papil
30	49	100.0	151	2 Q89708	Q89708 human papil
31	49	100.0	151	2 Q89755	Q89755 human papil

RESULT 1
Q80886 PRELIMINARY; PRT; 81 AA.
AC Q80886;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-OCT-2003 (TrEMBLrel. 01, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G.; Galutira D.F.; Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14515; AAB60569.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR InterPro; IPR001334; B6.
DR Pfam; PF00518; B6; 1.
FT NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA; 9784 MW; D5FEDBC9F845B97 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYSKI 9
|||
Db 24 KCLKFYSKI 32

RESULT 2
Q80882 PRELIMINARY; PRT; 84 AA.
AC Q80882;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=HPV16; TISSUE=Cervical;
RA Haegert D.G.; Galutira D.F.; Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14511; AAB60565.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.

Q89852 human papil
Q89887 human papil
Q85564 human papil
Q8bb19 human papil
Q8bb20 human papil
Q8bb21 human papil
Q8w8c3 human papil
Q8w931 human papil
Q8wmp2 human papil
Q8wmp3 human papil
Q8wmp4 human papil
Q8wmp5 human papil
P03126 human papil
Q8jmu8 human papil

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DR GO: 0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 84
SQ SEQUENCE 84 AA; 10177 MW; 5AB6B896468E1CAA CRC64;

Query Match 100.0%; Score 49; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYSKI 9
Db 21 KCLKFYSKI 29

RESULT 3
ID Q80884 PRELIMINARY; PRT; 90 AA.
AC Q80884;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14513; AAB60567.2; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 11021 MW; 47F42BBEFAFACCC01 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYSKI 9
Db 24 KCLKFYSKI 32

RESULT 4
ID Q80885 PRELIMINARY; PRT; 90 AA.
AC Q80885;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14514; AAB60568.2; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 99

RESULT 5
ID Q80887 PRELIMINARY; PRT; 91 AA.
AC Q80887;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14516; AAB60570.1; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 91
SQ SEQUENCE 91 AA; 11136 MW; 22FDF3EA185ACBA7 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYSKI 9
Db 24 KCLKFYSKI 32

RESULT 6
ID Q919B2 PRELIMINARY; PRT; 99 AA.
AC Q919B2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040704; AAL01365.1; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 99

```

SQ SEQUENCE 99 AA; 12005 MW; C2B96025EC370B38 CRC64;
 Query Match 100.0%; Score 49; DB 2; Length 99;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCLKFYYSKI 9
 |||||
 DB 41 KCLKFYYSKI 49

RESULT 7
 Q919D6 PRELIMINARY; PRT; 103 AA.
 ID Q919D6
 AC Q919D6
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404692; AAL01342.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 103 AA; 12422 MW; 6F90CB4F1F25449B CRC64;

Query Match 100.0%; Score 49; DB 2; Length 103;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCLKFYYSKI 9
 |||||
 DB 17 KCLKFYYSKI 25

RESULT 8
 Q919B4 PRELIMINARY; PRT; 130 AA.
 ID Q919B4
 AC Q919B4
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404703; AAL01363.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227BEDDC CRC64;

Query Match 100.0%; Score 49; DB 2; Length 130;

Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KCLKFYYSKI 9
 |||||
 DB 44 KCLKFYYSKI 52

RESULT 9
 Q919B8 PRELIMINARY; PRT; 130 AA.
 ID Q919B8
 AC Q919B8
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404701; AAL01359.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 130 AA; 15775 MW; 92D3C07BF96B092F CRC64;

Query Match 100.0%; Score 49; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCLKFYYSKI 9
 |||||
 DB 44 KCLKFYYSKI 52

RESULT 10
 Q919C0 PRELIMINARY; PRT; 130 AA.
 ID Q919C0
 AC Q919C0
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404700; AAL01357.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYSKI 9
|||||
Db 44 KCLKFYSKI 52

RESULT 11

Q919C2 ID Q919C2 PRELIMINARY; PRT; 130 AA.
AC Q919C2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404699; AAL01355.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYSKI 9
|||||
Db 44 KCLKFYSKI 52

RESULT 12

Q919C8 ID Q919C8 PRELIMINARY; PRT; 130 AA.
AC Q919C8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404696; AAL01349.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYSKI 9
|||||
Db 44 KCLKFYSKI 52

RESULT 13

Q919D0 ID Q919D0 PRELIMINARY; PRT; 130 AA.
AC Q919D0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404695; AAL01347.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15735 MW; 9FB30EEDCA21AF3 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYSKI 9
|||||
Db 44 KCLKFYSKI 52

RESULT 14

Q919D2 ID Q919D2 PRELIMINARY; PRT; 138 AA.
AC Q919D2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404694; AAL01345.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 138 AA; 16696 MW; 481E5AEA90895FC2 CRC64;

Query Match 100.0%; Score 49; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYSKI 9
|||||
Db 52 KCLKFYSKI 60

RESULT 15

Q919B6
 ID Q919B6 PRELIMINARY; PRT; 143 AA.
 AC Q919B6;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404702; AAL01361.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;
 Query Match 100.0%; Score 49; DB 2; Length 143;
 Best Local Similarity 100.0%; Pred. No. 0.22;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KCLKFYSKI 9
 Db 57 KCLKFYSKI 65

Search completed: June 29, 2005, 01:34:48
 Job time : 54.2473 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:32:21 ; Search time 11.2747 Seconds
(without alignments)
76.805 Million cell updates/sec

Title: US-08-170-344-69

Perfect score: 49

Sequence: 1 KCLKFYSKI 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	100.0	149	1 W6WLJ35	E6 protein - human
2	49	100.0	158	1 W6WLH35	protein E6 - human
3	45	91.8	149	1 W6WLJ31	E6 protein - human
4	41	83.7	191	1 W6WLK1	E6 protein - rhesu
5	40	81.6	154	2 S36584	E6 protein - human
6	39	79.6	142	2 S36509	E6 protein - human
7	39	79.6	158	1 W6WLJ39	E6 protein - human
8	39	79.6	158	1 W6WLPR	E6 protein - human
9	38	77.6	151	1 W6WLJ51	E6 protein - human
10	38	77.6	158	1 W6WLJ18	E6 protein - human
11	38	77.6	158	2 S36561	E6 protein - human
12	38	77.6	443	2 T39200	hypothetical prote
13	38	77.6	918	2 S45872	hypothetical prote
14	37	75.5	202	2 F81293	probable ATP/GTP-b
15	37	75.5	211	2 S55129	transcription fact
16	36	73.5	120	2 JE0177	lymphocyte and mon
17	36	73.5	138	2 T14244	NADH2 dehydrogenas
18	36	73.5	148	2 S36515	E6 protein - human
19	36	73.5	153	2 S36503	E6 protein - human
20	36	73.5	154	2 S36527	E6 protein - human
21	36	73.5	155	1 W6WLJ56	E6 protein - human
22	36	73.5	155	2 A44890	E6 protein - human
23	36	73.5	391	2 S61704	probable transcrip
24	36	73.5	558	2 S63148	probable membrane
25	36	73.5	670	2 G90091	hypothetical prote
26	35	71.4	150	2 S36544	E6 protein - human
27	35	71.4	182	2 S36588	hypothetical prote
28	35	71.4	354	2 T32319	hypothetical prote
29	35	71.4	439	2 A35744	clusterin precurs

ALIGNMENTS

RESULT 1

W6WLJ35

E6 protein - human papillomavirus type 35

A;Species: human papillomavirus type 35

A;Note: host Homo sapiens (man)

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C;Accession: E40824; S36521

R;Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.

Virology 186, 770-776, 1992

A;Title: The phylogenetic relationship and complete nucleotide sequence of human papill

A;Reference number: A40824; MUID:92124753; PMID:1310198

A;Accession: E40824

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-149 <MAR>

A;Cross-references: UNIPROT:P27228; GB:M74117; NID:g333050; PIDN:AAA46966.1; PID:g33305

R;Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A;Description: Primer-directed sequencing of human papillomavirus types.

A;Reference number: S36469

A;Accession: S36521

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-149

A;Cross-references: EMBL:X74477; NID:g396997; PIDN:CAA52561.1; PID:g396998

A;Experimental source: strain 35H

C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; zinc finger

F;30-66/Region: zinc finger CCCC motif

F;103-139/Region: zinc finger CCCC motif

Query Match 100.0%; Score 49; DB 1; Length 149;

Best Local Similarity 100.0%; Pred. No. 0.041;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYSKI 9

Db 65 KCLKFYSKI 73

RESULT 2

W6WLH35

protein E6 - human papillomavirus type 16

C;Species: human papillomavirus type 16

C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C;Accession: A03682; T10427

R;Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virology 145, 181-195, 1985

A;Title: Human papillomavirus type 16 DNA sequence.

A;Reference number: A22355; MUID:85246220; PMID:2990099

A;Accession: A03682

A;Molecule type: DNA

A;Residues: 1-158 <SBE>
A;Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
R;Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A;Title: A negative element in the human papillomavirus type 16 genome acts at the level of transcriptional activation
A;Reference number: 217014; MUID:91162763; PMID:1848319
A;Accession: F10427
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-158 <KEN>
A;Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
C;Genetics:
A;Gene: E6
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;37-73/Region: zinc finger CCCC motif
F;110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 49; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCLKFYSKI 9
|||||
Db 72 KCLKFYSKI 80

RESULT 3
W6WL31
E6 protein - human papillomavirus type 31
C;Species: human papillomavirus type 31
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: A32444
R;Goldsbrough, M.D.; Disilvestre, D.; Temple, G.F.; Lorincz, A.T.
Virology 171, 306-311, 1989
A;Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associated DNA
A;Reference number: A94398; MUID:89299478; PMID:2545036
A;Accession: A32444
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-149 <GOL>
A;Cross-references: UNIPROT:P17386; GB:J04353; NID:G333048; PIDN:AAA46950.1; PID:G459916
C;Comment: This protein may be involved in the oncogenic potential of this virus.
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif

Query Match 91.8%; Score 45; DB 1; Length 149;
Best Local Similarity 77.8%; Pred. No. 0.24;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCLKFYSKI 9
|||||
Db 65 KCLKFYSKV 73

RESULT 4
W6WL31
E6 protein - rhesus papillomavirus (type 1)
C;Species: rhesus papillomavirus
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: A38503
R;Ostrow, R.S.; LaBresh, K.V.; Faras, A.J.
Virology 181, 424-429, 1991
A;Title: Characterization of the complete RhpV 1 genomic sequence and an integration locus
A;Reference number: A38503; MUID:91135018; PMID:1847267
A;Accession: A38503
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-191 <OST>
A;Cross-references: UNIPROT:P22159; EMBL:M37717

C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;60-96/Region: zinc finger CCCC motif
F;133-169/Region: zinc finger CCCC motif

Query Match 83.7%; Score 41; DB 1; Length 191;
Best Local Similarity 87.5%; Pred. No. 1.7;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 CLKFYSKI 9
|||||
Db 96 CLKFYSKI 103

RESULT 5
S36584
E6 protein - human papillomavirus type 7
C;Species: human papillomavirus type 7
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36584
R;Deilius, H.; Hofmann, B.
Submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36584
A;Molecule type: DNA
A;Residues: 1-154
A;Cross-references: UNIPROT:P36800; EMBL:X74463; NID:G397060; PIDN:CAA52476.1; PID:G397
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 81.6%; Score 40; DB 2; Length 154;
Best Local Similarity 66.7%; Pred. No. 2.2;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCLKFYSKI 9
|||||
Db 65 KCLKFYGV 73

RESULT 6
S36509
E6 protein - human papillomavirus type 32
C;Species: human papillomavirus type 32
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36509
R;Deilius, H.; Hofmann, B.
Submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36509
A;Molecule type: DNA
A;Residues: 1-142
A;Cross-references: UNIPROT:P36810; EMBL:X74475; NID:G396981; PIDN:CAA52549.1; PID:G396
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 79.6%; Score 39; DB 2; Length 142;
Best Local Similarity 75.0%; Pred. No. 3.2;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 CLKFYSKI 9
|||||
Db 67 CLKFYGV 74

RESULT 7
W6WL39
E6 protein - human papillomavirus type 39
C;Species: human papillomavirus type 39
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: A38502

R;Volpers, C.; Streeck, R.E.

Virology 181, 419-423, 1991

A;Title: Genome organization and nucleotide sequence of human papillomavirus type 39.

A;Reference number: A38502; MUID:91135017; PMID:1847266

A;Accession: A38502

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-158 <VOL>

A;Cross-references: UNIPROT:P24835; GB:M62849; EMBL:M38185; NID:G333245; PIDN:AAA47050.1

C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; transforming protein; zinc finger

F;32-68/Region: zinc finger CCCC motif

F;103-141/Region: zinc finger CCCC motif

Query Match 79.6%; Score 39; DB 1; Length 158;

Best Local Similarity 75.0%; Pred. No. 3.5;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CLKFYSKI 9

Db 68 CIKFYAKI 75

RESULT 8

W6WLPX

E6 protein - human papillomavirus type ME180 (provirus)

C;Species: human papillomavirus type ME180

A;Note: host Homo sapiens (man)

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C;Accession: C40509

J;Reuter, S.; Delius, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.

J. Virol. 65, 5564-5568, 1991

A;Title: Characterization of a novel human papillomavirus DNA in the cervical carcinoma

A;Reference number: A40509; MUID:91374616; PMID:1716694

A;Accession: C40509

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-158 <REU>

A;Cross-references: UNIPROT:P27962; GB:M73258

C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; zinc finger

F;32-68/Region: zinc finger CCCC motif

F;103-141/Region: zinc finger CCCC motif

Query Match 79.6%; Score 39; DB 1; Length 158;

Best Local Similarity 75.0%; Pred. No. 3.5;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CLKFYSKI 9

Db 68 CIKFYAKI 75

RESULT 9

W6WLS1

E6 protein - human papillomavirus type 51

C;Species: human papillomavirus type 51

A;Note: host Homo sapiens (man)

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C;Accession: E40415

R;Lungu, O.; Crum, C.P.; Silverstein, S.J.

J. Virol. 65, 4216-4225, 1991

A;Title: Biologic properties and nucleotide sequence analysis of human papillomavirus ty

A;Reference number: A40415; MUID:91303675; PMID:1649326

A;Accession: E40415

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-151 <LUN>

A;Cross-references: UNIPROT:P26554; GB:M62877

C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; zinc finger

F;30-66/Region: zinc finger CCCC motif

F;103-139/Region: zinc finger CCCC motif

Query Match

Best Local Similarity 77.6%; Score 38; DB 1; Length 151;

Matches 7; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 KCLKFYSKI 9

Db 65 QCLLFYSKI 73

RESULT 10

W6WLI8

E6 protein - human papillomavirus type 18

C;Species: human papillomavirus type 18

C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004

C;Accession: A26165; G26251

R;Seedorf, K.; Oltersdorf, T.; Kraemmer, G.; Roewekamp, W.

EMBO J. 6, 139-144, 1987

A;Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 1

A;Reference number: A91068; MUID:87218459; PMID:3034571

A;Accession: A26165

A;Molecule type: DNA

A;Residues: 1-158 <SEE>

A;Cross-references: UNIPROT:P06463; GB:X04773; NID:G60876; PIDN:CAA28466.1; PID:G60877

R;Cole, S.T.; Danos, O.

J. Mol. Biol. 193, 599-608, 1987

A;Title: Nucleotide sequence and comparative analysis of the human papillomavirus type

A;Reference number: A92937; MUID:87283882; PMID:3039146

A;Accession: G26251

A;Molecule type: DNA

A;Residues: 1-158 <COL>

A;Cross-references: GB:X05015; NID:G60975; PIDN:CAA28664.1; PID:G60976

R;Matlashewski, G.; Banks, L.; Wu-Liao, J.; Spence, P.; Pim, D.; Crawford, L.

J. Gen. Virol. 67, 1909-1916, 1986

A;Title: The expression of human papillomavirus type 18 E6 protein in bacteria and the

A;Reference number: A92791; MUID:86306665; PMID:3018129

A;Contents: annotation; identification of the protein

C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; transforming protein; zinc finger

F;32-68/Region: zinc finger CCCC motif

F;105-141/Region: zinc finger CCCC motif

Query Match 77.6%; Score 38; DB 1; Length 158;

Best Local Similarity 66.7%; Pred. No. 5.4;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCLKFYSKI 9

Db 67 KCIDFYSKI 75

RESULT 11

S36561

E6 protein - human papillomavirus type 45

C;Species: human papillomavirus type 45

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C;Accession: S36561

R;Deilius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A;Description: Primer-directed sequencing of human papillomavirus types.

A;Reference number: S36469

A;Accession: S36561

A;Molecule type: DNA

A;Residues: 1-158

A;Cross-references: UNIPROT:P21735; EMBL:X74479; NID:G397022; PIDN:CAAS2573.1; PID:G397

C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 77.6%; Score 38; DB 2; Length 158;

Best Local Similarity 66.7%; Pred. No. 5.4;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCLKFYSKI 9

Db 67 KCIDFYSGRI 75
||: |||:|

RESULT 12

T39200
hypothetical protein SPAC926.02 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T39200
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Ramsperger, U.; Pohl, T.
submitted to the EMBL Data Library, September 1999
A:Reference number: Z21835
A:Accession: T39200
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-443 <WOO>
A:Cross-references: UNIPROT:O9JUG6; EMBL:AL110469; PIDN:CAB54150.1; GSPDB:GN00066; SPDB:
A:Experimental source: strain 972h-; cosmid c926
C:Genetics:
A:Gene: SPDB:SPAC926.02
A:Map position: 1
A:Introns: 48/3
C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC926.02

Query Match 77.6%; Score 38; DB 2; Length 443;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCLKFYSK 8
|||: ||| |
Db 48 KCLRFYQK 55

RESULT 13

S45872
hypothetical protein YBR017c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein YBR0224
C:Species: Saccharomyces cerevisiae
C:Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C:Accession: S45872; S50812; S50321
R:Entian, K.D.; Koetter, P.; Rose, M.; Li, Z.; Thermann, R.; Brendel, M.; Baur, A.; Bole
submitted to the Protein Sequence Database, August 1994
A:Reference number: S45862
A:Accession: S45872
A:Molecule type: DNA
A:Residues: 1-918 <ENT>
A:Cross-references: UNIPROT:P38217; EMBL:Z35886; NID:G536217; PIDN:CAA84959.1; PID:G5362
A:Experimental source: strain S288C
R:Schaaff-Gerstenschlaeger, I.; Schindwolf, T.; Lehnert, W.; Rose, M.; Zimmermann, F.K.
Yeast 11, 79-83, 1995
A:Title: Sequence and functional analysis of a 7.2 kb fragment of Saccharomyces cerevis
A:Reference number: S50812; MUID:95282516; PMID:7762304
A:Accession: S50812
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-918 <SCW>
A:Cross-references: EMBL:X81324; NID:G587572; PIDN:CAA57104.1; PID:G587573
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:KAP104
A:Cross-references: SGD:S0000221; MIPS:YBR017c
A:Map position: 2R

Query Match 77.6%; Score 38; DB 2; Length 918;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCLKFYSK 8
|||: ||| |
Db 553 KCLKYKK 560

RESULT 14

F81293
probable ATP/GTP-binding protein Cj1473c [imported] - Campylobacter jejuni (strain NCTC
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: F81293
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilli
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hy
A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: F81293
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-202 <PAR>
A:Cross-references: UNIPROT:Q9PMI9; GB:AL111168; NID:G6968723; PIDN:CAB73
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: Cj1473c

Query Match 75.5%; Score 37; DB 2; Length 202;
Best Local Similarity 77.8%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KCLKFYSKI 9
|||: ||| |
Db 151 KCLKFLQKI 159

RESULT 15

S55129
transcription factor RGM1 - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YMR010.12c; protein YMR182c
C:Species: Saccharomyces cerevisiae
C:Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S55129; S17249
R:Churcher, C.M.
submitted to the EMBL Data Library, June 1995
A:Reference number: S55118
A:Accession: S55129
A:Molecule type: DNA
A:Residues: 1-211 <CHU>
A:Cross-references: UNIPROT:Q00453; EMBL:Z49808; NID:G854440; PID:G854452; MIPS:YMR182c
A:Experimental source: strain AB972
R:Estreich, F.
Nucleic Acids Res. 19, 4873-4877, 1991
A:Title: The yeast putative transcriptional repressor RGM1 is a proline-rich zinc finger
A:Reference number: S17249; MUID:92020118; PMID:1923755
A:Accession: S17249
A:Molecule type: DNA
A:Residues: 1-113, 'V', 115-211 <EST>
A:Cross-references: EMBL:X59861; NID:G4317; PIDN:CAA42521.1; PID:G4318
C:Genetics:
A:Gene: SGD:RGM1
A:Cross-references: SGD:S0004794; MIPS:YMR182c
A:Map position: 13R
C:Keywords: DNA binding; transcription factor; zinc finger

Query Match 75.5%; Score 37; DB 2; Length 211;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CLKFYSKI 9
|||: ||| |
Db 55 CLKFFSRI 62

Search completed: June 29, 2005, 01:38:45
Job time : 12.2747 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 05:18:25 ; Search time 53.8517 Seconds
(without alignments)
64.268 Million cell updates/sec

Title: US-08-170-344-69
Perfect score: 49
Sequence: 1 KCLKFYSKI 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	49	100.0	20	16	US-10-476-570-11
2	49	100.0	22	14	Sequence 11, Appli
3	49	100.0	151	14	Sequence 4, Appli
4	49	100.0	151	17	Sequence 6, Appli
5	49	100.0	151	17	Sequence 20, Appli
6	49	100.0	158	17	Sequence 27, Appli
7	49	100.0	158	17	Sequence 2, Appli
8	49	100.0	171	16	Sequence 16, Appli
9	49	100.0	266	9	Sequence 2, Appli
10	49	100.0	273	13	Sequence 1, Appli
11	49	100.0	273	17	Sequence 4, Appli

12	49	100.0	292	13	US-10-000-903-10	Sequence 10, Appli
13	49	100.0	292	17	US-10-899-771-10	Sequence 10, Appli
14	49	100.0	371	13	US-10-000-903-6	Sequence 6, Appli
15	49	100.0	371	17	US-10-899-771-6	Sequence 6, Appli
16	49	100.0	390	13	US-10-000-903-14	Sequence 14, Appli
17	49	100.0	390	17	US-10-899-771-14	Sequence 14, Appli
18	38	77.6	158	16	US-10-800-023-27	Sequence 27, Appli
19	38	77.6	172	16	US-10-472-724-6	Sequence 6, Appli
20	38	77.6	278	13	US-10-000-903-21	Sequence 21, Appli
21	38	77.6	278	17	US-10-899-771-21	Sequence 21, Appli
22	38	77.6	383	13	US-10-000-903-23	Sequence 23, Appli
23	38	77.6	383	17	US-10-899-771-23	Sequence 23, Appli
24	36	73.5	65	16	US-10-437-963-198440	Sequence 198440,
25	36	73.5	82	16	US-10-803-960-9	Sequence 9, Appli
26	36	73.5	96	16	US-10-398-457-36	Sequence 36, Appli
27	36	73.5	97	15	US-10-332-038A-14	Sequence 14, Appli
28	36	73.5	97	16	US-10-779-267-3	Sequence 3, Appli
29	36	73.5	97	17	US-10-839-017-6	Sequence 6, Appli
30	36	73.5	97	17	US-10-332-039A-14	Sequence 14, Appli
31	36	73.5	120	14	US-10-293-705-2	Sequence 2, Appli
32	36	73.5	120	15	US-10-412-548-24	Sequence 24, Appli
33	36	73.5	120	16	US-10-779-267-2	Sequence 2, Appli
34	36	73.5	863	16	US-10-437-963-192423	Sequence 192423,
35	35	71.4	15	9	US-09-459-749D-11	Sequence 11, Appli
36	35	71.4	15	14	US-10-270-871-11	Sequence 11, Appli
37	35	71.4	16	14	US-10-120-508-7	Sequence 7, Appli
38	35	71.4	19	14	US-10-120-508-8	Sequence 8, Appli
39	35	71.4	75	16	US-10-425-115-266253	Sequence 266253,
40	35	71.4	111	15	US-10-424-599-251917	Sequence 251917,
41	35	71.4	225	15	US-10-264-049-3927	Sequence 3927, Ap
42	35	71.4	349	17	US-10-491-213-45	Sequence 45, Appli
43	35	71.4	363	10	US-09-832-129-34	Sequence 34, Appli
44	35	71.4	363	11	US-09-833-245-2248	Sequence 2248, Ap
45	35	71.4	363	16	US-10-733-368-34	Sequence 34, Appli

ALIGNMENTS

RESULT 1
US-10-476-570-11
; Sequence 11, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 20
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 61-80
US-10-476-570-11

Query Match 100.0%; Score 49; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYSKI 9
 Db 12 KCLKFYSKI 20

RESULT 2

US-10-612-818-4
 ; Sequence 4, Application US/10612818
 ; Publication No. US20040110925A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Impact Diagnostics
 ; APPLICANT: Impact Diagnostics
 ; TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomavirus
 ; TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Papillomavirus
 ; TITLE OF INVENTION: Associated Cancers
 ; FILE REFERENCE: 3352-2-2
 ; CURRENT APPLICATION NUMBER: US/10/612,818
 ; CURRENT FILING DATE: 2003-07-01
 ; PRIOR APPLICATION NUMBER: US 60/394,172
 ; PRIOR FILING DATE: 2002-07-02
 ; PRIOR APPLICATION NUMBER: US 09/828,645
 ; PRIOR FILING DATE: 2001-04-05
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 22
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Derived from the E6 early coding region of HPV 16
 US-10-612-818-4

Query Match 100.0%; Score 49; DB 16; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.064;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYSKI 9
 Db 11 KCLKFYSKI 19

RESULT 3

US-10-177-390-6
 ; Sequence 6, Application US/10177390
 ; Publication No. US20030143743A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schuler, Gerold
 ; APPLICANT: N.V. Antwerps Innovatiecentrum
 ; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
 ; TITLE OF INVENTION: Polynucleotides by Electroporation
 ; FILE REFERENCE: 021505wo/JH/ml
 ; CURRENT APPLICATION NUMBER: US/10/177,390
 ; CURRENT FILING DATE: 2002-06-20
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 151
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus type 16
 US-10-177-390-6

Query Match 100.0%; Score 49; DB 14; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYSKI 9
 Db 65 KCLKFYSKI 73

RESULT 4

US-10-484-063-20
 ; Sequence 20, Application US/10484063

; Publication No. US20050048467A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SASTRY, K. JAGANNADHA
 ; APPLICANT: TORTOLERO-LUNA, GUILLERMO
 ; APPLICANT: FOLLEN, MICHELE
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
 ; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
 ; FILE REFERENCE: UTSC:560US
 ; CURRENT APPLICATION NUMBER: US/10/484,063
 ; CURRENT FILING DATE: 2004-01-16
 ; PRIOR APPLICATION NUMBER: PCT/US02/23198
 ; PRIOR FILING DATE: 2002-07-19
 ; PRIOR APPLICATION NUMBER: 60/306,809
 ; PRIOR FILING DATE: 2001-07-20
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 20
 ; LENGTH: 151
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus
 US-10-484-063-20

Query Match 100.0%; Score 49; DB 17; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYSKI 9
 Db 65 KCLKFYSKI 73

RESULT 5

US-10-484-063-27
 ; Sequence 27, Application US/10484063
 ; Publication No. US20050048467A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SASTRY, K. JAGANNADHA
 ; APPLICANT: TORTOLERO-LUNA, GUILLERMO
 ; APPLICANT: FOLLEN, MICHELE
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
 ; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
 ; FILE REFERENCE: UTSC:560US
 ; CURRENT APPLICATION NUMBER: US/10/484,063
 ; CURRENT FILING DATE: 2004-01-16
 ; PRIOR APPLICATION NUMBER: PCT/US02/23198
 ; PRIOR FILING DATE: 2002-07-19
 ; PRIOR APPLICATION NUMBER: 60/306,809
 ; PRIOR FILING DATE: 2001-07-20
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 27
 ; LENGTH: 151
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus type 16
 US-10-484-063-27

Query Match 100.0%; Score 49; DB 17; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYSKI 9
 Db 65 KCLKFYSKI 73

RESULT 6

US-10-858-384-2
 ; Sequence 2, Application US/10858384
 ; Publication No. US2005003025A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHOPPIN, JEANNINE
 ; APPLICANT: BOURGAULT VILLADA, ISABELLE
 ; APPLICANT: GUILLET, JEAN-GERARD

```

; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match      100.0%; Score 49; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KCLKFYSKI 9
Db      72 KCLKFYSKI 80

RESULT 7
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match      100.0%; Score 49; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KCLKFYSKI 9
Db      72 KCLKFYSKI 80

RESULT 8
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7

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; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

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Query Match      100.0%; Score 49; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 KCLKFYSKI 9
Db      77 KCLKFYSKI 85

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RESULT 9
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

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Query Match      100.0%; Score 49; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 KCLKFYSKI 9
Db      72 KCLKFYSKI 80

```

```

RESULT 10
US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4

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; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4

Query Match      100.0%; Score 49; DB 13; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYSKI 9
   |||||
Db 178 KCLKFYSKI 186

RESULT 11
US-10-899-771-4
; Sequence 4, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: Influenzae B and B6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-4

Query Match      100.0%; Score 49; DB 17; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYSKI 9
   |||||
Db 178 KCLKFYSKI 186

RESULT 12
US-10-000-903-10
; Sequence 10, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-10

Query Match      100.0%; Score 49; DB 13; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.74;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYSKI 9
   |||||
Db 197 KCLKFYSKI 205

RESULT 13
US-10-899-771-10
; Sequence 10, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (Clyta from Streptococcus
; OTHER INFORMATION: pneumoniae and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-10

Query Match      100.0%; Score 49; DB 17; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.74;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYSKI 9
   |||||
Db 197 KCLKFYSKI 205

RESULT 14
US-10-000-903-6
; Sequence 6, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
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; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-6

Query Match      100.0%; Score 49; DB 13; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.92;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KCLKFYSKI 9
Db      178 KCLKFYSKI 186

RESULT 15
US-10-899-771-6
; Sequence 6, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein (protein D from Haemophilus
; OTHER INFORMATION: Influenzae B and B6E7 fusion from Human papilloma
; OTHER INFORMATION: virus type 16)
US-10-899-771-6

Query Match      100.0%; Score 49; DB 17; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.92;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KCLKFYSKI 9
Db      178 KCLKFYSKI 186

Search completed: June 29, 2005, 05:48:14
Job time : 54.8517 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:37:59 ; Search time 16.8626 Seconds
(without alignments)
39.842 Million cell updates/sec

Title: US-08-170-344-69
Perfect score: 49
Sequence: 1 KCLKFYSKI 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	20	2	US-08-934-915-162
2	49	100.0	158	4	US-08-980-523A-2
3	49	100.0	162	1	US-08-316-239B-3
4	49	100.0	162	1	US-08-316-239B-4
5	49	100.0	172	3	US-08-860-165-12
6	49	100.0	172	3	US-08-860-165-14
7	49	100.0	172	3	US-08-359-382-12
8	49	100.0	172	3	US-08-359-382-14
9	49	100.0	266	3	US-08-860-165-10
10	49	100.0	266	3	US-08-359-382-10
11	49	100.0	266	4	US-09-367-309A-1
12	49	100.0	273	3	US-09-485-885-4
13	49	100.0	292	3	US-09-485-885-10
14	49	100.0	371	3	US-09-485-885-6
15	49	100.0	390	3	US-09-485-885-14
16	40	81.6	9	3	US-08-159-339A-137
17	38	77.6	32	1	US-08-466-285-4
18	38	77.6	32	3	US-08-164-768-4
19	38	77.6	158	2	US-08-247-904B-10
20	38	77.6	158	3	US-08-767-942A-19
21	38	77.6	271	1	US-08-117-083-14
22	38	77.6	278	3	US-09-485-885-21
23	38	77.6	383	3	US-09-485-885-23
24	37	75.5	505	4	US-09-270-767-43800
25	36	73.5	9	3	US-08-159-339A-74
26	36	73.5	10	3	US-08-159-339A-561
27	36	73.5	82	4	US-09-567-225-9

28	36	73.5	120	1	US-08-347-492B-2	Sequence 2, Appli
29	36	73.5	120	2	US-08-798-143-2	Sequence 2, Appli
30	36	73.5	120	5	PCT-US95-15484-2	Sequence 2, Appli
31	36	73.5	136	5	PCT-US95-07171-2	Sequence 2, Appli
32	36	73.5	191	5	PCT-US95-07171-3	Sequence 3, Appli
33	35	71.4	15	4	US-09-459-749D-11	Sequence 11, Appli
34	35	71.4	63	4	US-09-248-796A-22995	Sequence 22995, A
35	35	71.4	200	4	US-09-248-796A-15345	Sequence 15345, A
36	35	71.4	464	4	US-09-949-016-11532	Sequence 11532, A
37	34	69.4	85	4	US-09-270-767-32609	Sequence 32609, A
38	34	69.4	85	4	US-09-270-767-47826	Sequence 47826, A
39	34	69.4	264	2	US-08-460-309-10	Sequence 10, Appli
40	34	69.4	264	2	US-08-125-077-10	Sequence 10, Appli
41	34	69.4	350	4	US-08-637-670-25	Sequence 25, Appli
42	34	69.4	972	3	US-08-335-844A-23	Sequence 23, Appli
43	34	69.4	972	4	US-09-129-366-23	Sequence 23, Appli
44	34	69.4	2123	4	US-09-949-016-7517	Sequence 7517, Ap
45	34	69.4	3070	4	US-09-961-403-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-934-915-162
; Sequence 162, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 162:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-934-915-162
Query Match 100.0%; Score 49; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.029;

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYSKI 9
    |||||
Db 11 KCLKFYSKI 19

RESULT 2
US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCES
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO/91 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 49; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYSKI 9
    |||||
Db 72 KCLKFYSKI 80

RESULT 3
US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 100.0%; Score 49; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 100.0%; Score 49; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYSKI 9
    |||||
Db 72 KCLKFYSKI 80

RESULT 4
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 100.0%; Score 49; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 KCLKFYSKI 9
      |||||
Db      72 KCLKFYSKI 80

RESULT 5
US-08-860-165-12
; Sequence 12, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12

Query Match      100.0%; Score 49; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.2; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KCLKFYSKI 9
      |||||
Db      10 KCLKFYSKI 18

RESULT 6
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14

Query Match      100.0%; Score 49; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.2; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KCLKFYSKI 9
      |||||
Db      10 KCLKFYSKI 18

RESULT 7
US-09-359-382-12
; Sequence 12, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-12

Query Match      100.0%; Score 49; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.2; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KCLKFYSKI 9
      |||||
Db      10 KCLKFYSKI 18

RESULT 8
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match      100.0%; Score 49; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.2; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KCLKFYSKI 9
      |||||
Db      10 KCLKFYSKI 18
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Db 141 KCLKFYYSKI 149
|||||||

RESULT 9
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860.165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1993-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 49; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYYSKI 9
|||||||

Db 72 KCLKFYYSKI 80

RESULT 10
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359.382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860.165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 49; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYYSKI 9
|||||||

Db 72 KCLKFYYSKI 80

RESULT 11
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367.309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 49; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYYSKI 9
|||||||

Db 72 KCLKFYYSKI 80

RESULT 12
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485.885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match 100.0%; Score 49; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYYSKI 9
|||||||

Db 178 KCLKFYYSKI 186

RESULT 13
US-09-485-885-10
; Sequence 10, Application US/09485885

; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10

Query Match 100.0%; Score 49; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYSKI 9
|||
Db 197 KCLKFYSKI 205

RESULT 14
US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6

Query Match 100.0%; Score 49; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYSKI 9
|||
Db 178 KCLKFYSKI 186

RESULT 15
US-09-485-885-14
; Sequence 14, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine

; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-14

Query Match 100.0%; Score 49; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCLKFYSKI 9
|||
Db 197 KCLKFYSKI 205

Search completed: June 29, 2005, 01:44:26
Job time : 17.9126 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:28:22 ; Search time 54.2473 Seconds
(without alignments)

84.958 Million cell updates/sec

Title: US-08-170-344-68
Perfect score: 55
Sequence: 1 PYAVCDKCL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	81	2	Q80886 human papil
2	55	100.0	84	2	Q80882 human papil
3	55	100.0	90	2	Q80883 human papil
4	55	100.0	90	2	Q80884 human papil
5	55	100.0	90	2	Q80885 human papil
6	55	100.0	91	2	Q80887 human papil
7	55	100.0	99	2	Q919B2 human papil
8	55	100.0	103	2	Q919D6 human papil
9	55	100.0	130	2	Q919B4 human papil
10	55	100.0	130	2	Q919B8 human papil
11	55	100.0	130	2	Q919C0 human papil
12	55	100.0	130	2	Q919C2 human papil
13	55	100.0	130	2	Q919C8 human papil
14	55	100.0	130	2	Q919D0 human papil
15	55	100.0	138	2	Q919D2 human papil
16	55	100.0	143	2	Q919B6 human papil
17	55	100.0	143	2	Q919C4 human papil
18	55	100.0	151	2	O12335 human papil
19	55	100.0	151	2	O12336 human papil
20	55	100.0	151	2	O767TS0 human papil
21	55	100.0	151	2	O778I6 human papil
22	55	100.0	151	2	O77E16 human papil
23	55	100.0	151	2	O77J7C7 human papil
24	55	100.0	151	2	O77ZJ5 human papil
25	55	100.0	151	2	O80963 human papil
26	55	100.0	151	2	O80966 human papil
27	55	100.0	151	2	O80968 human papil
28	55	100.0	151	2	O89640 human papil
29	55	100.0	151	2	O89708 human papil
30	55	100.0	151	2	O89755 human papil
31	55	100.0	151	2	O89852 human papil

32 55 100.0 151 2 Q89887 human papil
33 55 100.0 151 2 Q8B564 human papil
34 55 100.0 151 2 Q8BB19 human papil
35 55 100.0 151 2 Q8BB20 human papil
36 55 100.0 151 2 Q8BB21 human papil
37 55 100.0 151 2 Q8W8C3 human papil
38 55 100.0 151 2 Q9W931 human papil
39 55 100.0 151 2 Q9WMP2 human papil
40 55 100.0 151 2 Q9WMP4 human papil
41 55 100.0 151 2 Q9WMP5 human papil
42 55 100.0 158 1 VE6_HPVI6
43 55 100.0 158 2 Q8JMU8 human papil
44 55 100.0 158 2 Q8QHNO human papil
45 55 100.0 158 2 Q8QHP5 human papil

ALIGNMENTS

RESULT 1
Q80886 PRELIMINARY; PRT; 81 AA.
AC Q80886;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galuira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14515; AAB60569.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR NON_TER 1
FT NON_TER 81
SQ SEQUENCE 81 AA; 9784 MW; DDSPEDBC9F845B97 CRC64;
Query Match 100.0%; Score 55; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 18 PYAVCDKCL 26

RESULT 2
Q80882 PRELIMINARY; PRT; 84 AA.
AC Q80882;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical;
RA Haegert D.G., Galuira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14511; AAB60565.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.

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DR GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 84 AA; 10177 MW; 5AB6B896468E1CAA CRC64;
Query Match 100.0%; Score 55; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 15 PYAVCDKCL 23

RESULT 3
Q80883 ID Q80883 PRELIMINARY; PRT; 90 AA.
AC Q80883;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14512; AAB60566.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 10904 MW; 5D3ADF843AD6060B CRC64;
Query Match 100.0%; Score 55; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 18 PYAVCDKCL 26

RESULT 4
Q80884 ID Q80884 PRELIMINARY; PRT; 90 AA.
AC Q80884;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14513; AAB60567.2; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 91
SQ SEQUENCE 91 AA; 11136 MW; 22PDF3EA185ACBA7 CRC64;

FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 11021 MW; 47F42BBEFACCCC01 CRC64;
Query Match 100.0%; Score 55; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 18 PYAVCDKCL 26

RESULT 5
Q80885 ID Q80885 PRELIMINARY; PRT; 90 AA.
AC Q80885;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14514; AAB60568.2; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 10964 MW; BC2531643ACBA76C CRC64;
Query Match 100.0%; Score 55; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 18 PYAVCDKCL 26

RESULT 6
Q80887 ID Q80887 PRELIMINARY; PRT; 91 AA.
AC Q80887;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14516; AAB60570.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 91
SQ SEQUENCE 91 AA; 11136 MW; 22PDF3EA185ACBA7 CRC64;

```

Query Match 100.0%; Score 55; DB 2; Length 91;
 Best Local Similarity 100.0%; Pred. No. 0.05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PYAVCDKCL 9
 |||||
 DB 18 PYAVCDKCL 26

RESULT 7

Q919B2 ID Q919B2 PRELIMINARY; PRT; 99 AA.
 AC Q919B2; MEDLINE=21846229; PubMed=11857370;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF040704; AAL01342.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON_TER 1
 FT NON_TER 99
 SQ SEQUENCE 99 AA; 12005 MW; C2B96025EC370E38 CRC64;

Query Match 100.0%; Score 55; DB 2; Length 99;
 Best Local Similarity 100.0%; Pred. No. 0.054;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PYAVCDKCL 9
 |||||
 DB 35 PYAVCDKCL 43

RESULT 8

Q919D6 ID Q919D6 PRELIMINARY; PRT; 103 AA.
 AC Q919D6; MEDLINE=21846229; PubMed=11857370;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF040692; AAL01342.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON_TER 1
 FT NON_TER 103
 SQ SEQUENCE 103 AA; 12422 MW; 6F90CBAF1F25449B CRC64;

Query Match 100.0%; Score 55; DB 2; Length 103;

Best Local Similarity 100.0%; Pred. No. 0.056;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PYAVCDKCL 9
 |||||
 DB 11 PYAVCDKCL 19

RESULT 9

Q919B4 ID Q919B4 PRELIMINARY; PRT; 130 AA.
 AC Q919B4; MEDLINE=21846229; PubMed=11857370;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF040703; AAL01363.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON_TER 1
 FT NON_TER 130
 SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227EEDDC CRC64;

Query Match 100.0%; Score 55; DB 2; Length 130;

Best Local Similarity 100.0%; Pred. No. 0.069;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PYAVCDKCL 9
 |||||
 DB 38 PYAVCDKCL 46

RESULT 10

Q919B8 ID Q919B8 PRELIMINARY; PRT; 130 AA.
 AC Q919B8; MEDLINE=21846229; PubMed=11857370;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF040701; AAL01359.1; -;
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON_TER 1
 FT NON_TER 130
 SQ SEQUENCE 130 AA; 15775 MW; 92D3C07BF96B092F CRC64;

Query Match 100.0%; Score 55; DB 2; Length 130;

Best Local Similarity 100.0%; Pred. No. 0.069;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
 Db 38 PYAVCDKCL 46

RESULT 11

Q919C0 Q919C0 PRELIMINARY; PRT; 130 AA.
 AC Q919C0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404700; AAL01357.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 55; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.069;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
 Db 38 PYAVCDKCL 46

RESULT 12

Q919C2 Q919C2 PRELIMINARY; PRT; 130 AA.
 AC Q919C2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404699; AAL01355.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 55; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.069;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
 Db 38 PYAVCDKCL 46

RESULT 13

Q919C8 Q919C8 PRELIMINARY; PRT; 130 AA.
 AC Q919C8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404696; AAL01349.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;

Query Match 100.0%; Score 55; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.069;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
 Db 38 PYAVCDKCL 46

RESULT 14

Q919D0 Q919D0 PRELIMINARY; PRT; 130 AA.
 AC Q919D0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404695; AAL01347.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 130 AA; 15735 MW; 9EFB30EEDCA21AF3 CRC64;

Query Match 100.0%; Score 55; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.069;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
 Db 38 PYAVCDKCL 46

RESULT 15

Q919D2
ID Q919D2 PRELIMINARY; PRT; 138 AA.
AC Q919D2;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia."
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404694; AAL01345.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 138 AA; 16696 MW; 481E5AEA90895FC2 CRC64;
Query Match 100.0%; Score 55; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PYAVCDKCL 9
Db 46 PYAVCDKCL 54

Search completed: June 29, 2005, 01:34:48
Job time : 54.2473 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:32:21 ; Search time 11.2747 Seconds
(without alignments)
76.805 Million cell updates/sec

Title: US-08-170-344-68
Perfect score: 55
Sequence: 1 PYAVCDKCL 9
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	158	1 W6WLS	protein E6 - human
2	44	80.0	151	1 W6WLS1	E6 protein - human
3	43	78.2	153	1 S15621	E6 protein - human
4	42	76.4	149	1 W6WLS5	E6 protein - human
5	42	76.4	153	2 S36503	E6 protein - human
6	42	76.4	1891	2 T13594	hypothetical prote
7	42	76.4	1920	2 T13893	gene hindsight pro
8	41	74.5	169	2 B82757	transcription regu
9	41	74.5	740	2 E69420	hydrogenase expres
10	40	72.7	155	1 W6WLS6	E6 protein - human
11	40	72.7	155	2 A44890	E6 protein - human
12	40	72.7	605	2 G70409	high affinity sulf
13	40	72.7	951	2 T45726	hypothetical prote
14	39	70.9	149	1 W6WLS1	E6 protein - human
15	38	69.1	123	2 D72856	AcOrf-52 protein -
16	38	69.1	150	2 S36544	E6 protein - human
17	38	69.1	154	2 S36584	E6 protein - human
18	38	69.1	187	2 T32826	hypothetical prote
19	38	69.1	194	2 T41796	AcMNPV orf52 - Bom
20	38	69.1	401	2 A96941	hypothetical prote
21	38	69.1	552	2 S45886	hypothetical prote
22	37	67.3	149	1 W6WLS8	E6 protein - human
23	37	67.3	158	1 W6WLS18	E6 protein - human
24	36	65.5	101	2 E71607	metal binding prot
25	36	65.5	117	2 E64628	hydrogenase expres
26	36	65.5	148	2 A61237	E6 protein - human
27	36	65.5	148	2 S36532	E6 protein - human
28	36	65.5	148	2 S36573	E6 protein - human
29	36	65.5	152	2 S36550	E6 protein - human

ALIGNMENTS

RESULT 1

W6WLS

protein E6 - human papillomavirus type 16

C;Species: human papillomavirus type 16

C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C;Accession: A03682; T10427

R;Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virology 145, 181-185, 1985

A;Title: Human papillomavirus type 16 DNA sequence.

A;Reference number: A22355; MUID:85246220; PMID:2990099

A;Accession: A03682

A;Molecule type: DNA

A;Residues: 1-158 <SEE>

A;Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333033

R;Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A;Title: A negative element in the human poapillomavirus type 16 genome acts at the lev

A;Reference number: Z17014; MUID:91162763; PMID:1848319

A;Accession: T10427

A;Status: preliminary; translated from GB/EMBL/DBDJB

A;Molecule type: DNA

A;Residues: 1-158 <KEN>

A;Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

C;Genetics:

A;Gene: E6

C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; zinc finger

F;37-73/Region: zinc finger CCCC motif

F;110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 55; DB 1; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.069;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9

|||||

Db 66 PYAVCDKCL 74

RESULT 2

W6WLS1

E6 protein - human papillomavirus type 51

C;Species: human papillomavirus type 51

C;Note: Host Homo sapiens (man)

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C;Accession: E40415

R;Lungu, O.; Crum, C.P.; Silverstein, S.J.

J. Virol. 65, 4216-4225, 1991

A;Title: Biologic properties and nucleotide sequence analysis of human papillomavirus t

A;Reference number: A40415; MUID:91303675; PMID:1649326

A;Accession: E40415

A;Status: translation not shown

A:Molecule type: DNA
A:Residues: 1-151 <LUN>
A:Cross-references: UNIPROT:P26554; GB:MG2877
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match 80.0%; Score 44; DB 1; Length 151;
Best Local Similarity 77.8%; Pred. No. 3.8;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 59 PYGCKQCL 67

RESULT 3
S15621
E6 protein - human papillomavirus type 57
C:Species: human papillomavirus type 57
A:Note: host Homo sapiens (man)
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C:Accession: S15621
R:Hirsch-Bennam, A.; Delius, H.; de Villiers, E.M.
Virus Res. 18, 81-98, 1990
A:Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and 2b
A:Reference number: S15614; MUID:91188699; PMID:1964523
A:Accession: S15621
A:Molecule type: DNA
A:Residues: 1-153 <HR>
A:Cross-references: UNIPROT:P22158; EMBL:X55965; NID:g60882; PIDN:CAA39430.1; PID:g60883
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; transforming protein; zinc finger
F:29-65/Region: zinc finger CCCC motif
F:102-138/Region: zinc finger CCCC motif

Query Match 78.2%; Score 43; DB 1; Length 153;
Best Local Similarity 66.7%; Pred. No. 5.5;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 58 PYGACEKCL 66

RESULT 4
W6WL35
E6 protein - human papillomavirus type 35
C:Species: human papillomavirus type 35
A:Note: host Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: E40824; S36521
R:Marich, J.E.; Pontaler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776, 1992
A:Title: The phylogenetic relationship and complete nucleotide sequence of human papillomavirus type 35
A:Reference number: A40824; MUID:92124753; PMID:1310198
A:Accession: E40824
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-149 <MAR>
A:Cross-references: UNIPROT:P27228; GB:M74117; NID:g333050; PIDN:AAA46966.1; PID:g333051
F:Delius, H.; Hofmann, B.
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36521
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-149
A:Cross-references: EMBL:X74477; NID:g396997; PIDN:CAA52561.1; PID:g396998
A:Experimental source: strain 35H
C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match 76.4%; Score 42; DB 1; Length 149;
Best Local Similarity 77.8%; Pred. No. 7.8;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 59 PYGVCMKCL 67

RESULT 5
S36503
E6 protein - human papillomavirus type 30
C:Species: human papillomavirus type 30
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36503
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36503
A:Molecule type: DNA
A:Residues: 1-153
A:Cross-references: UNIPROT:P36809; EMBL:X74474; NID:g396973; PIDN:CAA52543.1; PID:g396999
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 76.4%; Score 42; DB 2; Length 153;
Best Local Similarity 77.8%; Pred. No. 8;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 62 PYAVCNFCL 70

RESULT 6
T13594
hypothetical protein peb - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T13594
R:Ferraz, C.; Vidal, S.; Brun, C.; Bucheton, A.; Demaille, J.G.
submitted to the EMBL Data Library, October 1998
A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A:Reference number: Z17692
A:Accession: T13594
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1891 <FER>
A:Cross-references: UNIPROT:O77275; EMBL:AL031227; NID:e1330103; PID:e1316856; PIDN:CAA
C:Genetics:
A:Gene: peb
A:Cross-references: FlyBase:FBgn0003053
A:Introns: 289/3

Query Match 76.4%; Score 42; DB 2; Length 1891;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDK 7
Db 747 PYAVCDK 753

RESULT 7
T13893
gene hindsight protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C;Accession: T13893
 R;Yip, M.L.R.; Lamka, M.L.; Lipshitz, H.D.
 Development 124, 2129-2141, 1997
 A;Title: Control of germ-band retraction in *Drosophila* by the zinc-finger protein HINDS1
 A;Reference number: Z17807; MUID:97330681; PMID:9187140
 A;Accession: T13893
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-1920 <YIP>
 A;Cross-references: UNIPROT:O46205; EMBL:U86010; NID:g2769709; PID:g2769710; PIDN:AAB956
 C;Genetics:
 A;Gene: hindsight
 A;Cross-references: FlyBase:FBgn003053
 C;Function:
 A;Description: probably function as a transcription factor
 C;Keywords: nucleus; zinc finger

Query Match 76.4%; Score 42; DB 2; Length 1920;
 Best Local Similarity 100.0%; Pred. No. 55;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDK 7
 Db 747 PYAVCDK 753
 |||||

RESULT 8
 B82757
 Transcription regulator Fur family XP0821 [imported] - *Xylella fastidiosa* (strain 9a5c)
 C;Species: *Xylella fastidiosa*
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C;Accession: B82757
 R;anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequen
 Nature 406, 151-157, 2000
 A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
 A;Reference number: A82515; MUID:20365717; PMID:10910347
 A;Note: for a complete list of authors see reference number A59328 below
 A;Accession: B82757
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-169 <SIN>
 A;Cross-references: UNIPROT:Q9PF57; GB:AE003922; GB:AE003849; NID:g9105722; PIDN:AAF8363
 A;Experimental source: strain 9a5c
 R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
 as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohn
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, E.E.; Laig
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, H
 A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Tshahoko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A;Reference number: A59328
 A;Contents: annotation
 C;Genetics:
 A;Gene: XF0821

Query Match 74.5%; Score 41; DB 2; Length 169;
 Best Local Similarity 62.5%; Pred. No. 12;
 Matches 5; Conservative 2; Mismatches 2; Indels 1; Gaps 0;

Qy 1 PYAVCDK 8
 Db 112 PFLICDKC 119
 ||:||||

RESULT 9
 B69420
 hydrogenase expression/formation regulatory protein (hypF) homolog - *Archaeoglobus fulgi*
 C;Species: *Archaeoglobus fulgidus*

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 14-Apr-2003
 C;Accession: B69420
 R;Klenk, H.P.; Clayton, R.A.; Tomb, J.P.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodge
 ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.
 Glodok, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
 A;Reference number: A69250; MUID:98049343; PMID:9389475
 A;Accession: B69420
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-740 <KLE>
 A;Cross-references: GB:AE001009; GB:AE000782; NID:g2689332; PIDN:AAB89876.1; PID:g26492
 C;Superfamily: carbamoyl phosphate-converting enzyme (Nife)-hydrogenase maturation fac

Query Match 74.5%; Score 41; DB 2; Length 740;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AVCDKCL 9
 Db 100 AVCDKCL 106
 |||||

RESULT 10
 W6W156
 E6 protein - human papillomavirus type 56
 C;Species: human papillomavirus type 56
 C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
 C;Accession: A33377; S36579
 R;Loerincz, A.T.; Quinn, A.P.; Goldeborough, M.D.; McAllister, P.; Temple, G.F.
 J. Gen. Virol. 70, 3099-3104, 1989
 A;Title: Human papillomavirus type 56: a new virus detected in cervical cancers.
 A;Reference number: A33377; MUID:90063558; PMID:2555440
 A;Accession: A33377
 A;Molecule type: DNA
 A;Residues: 1-155 <LOE>
 A;Cross-references: UNIPROT:P24836
 R;Dellius, H.; Hofmann, B.
 submitted to the EMBL Data Library, August 1993
 A;Description: Primer-directed sequencing of human papillomavirus types.
 A;Reference number: S36469
 A;Accession: S36579
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-155
 A;Cross-references: EMBL:X74483; NID:g397053; PIDN:CAA52596.1; PID:g397054
 C;Superfamily: papillomavirus E6 protein
 C;Keywords: DNA binding; early protein; transforming protein; zinc finger
 F;33-69/Region: zinc finger CCCC motif
 F;106-142/Region: zinc finger CCCC motif

Query Match 72.7%; Score 40; DB 1; Length 155;
 Best Local Similarity 77.8%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
 Db 62 PYAVCRVCL 70
 |||||

RESULT 11
 A44890
 E6 protein - human papillomavirus type 66
 C;Species: human papillomavirus type 66
 C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
 C;Accession: A44890
 R;Lawhead, A.R.; Beaudenon, S.; Favre, M.; Orth, G.
 J. Clin. Microbiol. 29, 2656-2660, 1991
 A;Title: Characterization of human papillomavirus type 66 from an invasive carcinoma of
 A;Reference number: A44890; MUID:92129556; PMID:1663515

A;Accession: A44890

A;Molecule type: DNA

A;Residues: 1-155 <TAW>

A;Cross-references: UNIPROT:Q80955

A;Note: sequence extracted from NCBI backbone (NCBIN:78637, NCBIPI:78638)

C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; transforming protein; zinc finger

F;33-69/Region: zinc finger CCCC motif

F;106-142/Region: zinc finger CCCC motif

Query Match 72.7%; Score 40; DB 2; Length 155;

Best Local Similarity 77.8%; Pred. No. 17;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9

Db 62 PYAVCRVCL 70

RESULT 12

G70409 high affinity sulfate transporter - Aquifex aeolicus

C;Species: Aquifex aeolicus

C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004

C;Accession: G70409

F;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov

Nature 392, 353-358, 1998

A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A;Reference number: A70300; MUID:98196666; PMID:9537320

A;Accession: G70409

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-605 <AQF>

A;Cross-references: UNIPROT:O67306; GB:AE000732; NID:G2983704; PIDN:AAC07275.1; PID:G298

A;Experimental source: strain VF5

C;Genetics:

A;Gene: hvsr

C;Superfamily: integral membrane protein HP0228

Query Match

Best Local Similarity 72.7%; Score 40; DB 2; Length 605;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9

Db 582 PYAVFDECL 590

RESULT 13

T45726

hypothetical protein FIP2.210 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004

C;Accession: T45726

F;Choisme, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa

submitted to the Protein Sequence Database, November 1999

A;Reference number: Z23010

A;Accession: T45726

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-951 <CHO>

A;Cross-references: UNIPROT:Q9SN72; EMBL:AL132955

A;Experimental source: cultivar Columbia; BAC clone FIP2

C;Genetics:

A;Map position: 3

A;Introns: 16/3; 45/3; 75/3; 102/3; 163/3; 883/3; 932/3

A;Note: FIP2.210

Query Match

Best Local Similarity 72.7%; Score 40; DB 2; Length 951;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PYAVCDKC 8

Db 686 PYRVCDDC 693

RESULT 14

W6WL31

E6 protein - human papillomavirus type 31

C;Species: human papillomavirus type 31

A;Note: host Homo sapiens (man)

C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004

C;Accession: A32444

R;Goldsbrough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.

Virology 171, 306-311, 1989

A;Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-asso

A;Reference number: A94398; MUID:89299478; PMID:2545036

A;Accession: A32444

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-149 <GOL>

A;Cross-references: UNIPROT:PI7386; GB:J04353; NID:G333048; PIDN:AAA46950.1; PID:G45991

C;Comment: This protein may be involved in the oncogenic potential of this virus.

C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; zinc finger

F;30-66/Region: zinc finger CCCC motif

F;103-139/Region: zinc finger CCCC motif

Query Match

Best Local Similarity 70.9%; Score 39; DB 1; Length 149;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9

Db 59 PHGVCTKCL 67

RESULT 15

D72856

AcOrf-52 protein - Autographa californica nuclear polyhedrosis virus

C;Species: Autographa californica nuclear polyhedrosis virus, AcMNPV

A;Note: dsDNA virus

C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004

C;Accession: D72856

R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.

Virology 202, 586-605, 1994

A;Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus

A;Reference number: A72850; MUID:94303173; PMID:8030224

A;Accession: D72856

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-123 <AYR>

A;Cross-references: UNIPROT:P41456; GB:L22858; NID:G510708; PIDN:AAA66682.1; PID:G55912

C;Genetics:

A;Gene: AcOrf-52

Query Match

Best Local Similarity 69.1%; Score 38; DB 2; Length 123;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YAVCDKCL 9

Db 73 YLCDDKCL 80

Search completed: June 29, 2005, 01:38:44

Job time : 12.2747 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 05:18:25 ; Search time 53.8517 Seconds
(without alignments)
64.268 Million cell updates/sec

Title: US-08-170-344-68
Perfect score: 55
Sequence: 1 PYAVCDKCL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	9	17	US-10-484-063-6
2	55	100.0	10	8	US-08-344-824-237
3	55	100.0	20	16	US-10-476-570-11
4	55	100.0	22	16	US-10-612-818-4
5	55	100.0	151	14	US-10-177-390-6
6	55	100.0	151	17	US-10-484-063-20
7	55	100.0	151	17	US-10-484-063-27
8	55	100.0	158	17	US-10-858-384-2
9	55	100.0	158	17	US-10-367-057-16
10	55	100.0	171	16	US-10-472-724-2
11	55	100.0	266	9	US-09-367-309A-1

12	55	100.0	273	13	US-10-000-903-4	Sequence 4, Appli
13	55	100.0	273	17	US-10-899-771-4	Sequence 4, Appli
14	55	100.0	292	13	US-10-000-903-10	Sequence 10, Appl
15	55	100.0	292	17	US-10-899-771-10	Sequence 10, Appl
16	55	100.0	371	13	US-10-000-903-6	Sequence 6, Appli
17	55	100.0	371	17	US-10-899-771-6	Sequence 6, Appli
18	55	100.0	390	13	US-10-000-903-14	Sequence 14, Appl
19	55	100.0	390	17	US-10-899-771-14	Sequence 14, Appl
20	51	92.7	9	8	US-08-344-824-346	Sequence 346, App
21	45	81.8	781	15	US-10-424-599-265840	Sequence 265840,
22	43	78.2	292	15	US-10-424-599-205655	Sequence 205655,
23	43	78.2	467	16	US-10-437-963-163687	Sequence 163687,
24	41	74.5	140	16	US-10-767-701-38586	Sequence 38586, A
25	41	74.5	158	16	US-10-425-115-306006	Sequence 306006,
26	41	74.5	209	16	US-10-767-701-61305	Sequence 61305, A
27	41	74.5	315	16	US-10-425-115-281736	Sequence 281736,
28	41	74.5	462	15	US-10-424-599-252512	Sequence 252512,
29	41	74.5	517	16	US-10-425-115-282885	Sequence 282885,
30	41	74.5	917	16	US-10-437-963-113217	Sequence 113217,
31	41	74.5	940	15	US-10-282-122A-52332	Sequence 52332, A
32	41	74.5	1082	16	US-10-437-963-167162	Sequence 167162,
33	41	74.5	1086	16	US-10-437-963-104962	Sequence 104962,
34	41	74.5	1158	16	US-10-437-963-126051	Sequence 126051,
35	41	74.5	1169	16	US-10-437-963-156044	Sequence 156044,
36	40	72.7	427	16	US-10-425-115-304190	Sequence 304190,
37	39	70.9	824	16	US-10-739-930-6146	Sequence 6146, Ap
38	38	69.1	16	9	US-09-767-395-18	Sequence 18, Appl
39	38	69.1	154	17	US-10-873-332-8	Sequence 8, Appli
40	38	69.1	160	17	US-10-873-332-66	Sequence 66, Appl
41	38	69.1	467	15	US-10-425-114-38299	Sequence 38299, A
42	37	67.3	10	8	US-08-344-824-241	Sequence 241, App
43	37	67.3	81	15	US-10-424-599-228359	Sequence 228359,
44	37	67.3	113	16	US-10-767-701-41187	Sequence 41187, A
45	37	67.3	158	16	US-10-800-023-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-10-484-063-6
; Sequence 6, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-6

Query Match 100.0%; Score 55; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PYAVCDKCL 9
Db 1 PYAVCDKCL 9

RESULT 2
US-08-344-824-237
; Sequence 237, Application US/08344824
; Publication No. US20030152580A1
; GENERAL INFORMATION:
; APPLICANT: SETTE, Alessandro
; APPLICANT: SIDNEY, John
; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
; NUMBER OF SEQUENCES: 399
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: One Market Plaza, Steuart Street Tower, 20th
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/344,824
; FILING DATE: 23-NOV-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,634
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 14137-80-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 237:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-824-237

Query Match 100.0%; Score 55; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 2 PYAVCDKCL 10

RESULT 3
US-10-476-570-11
; Sequence 11, Application US/10476570
; Publication No. US20040170643A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980

; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 20
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 61-80
US-10-476-570-11

Query Match 100.0%; Score 55; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 6 PYAVCDKCL 14

RESULT 4
US-10-612-818-4
; Sequence 4, Application US/10612818
; Publication No. US20040110925A1
; GENERAL INFORMATION:
; APPLICANT: Impact Diagnostics
; APPLICANT: Impact Diagnostics
; TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomavirus
; TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Papillomavirus
; FILE REFERENCE: 3352-2-2
; CURRENT APPLICATION NUMBER: US/10/612,818
; CURRENT FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 60/394,172
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 09/828,645
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from the E6 early coding region of HPV 16
US-10-612-818-4

Query Match 100.0%; Score 55; DB 16; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 5 PYAVCDKCL 13

RESULT 5
US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerp Innovatiescentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT

; ORGANISM: Human papillomavirus type 16
US-10-177-390-6

Query Match 100.0%; Score 55; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.35; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 59 PYAVCDKCL 67
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RESULT 6

US-10-484-063-20
; Sequence 20, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-20

Query Match 100.0%; Score 55; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.35; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 59 PYAVCDKCL 67
|||||

RESULT 7

US-10-484-063-27
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-484-063-27

Query Match 100.0%; Score 55; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.35;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 59 PYAVCDKCL 67
|||||

RESULT 8

US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match 100.0%; Score 55; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.36; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 66 PYAVCDKCL 74
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RESULT 9

US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match 100.0%; Score 55; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 66 PYAVCDKCL 74
|||||

```
RESULT 10
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match      100.0%; Score 55; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 PYAVCDKCL 9
Db      71 PYAVCDKCL 79

RESULT 11
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JTM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 01727/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match      100.0%; Score 55; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 PYAVCDKCL 9
Db      66 PYAVCDKCL 74

RESULT 12
US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
```

```
; APPLICANT: Caberon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4

Query Match      100.0%; Score 55; DB 13; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 PYAVCDKCL 9
Db      172 PYAVCDKCL 180

RESULT 13
US-10-899-771-4
; Sequence 4, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried I.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-4

Query Match      100.0%; Score 55; DB 17; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 PYAVCDKCL 9
Db      172 PYAVCDKCL 180

RESULT 14
US-10-000-903-10
; Sequence 10, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
```

; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-10

Query Match 100.0%; Score 55; DB 13; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.62; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 191 PYAVCDKCL 199

RESULT 15
US-10-899-771-10
; Sequence 10, Application US/10899771
; Publication No: US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (Clyta from Streptococcus
; OTHER INFORMATION: pneumoniae and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-10

Query Match 100.0%; Score 55; DB 17; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.62; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 191 PYAVCDKCL 199

Search completed: June 29, 2005, 05:48:13
Job time : 53.8517 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:37:59 ; Search time 16.8626 Seconds
(without alignments)
39,842 Million cell updates/sec

Title: US-08-170-344-68

Perfect score: 55

Sequence: 1 PYAVCDKOL 9

Scoring table: BLOSUM62

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	11	3	US-08-159-339A-1170
2	55	100.0	158	4	US-08-980-523A-2
3	55	100.0	162	1	US-08-316-239B-3
4	55	100.0	162	1	US-08-316-239B-3
5	55	100.0	172	3	US-08-860-165-12
6	55	100.0	172	3	US-08-860-165-12
7	55	100.0	172	3	US-08-359-382-12
8	55	100.0	172	3	US-08-359-382-12
9	55	100.0	266	3	US-08-860-165-10
10	55	100.0	266	3	US-08-359-382-10
11	55	100.0	266	4	US-08-367-309A-1
12	55	100.0	273	3	US-08-485-885-4
13	55	100.0	292	3	US-08-485-885-10
14	55	100.0	371	3	US-08-485-885-6
15	55	100.0	390	3	US-08-485-885-14
16	50	90.9	20	2	US-08-934-915-162
17	41	74.5	8	3	US-08-159-339A-1169
18	41	74.5	10	3	US-08-159-339A-561
19	39	70.9	74	4	US-08-513-939C-7370
20	38	69.1	16	2	US-08-889-291-18
21	38	69.1	16	3	US-08-098-244-18
22	38	69.1	16	3	US-08-375-314-18
23	38	69.1	16	4	US-08-767-395-18
24	37	67.3	9	3	US-08-159-339A-74
25	37	67.3	9	3	US-08-159-339A-249
26	37	67.3	158	2	US-08-247-904B-10
27	37	67.3	158	3	US-08-767-942A-19

Sequence 14, Appl
Sequence 21, Appl
Sequence 23, Appl
Sequence 8725, Ap
Sequence 8726, Ap
Sequence 8727, Ap
Sequence 8728, Ap
Sequence 8729, Ap
Sequence 8730, Ap
Sequence 7517, Ap
Sequence 7, Appl
Sequence 8, Appl
Sequence 4, Appl
Sequence 6, Appl
Sequence 7, Appl
Sequence 86, Appl
Sequence 5937, Ap

ALIGNMENTS

RESULT 1
US-08-159-339A-1170
; Sequence 1170, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq For Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 1170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-1170

Query Match 100.0%; Score 55; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 1 PYAVCDKCL 9

RESULT 2

US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO81 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 55; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 66 PYAVCDKCL 74

RESULT 3

US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 100.0%; Score 55; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 66 PYAVCDKCL 74

RESULT 4

US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 100.0%; Score 55; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 66 PYAVCDKCL 74

RESULT 5
US-08-860-165-12
; Sequence 12, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12

Query Match 100.0%; Score 55; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 4 PYAVCDKCL 12

RESULT 6
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14

Query Match 100.0%; Score 55; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 135 PYAVCDKCL 143

RESULT 7
US-09-359-382-12
; Sequence 12, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-12

Query Match 100.0%; Score 55; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 4 PYAVCDKCL 12

RESULT 8
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match 100.0%; Score 55; DB 3; Length 172;

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Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 135 PYAVCDKCL 143

RESULT 9
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 55; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 66 PYAVCDKCL 74

RESULT 10
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 55; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.12;

Qy 1 PYAVCDKCL 9
Db 172 PYAVCDKCL 180

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 55; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 66 PYAVCDKCL 74

RESULT 11
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 55; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 66 PYAVCDKCL 74

RESULT 12
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match 100.0%; Score 55; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 172 PYAVCDKCL 180
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RESULT 13

US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485.885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10

Query Match 100.0%; Score 55; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.13; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 191 PYAVCDKCL 199
|||||

RESULT 14

US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485.885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6

Query Match 100.0%; Score 55; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.16; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 172 PYAVCDKCL 180
|||||

RESULT 15

US-09-485-885-14

; Sequence 14, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485.885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-14

Query Match 100.0%; Score 55; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 0.17; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PYAVCDKCL 9
Db 191 PYAVCDKCL 199
|||||

Search completed: June 29, 2005, 01:44:25
Job time : 17.9126 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:28:22 ; Search time 54.2473 Seconds
(without alignments)
84.958 Million cell updates/sec

Title: US-08-170-344-67
Perfect score: 48
Sequence: 1 VYDFAFRDL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	81	2 Q80886	Q80886 human papil
2	48	100.0	90	2 Q80883	Q80883 human papil
3	48	100.0	90	2 Q80884	Q80884 human papil
4	48	100.0	90	2 Q80885	Q80885 human papil
5	48	100.0	91	2 Q80887	Q80887 human papil
6	48	100.0	99	2 Q91982	Q91982 human papil
7	48	100.0	130	2 Q91984	Q91984 human papil
8	48	100.0	130	2 Q91988	Q91988 human papil
9	48	100.0	130	2 Q919C0	Q919C0 human papil
10	48	100.0	130	2 Q919C2	Q919C2 human papil
11	48	100.0	130	2 Q919C8	Q919C8 human papil
12	48	100.0	138	2 Q919D2	Q919D2 human papil
13	48	100.0	143	2 Q919B6	Q919B6 human papil
14	48	100.0	143	2 Q919C4	Q919C4 human papil
15	48	100.0	151	2 Q12335	Q12335 human papil
16	48	100.0	151	2 Q12336	Q12336 human papil
17	48	100.0	151	2 Q76TS0	Q76TS0 human papil
18	48	100.0	151	2 Q77816	Q77816 human papil
19	48	100.0	151	2 Q77E16	Q77E16 human papil
20	48	100.0	151	2 Q77JC7	Q77JC7 human papil
21	48	100.0	151	2 Q77ZJ5	Q77ZJ5 human papil
22	48	100.0	151	2 Q80963	Q80963 human papil
23	48	100.0	151	2 Q80966	Q80966 human papil
24	48	100.0	151	2 Q80964	Q80964 human papil
25	48	100.0	151	2 Q89648	Q89648 human papil
26	48	100.0	151	2 Q89708	Q89708 human papil
27	48	100.0	151	2 Q89755	Q89755 human papil
28	48	100.0	151	2 Q89852	Q89852 human papil
29	48	100.0	151	2 Q89887	Q89887 human papil
30	48	100.0	151	2 Q8B564	Q8B564 human papil
31	48	100.0	151	2 Q8BB19	Q8BB19 human papil

32	48	100.0	151	2 Q8BB20	Q8BB20 human papil
33	48	100.0	151	2 Q8BB21	Q8BB21 human papil
34	48	100.0	151	2 Q9W8C3	Q9W8C3 human papil
35	48	100.0	151	2 Q9WMP2	Q9WMP2 human papil
36	48	100.0	151	2 Q9WMP3	Q9WMP3 human papil
37	48	100.0	151	2 Q9WMP4	Q9WMP4 human papil
38	48	100.0	151	2 Q9WMP5	Q9WMP5 human papil
39	48	100.0	156	1 VE6 HPV16	P03126 human papil
40	48	100.0	158	2 Q8JMU8	Q8JMU8 human papil
41	48	100.0	158	2 Q8QHN0	Q8QHN0 human papil
42	48	100.0	158	2 Q8QHP5	Q8QHP5 human papil
43	48	100.0	158	2 Q8QHT0	Q8QHT0 human papil
44	48	100.0	158	2 Q8QRD5	Q8QRD5 human papil
45	48	100.0	158	2 Q8QRD6	Q8QRD6 human papil

ALIGNMENTS

RESULT 1

Q80886 PRELIMINARY; PRT; 81 AA.
AC Q80886;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14515; AAB60569.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR InterPro: IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1 1
FT NON_TER 81 81
SQ SEQUENCE 81 AA; 9784 MW; DD5FEDBC9F845B97 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYDFAFRDL 9
|||
Db 1 VYDFAFRDL 9

RESULT 2

Q80883 PRELIMINARY; PRT; 90 AA.
AC Q80883;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14512; AAB60566.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.

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DR GO: 0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 10904 MW; 5D3ADF843AD6060B CRC64;

Query Match 100.0%; Score 48; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
Db 1 VYDFAFRDL 9

RESULT 3
Q80884 ID Q80884 PRELIMINARY; PRT; 90 AA.
AC Q80884;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14513; AAB60567.2; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 11021 MW; 47F42BBEFAACCC01 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
Db 1 VYDFAFRDL 9

RESULT 4
Q80885 ID Q80885 PRELIMINARY; PRT; 90 AA.
AC Q80885;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14514; AAB60568.2; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 11021 MW; 47F42BBEFAACCC01 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
Db 1 VYDFAFRDL 9

RESULT 5
Q80887 ID Q80887 PRELIMINARY; PRT; 91 AA.
AC Q80887;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14516; AAB60570.1; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 91
SQ SEQUENCE 91 AA; 11136 MW; 22FDF3EA185ACBA7 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.094;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
Db 1 VYDFAFRDL 9

RESULT 6
Q919B2 ID Q919B2 PRELIMINARY; PRT; 99 AA.
AC Q919B2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RL "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404704; AAL01365.1; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 99

```


SQ SEQUENCE 99 AA; 12005 MW; C2B96025EC370E38 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
Db 18 VYDFAFRDL 26

RESULT 7

Q919B4 ID Q919B4 PRELIMINARY; PRT; 130 AA.
AC Q919B4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040703; AAL01353.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227BEDDC CRC64;

Query Match 100.0%; Score 48; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
Db 21 VYDFAFRDL 29

RESULT 8

Q919B8 ID Q919B8 PRELIMINARY; PRT; 130 AA.
AC Q919B8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040701; AAL01359.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15775 MW; 92D3C07BF96B092F CRC64;

Query Match 100.0%; Score 48; DB 2; Length 130;

Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
Db 21 VYDFAFRDL 29

RESULT 9

Q919C0 ID Q919C0 PRELIMINARY; PRT; 130 AA.
AC Q919C0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040700; AAL01357.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
Db 21 VYDFAFRDL 29

RESULT 10

Q919C2 ID Q919C2 PRELIMINARY; PRT; 130 AA.
AC Q919C2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040699; AAL01355.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
 Db 21 VYDFAFRDL 29

RESULT 11

Q919C8 ID Q919C8 PRELIMINARY; PRT; 130 AA.
 AC Q919C8; 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF046936; AAL01345.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
 Db 21 VYDFAFRDL 29

RESULT 12

Q919D2 ID Q919D2 PRELIMINARY; PRT; 138 AA.
 AC Q919D2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF046934; AAL01345.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 138 AA; 16696 MW; 481E5AEA90895FC2 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 138;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
 Db 29 VYDFAFRDL 37

RESULT 13

Q919B6 ID Q919B6 PRELIMINARY; PRT; 143 AA.
 AC Q919B6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF047022; AAL01361.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;

Query Match 100.0%; Score 48; DB 2; Length 143;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
 Db 34 VYDFAFRDL 42

RESULT 14

Q919C4 ID Q919C4 PRELIMINARY; PRT; 143 AA.
 AC Q919C4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF04698; AAL01353.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 143;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
 Db 34 VYDFAFRDL 42

RESULT 15

Wed Jun 29 09:52:11 2005

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O12335
ID O12335 PRELIMINARY; PRT; 151 AA.
AC O12335;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
CX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003015; AAB70732.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR PIR; P00518; E6; 1.
SQ SEQUENCE 151 AA; 18238 MW; BFF32A8B016CC88B CRC64;

Query Match 100.0%; Score 48; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
Db 42 VYDFAFRDL 50

```

Search completed: June 29, 2005, 01:34:48
Job time : 55.2473 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:32:21 ; Search time 11.2747 Seconds
(without alignments)
76.805 Million cell updates/sec

Title: US-08-170-344-67

Perfect score: 48

Sequence: 1 VYDFAFRDL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	158	1 W6WLS	protein E6 - human
2	43	89.6	148	2 S36515	E6 protein - human
3	42	87.5	149	1 W6WLS3	E6 protein - human
4	39	81.2	158	2 S36561	E6 protein - human
5	38	79.2	149	1 W6WLS8	E6 protein - human
6	38	79.2	158	1 W6WLS39	E6 protein - human
7	37	77.1	158	1 W6WLS18	E6 protein - human
8	37	77.1	158	1 W6WLP	E6 protein - human
9	36	75.0	128	2 A81153	type I restriction
10	35	72.9	246	2 B65230	conserved hypotet
11	35	72.9	324	2 A97919	3-oxoacyl-[acyl-ca
12	35	72.9	324	2 C95048	fusion of Uroporph
13	35	72.9	483	2 A97295	E6 protein - human
14	34	70.8	149	1 W6WLS31	E6 protein - human
15	34	70.8	154	2 S36527	E6 protein - human
16	34	70.8	155	1 W6WLS43	E6 protein - human
17	34	70.8	195	2 A96779	hypothetical prote
18	34	70.8	285	2 B64712	ubiquinol cytochro
19	34	70.8	285	2 E71803	dihydrolipoamide S
20	34	70.8	544	2 C42653	hypothetical prote
21	33	68.8	88	2 A21937	E6 protein - human
22	33	68.8	149	1 W6WLS5	hypothetical prote
23	33	68.8	174	2 T50419	hypothetical prote
24	33	68.8	193	2 T16662	conserved hypotet
25	33	68.8	270	2 D90542	hypothetical prote
26	33	68.8	290	2 T47991	hypothetical prote
27	33	68.8	325	2 C86721	hypothetical prote
28	33	68.8	432	2 A84798	peptidylprolyl iso
29	33	68.8	434	2 AD0061	

RESULT 1

W6WLS

protein E6 - human papillomavirus type 16

C/Species: human papillomavirus type 16

C/Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C/Accession: A03682; T10427

R/Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virology 145, 181-185, 1985

A/Title: Human papillomavirus type 16 DNA sequence.

A/Reference number: A22355; MUID:85246220; PMID:2990099

A/Accession: A03682

A/Molecule type: DNA

A/Residues: 1-158 <SEE>

A/Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333033

R/Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A/Title: A negative element in the human poapillomavirus type 16 genome acts at the lev

A/Reference number: Z17014; MUID:91162763; PMID:1848319

A/Accession: T10427

A/Status: preliminary; translated from GB/EMBL/DBDJ

A/Molecule type: DNA

A/Residues: 1-158 <KEN>

A/Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G3330332

C/Genetics:

C/Superfamily: papillomavirus E6 protein

C/Keywords: DNA binding; early protein; zinc finger

F/37-73/Region: zinc finger CCCC motif

F/110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 48; DB 1; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.015; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9

Db 49 VYDFAFRDL 57

RESULT 2

S36515

E6 protein - human papillomavirus type 34

C/Species: human papillomavirus type 34

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C/Accession: S36515

R/Deliuss, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A/Description: Primer-directed sequencing of human papillomavirus types.

A/Reference number: S36469

A/Accession: S36515

A/Molecule type: DNA

A/Residues: 1-148

A;Cross-references: UNIPROT:P35811; EMBL:X74476; NID:g396989; PIDN:CAA52555.1; PID:g396989
 C;Superfamily: papillomavirus E6 protein
 C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 89.6%; Score 43; DB 2; Length 148;
 Best Local Similarity 88.9%; Pred. No. 0.15;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
 ||||| |||
 Db 43 VYDFIFRDL 51

RESULT 3
 W6WL33
 E6 protein - human papillomavirus type 33
 C;Species: human papillomavirus type 33
 C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
 C;Accession: A03683
 J;Cole, S.T.; Strebeck, R.E.
 J. Virol. 58, 991-995, 1986
 A;Title: Genome organization and nucleotide sequence of human papillomavirus type 33, which is a member of the gamma 1 group of papillomaviruses
 A;Reference number: A93020; MUID:86200464; PMID:3009902
 A;Accession: A03683
 A;Molecule type: DNA
 A;Residues: 1-149 <COL>
 A;Cross-references: UNIPROT:P06427; GB:M12732; NID:g333049; PIDN:AAA46958.1; PID:g463177
 C;Superfamily: papillomavirus E6 protein
 C;Keywords: DNA binding; early protein; zinc finger
 F;30-66/Region: zinc finger CCCC motif
 F;103-139/Region: zinc finger CCCC motif

Query Match 87.5%; Score 42; DB 1; Length 149;
 Best Local Similarity 88.9%; Pred. No. 0.25;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
 ||||| |||
 Db 42 VYDFAFADL 50

RESULT 4
 S36561
 E6 protein - human papillomavirus type 45
 C;Species: human papillomavirus type 45
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C;Accession: S36561
 R;Delius, H.; Hofmann, B.
 submitted to the EMBL Data Library, August 1993
 A;Description: Primer-directed sequencing of human papillomavirus types.
 A;Reference number: S36469
 A;Accession: S36561
 A;Molecule type: DNA
 A;Residues: 1-158
 A;Cross-references: UNIPROT:P21735; EMBL:X74479; NID:g397022; PIDN:CAA52573.1; PID:g397022
 C;Superfamily: papillomavirus E6 protein
 C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 81.2%; Score 39; DB 2; Length 158;
 Best Local Similarity 77.8%; Pred. No. 1.1;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
 ||||| |||
 Db 44 VYQFAFKDL 52

RESULT 5
 W6WL58
 E6 protein - human papillomavirus type 58
 C;Species: human papillomavirus type 58
 A;Note: host Homo sapiens (man)
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C;Accession: E36779
 R;Kirii, Y.; Iwamoto, S.; Matsukura, T.
 Virology 185, 424-427, 1991
 A;Title: Human papillomavirus type 58 DNA sequence.
 A;Reference number: A36779; MUID:92024102; PMID:1656594
 A;Accession: E36779
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-149 <KIR>
 A;Cross-references: UNIPROT:P26555; GB:D90400; NID:g222386; PIDN:BAA31845.1; PID:g333370
 C;Superfamily: papillomavirus E6 protein
 C;Keywords: DNA binding; early protein; zinc finger
 F;30-66/Region: zinc finger CCCC motif
 F;103-139/Region: zinc finger CCCC motif

Query Match 79.2%; Score 38; DB 1; Length 149;
 Best Local Similarity 77.8%; Pred. No. 1.6;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
 ||||| |||
 Db 42 VYDFVFDL 50

RESULT 6
 W6WL39
 E6 protein - human papillomavirus type 39
 C;Species: human papillomavirus type 39
 A;Note: host Homo sapiens (man)
 C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
 C;Accession: A38502
 R;Volpers, C.; Strebeck, R.E.
 Virology 181, 419-423, 1991
 A;Title: Genome organization and nucleotide sequence of human papillomavirus type 39.
 A;Reference number: A38502; MUID:91135017; PMID:1847266
 A;Accession: A38502
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-158 <VOL>
 A;Cross-references: UNIPROT:P24835; GB:M62849; EMBL:M38185; NID:g333245; PIDN:AAA47050.1
 C;Superfamily: papillomavirus E6 protein
 C;Keywords: DNA binding; early protein; transforming protein; zinc finger
 F;32-68/Region: zinc finger CCCC motif
 F;105-141/Region: zinc finger CCCC motif

Query Match 79.2%; Score 38; DB 1; Length 158;
 Best Local Similarity 77.8%; Pred. No. 1.8;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
 ||||| |||
 Db 44 VYEFAFSDL 52

RESULT 7
 W6WL18
 E6 protein - human papillomavirus type 18
 C;Species: human papillomavirus type 18
 C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
 C;Accession: A26165; G26251
 R;Seedorf, K.; Oltersdorf, T.; Kraemer, G.; Roewekamp, W.
 EMBO J. 6, 139-144, 1987
 A;Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 16)
 A;Reference number: A91068; MUID:87218459; PMID:3034571
 A;Accession: A26165
 A;Molecule type: DNA
 A;Residues: 1-158 <SEE>
 A;Cross-references: UNIPROT:P06463; GB:X04773; NID:g60876; PIDN:CAA28466.1; PID:g60877
 J. Mol. Biol. 193, 599-608, 1987
 A;Title: Nucleotide sequence and comparative analysis of the human papillomavirus type 16
 A;Reference number: A92937; MUID:87283882; PMID:3039146
 A;Accession: G26251

A:Molecule type: DNA
A:Residues: 1-158 <COL>
A:Cross-references: GB:X05015; NID:g60975; PIDN:CAA28664.1; PID:g60976
R:Mareshewski, G.; Banks, L.; Wu-Liao, J.; Spence, P.; Pim, D.; Crawford, L.
J. Gen. Virol. 67, 1909-1916, 1986
A:Title: The expression of human papillomavirus type 18 E6 protein in bacteria and the p
A:Contents: annotation; identification of the protein
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; transforming protein; zinc finger
F:32-68/Region: zinc finger CCCC motif
F:105-141/Region: zinc finger CCCC motif

Query Match 77.1%; Score 37; DB 1; Length 158;
Best Local Similarity 66.7%; Pred. No. 2.8;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
Db 44 VPEFAFKDL 52

RESULT 8
WVLRP
E6 protein - human papillomavirus type ME180 (provirus)
C:Species: human papillomavirus type ME180
A:Note: host Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: C40509
R:Reuter, S.; Dellus, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.
J. Virol. 65, 5564-5568, 1991
A:Title: Characterization of a novel human papillomavirus DNA in the cervical carcinoma
A:Reference number: A40509; MUID:91374616; PMID:1716694
A:Accession: C40509
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-158 <REU>
A:Cross-references: UNIPROT:P27962; GB:M73258
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:32-68/Region: zinc finger CCCC motif
F:105-141/Region: zinc finger CCCC motif

Query Match 77.1%; Score 37; DB 1; Length 158;
Best Local Similarity 77.8%; Pred. No. 2.8;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
Db 44 VVEFAFGDL 52

RESULT 9
A81153
type I restriction enzyme-related protein NMB0833 [imported] - Neisseria meningitidis (s
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: A81153
R:Tetelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.B.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.B.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
xi, H.; Qin, H.; Vamathevan, J.; Gall, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: A81153
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-128 <TET>
A:Cross-references: UNIPROT:Q9JZ29; GB:AE002436; GB:AE002098; NID:g7226062; PIDN:AAF4124
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0833

Query Match 75.0%; Score 36; DB 2; Length 128;
Best Local Similarity 75.0%; Pred. No. 3.6;
Matches 6; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 VYDFAFRDL 8
Db 108 IYDFAFDD 115

RESULT 10
B69230
conserved hypothetical protein MTH972 - Methanobacterium thermoautotrophicum (strain D
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: B69230
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiawani, T.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: B69230
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-246 <MTH>
A:Cross-references: UNIPROT:O27053; GB:AE000666; NID:g26222069; PIDN:AA8854
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH972

Query Match 72.9%; Score 35; DB 2; Length 246;
Best Local Similarity 87.5%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YDFAFRDL 9
Db 45 YDEAFRDL 52

RESULT 11
A97919
3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) [imported] - Streptococcus pneu
C:Species: Streptococcus pneumoniae
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C:Accession: A97919
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.;
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.;
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: A97919
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-324 <KUR>
A:Cross-references: UNIPROT:Q93NA1; GB:AE007317; PIDN:AAK99181.1; PID:gl5457938; GSPDB
C:Genetics:
A:Gene: fabH
C:Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase III
C:Keywords: acyltransferase

Query Match 72.9%; Score 35; DB 2; Length 324;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
Db 217 VDFAFRDLV 225

RESULT 12

C95048
3-oxoacyl-[acyl-carrier-protein] synthase III [imported] - Streptococcus pneumoniae (str
C/Species: Streptococcus pneumoniae
C/Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C/Accession: C95048
R/Tetelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Unyam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A/Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A/Title: Complete Genome Sequence of a Virulent isolate of Streptococcus pneumoniae.
A/Reference number: A95000; MUID:21357209; PMID:11463916
A/Accession: C95048
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-324 <KUR>
A/Cross-references: UNIPROT:Q9JNA1; GB:AE005672; PIDN:AAK74580.1; PID:gi4971886; GSPDB:C
A/Experimental source: strain TIGR4
C/Genetics:
A/Gene: SP0417
C/Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase III

Query Match 72.9%; Score 35; DB 2; Length 324;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
|:|:|:|:
Db 217 VFDFAIRDV 225

RESULT 13
A97295
fusion of Uroporphyrinogen-III methylase related protein and MAZG family protein, YABN B
C/Species: Clostridium acetobutylicum
C/Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-May-2004
C/Accession: A97295
R/Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A/Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A/Reference number: A96900; MUID:21359325; PMID:21359325
A/Accession: A97295
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-483 <KUR>
A/Cross-references: GB:AE001437; PIDN:AAK81148.1; PID:gi15026284; GSPDB:GN00168
A/Experimental source: Clostridium acetobutylicum ATCC824
C/Genetics:
A/Gene: CAC3212
C/Superfamily: bifunctional tetrapyrrole methylase/MazG NTP pyrophosphohydrolase; beta-l

Query Match 72.9%; Score 35; DB 2; Length 483;
Best Local Similarity 77.8%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
|:|:|:|:
Db 65 VYDFIARDL 73

RESULT 14
W6WL31
E6 protein - human papillomavirus type 31
C/Species: human papillomavirus type 31
A/Note: host Homo sapiens (man)
C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C/Accession: A32444
R/Goldsborough, M.D.; Disilvestre, D.; Temple, G.F.; Lorincz, A.T.
Virology 171, 306-311, 1989
A/Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associ
A/Reference number: A94398; MUID:89299478; PMID:2545036
A/Accession: A32444

A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-149 <GOL>
A/Cross-references: UNIPROT:P17386; GB:J04353; NID:g333048; PIDN:AAA46950.1; PID:g45991
C/Comment: This protein may be involved in the oncogenic potential of this virus.
C/Superfamily: papillomavirus E6 protein
C/Keywords: DNA binding; early protein; zinc finger
F/30-66/Region: zinc finger CCCC motif
F/103-139/Region: zinc finger CCCC motif

Query Match 70.8%; Score 34; DB 1; Length 149;
Best Local Similarity 77.8%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
|:|:|:|:
Db 42 VLDFAFITDL 50

RESULT 15
S36527
E6 protein - human papillomavirus type 53
C/Species: human papillomavirus type 53
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C/Accession: S36527
R/Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A/Description: Primer-directed sequencing of human papillomavirus types.
A/Reference number: S36469
A/Accession: S36527
A/Molecule type: DNA
A/Residues: 1-154
A/Cross-references: UNIPROT:P36815; EMBL:X74482; NID:g397046; PIDN:CAAS2591.1; PID:g397
C/Superfamily: papillomavirus E6 protein
C/Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 70.8%; Score 34; DB 2; Length 154;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
|:|:|:|:
Db 46 VYNFAITDL 54

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Job time : 12.2747 secs

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OM protein - protein search, using sw model

Run on: June 29, 2005, 05:18:25 ; Search time 53.8517 Seconds
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Title: US-08-170-344-67
Perfect score: 48
Sequence: 1 VYDFAFRDL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	9	17 US-10-751-845-84	Sequence 84, Appl
2	48	100.0	10	14 US-10-239-313A-291	Sequence 291, Appl
3	48	100.0	10	17 US-10-484-063-5	Sequence 5, Appl
4	48	100.0	10	17 US-10-751-845-92	Sequence 92, Appl
5	48	100.0	10	17 US-10-751-845-94	Sequence 94, Appl
6	48	100.0	15	17 US-10-484-063-4	Sequence 4, Appl
7	48	100.0	22	17 US-10-858-384-6	Sequence 6, Appl
8	48	100.0	24	17 US-10-751-845-65	Sequence 65, Appl
9	48	100.0	117	17 US-10-751-845-126	Sequence 126, Appl
10	48	100.0	151	14 US-10-177-390-6	Sequence 6, Appl
11	48	100.0	151	17 US-10-484-063-20	Sequence 20, Appl

12	48	100.0	151	17	US-10-484-063-27	Sequence 27, Appl
13	48	100.0	158	17	US-10-858-384-2	Sequence 2, Appl
14	48	100.0	158	17	US-10-367-057-16	Sequence 16, Appl
15	48	100.0	171	16	US-10-472-724-2	Sequence 2, Appl
16	48	100.0	236	17	US-10-751-845-157	Sequence 157, App
17	48	100.0	237	17	US-10-751-845-158	Sequence 158, App
18	48	100.0	261	17	US-10-751-845-160	Sequence 160, App
19	48	100.0	266	9	US-09-367-309A-1	Sequence 1, Appl
20	48	100.0	273	13	US-10-000-903-4	Sequence 4, Appl
21	48	100.0	273	17	US-10-899-771-4	Sequence 4, Appl
22	48	100.0	292	13	US-10-000-903-10	Sequence 10, Appl
23	48	100.0	292	17	US-10-899-771-10	Sequence 10, Appl
24	48	100.0	371	13	US-10-000-903-6	Sequence 6, Appl
25	48	100.0	371	17	US-10-899-771-6	Sequence 6, Appl
26	48	100.0	390	13	US-10-000-903-14	Sequence 14, Appl
27	48	100.0	390	17	US-10-899-771-14	Sequence 14, Appl
28	48	100.0	536	15	US-10-367-095-10	Sequence 10, Appl
29	48	100.0	536	15	US-10-368-046-10	Sequence 10, Appl
30	48	100.0	536	16	US-10-367-367-10	Sequence 10, Appl
31	48	100.0	536	17	US-10-918-337-10	Sequence 10, Appl
32	44	91.7	9	17	US-10-751-845-163	Sequence 163, App
33	44	91.7	15	16	US-10-476-570-28	Sequence 28, Appl
34	44	91.7	15	16	US-10-476-570-29	Sequence 29, Appl
35	37	77.1	9	17	US-10-751-845-89	Sequence 89, Appl
36	37	77.1	158	16	US-10-800-023-27	Sequence 27, Appl
37	37	77.1	172	16	US-10-472-724-6	Sequence 6, Appl
38	37	77.1	278	13	US-10-000-903-21	Sequence 21, Appl
39	37	77.1	278	17	US-10-899-771-21	Sequence 21, Appl
40	37	77.1	383	13	US-10-000-903-23	Sequence 23, Appl
41	37	77.1	383	17	US-10-899-771-23	Sequence 23, Appl
42	36	75.0	504	14	US-10-163-198-41	Sequence 41, Appl
43	36	75.0	1032	15	US-10-282-122A-65229	Sequence 65229, A
44	35	72.9	321	11	US-09-758-759-111	Sequence 111, App
45	35	72.9	324	9	US-09-815-242-13357	Sequence 13357, A

ALIGNMENTS

RESULT 1
US-10-751-845-84
; Sequence 84, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; PRIOR FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-84

Query Match 100.0%; Score 48; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VYDFAFRDL 9
Db 1 VYDFAFRDL 9

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RESULT 2
US-10-239-313A-291
; Sequence 291, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
; TITLE OF INVENTION: OF A PHARMACEUTICAL INTEREST COMPRISING AT ITS
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 291
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-239-313A-291

Query Match      100.0%; Score 48; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
Db 2 VYDFAFRDL 10

RESULT 3
US-10-484-063-5
; Sequence 5, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-5

Query Match      100.0%; Score 48; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
Db 1 VYDFAFRDL 9

RESULT 4
US-10-751-845-92
```

```
; Sequence 92, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTOPE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-92
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```
Query Match      100.0%; Score 48; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 VYDFAFRDL 9
Db 2 VYDFAFRDL 10
```

```
RESULT 5
US-10-751-845-94
; Sequence 94, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTOPE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 94
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-94
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```
Query Match      100.0%; Score 48; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 VYDFAFRDL 9
Db 1 VYDFAFRDL 9
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RESULT 6
US-10-484-063-4
; Sequence 4, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
```

```
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US/10/484,063
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-4

Query Match      100.0%; Score 48; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
Db 7 VYDFAFRDL 15

RESULT 7
US-10-858-384-6
; Sequence 6, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; FILE REFERENCE: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 6
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
US-10-858-384-6

Query Match      100.0%; Score 48; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
Db 4 VYDFAFRDL 12

RESULT 8
US-10-751-845-65
; Sequence 65, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
```

```
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTOPE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-65

Query Match      100.0%; Score 48; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
Db 6 VYDFAFRDL 14

RESULT 9
US-10-751-845-126
; Sequence 126, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTOPE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-126

Query Match      100.0%; Score 48; DB 17; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
Db 26 VYDFAFRDL 34

RESULT 10
US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerps Innovatiecentrum
```

```
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides By Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6

Query Match      100.0%; Score 48; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VYDFAFRDL 9
Db      42 VYDFAFRDL 50

RESULT 11
US-10-484-063-20
; Sequence 20, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-20

Query Match      100.0%; Score 48; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VYDFAFRDL 9
Db      42 VYDFAFRDL 50

RESULT 12
US-10-484-063-27
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
```

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; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-484-063-27

Query Match      100.0%; Score 48; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VYDFAFRDL 9
Db      42 VYDFAFRDL 50

RESULT 13
US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match      100.0%; Score 48; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VYDFAFRDL 9
Db      49 VYDFAFRDL 57

RESULT 14
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraSequist version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-367-057-16

Query Match 100.0%; Score 48; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYDFAFRDL 9
Db 49 VYDFAFRDL 57

RESULT 15

US-10-472-724-2

; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct

US-10-472-724-2

Query Match 100.0%; Score 48; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VYDFAFRDL 9
Db 54 VYDFAFRDL 62

Search completed: June 29, 2005, 05:48:13
Job time : 53.8517 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:37:59 ; Search time 16.8626 Seconds
(without alignments)
39.842 Million cell updates/sec

Title: US-08-170-344-67
Perfect score: 48
Sequence: 1 VYDFAFRDL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	48	100.0	9	3	US-08-159-339A-246
2	48	100.0	9	3	Sequence 246, App
3	48	100.0	14	1	US-07-909-122-4
4	48	100.0	22	4	US-09-980-523A-6
5	48	100.0	23	4	US-09-601-729-276
6	48	100.0	158	4	US-09-980-523A-2
7	48	100.0	162	1	US-08-316-239B-3
8	48	100.0	162	1	US-08-316-239B-4
9	48	100.0	172	3	US-08-860-165-14
10	48	100.0	172	3	US-09-359-382-14
11	48	100.0	182	1	US-08-117-083-10
12	48	100.0	266	3	US-08-860-165-10
13	48	100.0	266	3	US-09-359-382-10
14	48	100.0	266	4	US-09-367-309A-1
15	48	100.0	273	3	US-09-485-885-4
16	48	100.0	292	3	US-09-485-885-10
17	48	100.0	371	3	US-09-485-885-6
18	48	100.0	390	3	US-09-485-885-14
19	43	89.6	342	4	US-08-328-352-5375
20	38	79.2	20	2	US-08-934-915-161
21	37	77.1	158	2	US-08-247-904B-10
22	37	77.1	158	3	US-08-767-942A-19
23	37	77.1	271	1	US-08-117-083-14
24	37	77.1	278	3	US-09-485-885-21
25	37	77.1	383	3	US-09-485-885-23
26	35	72.9	188	4	US-09-583-110-3915
27	35	72.9	290	4	US-09-248-796A-17543

Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 8, Appli
Sequence 36699, A
Sequence 51916, A
Sequence 5878, Ap
Sequence 4066, Ap
Sequence 6351, Ap
Sequence 4634, Ap
Sequence 44, Appli
Sequence 46, Appli
Sequence 41497, A
Sequence 16878, A
Sequence 17939, A
Sequence 18343, A
Sequence 11, Appli

US-08-746-797-2
US-08-927-387-2
US-08-918-058-2
US-09-810-836B-8
US-09-270-767-36699
US-09-270-767-51916
US-09-107-532A-5878
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US-09-583-110-4066
US-09-543-681A-6351
US-09-107-532A-4634
US-09-452-239-44
US-09-452-239-46
US-09-270-767-41497
US-09-252-991A-16878
US-09-248-796A-17939
US-09-248-796A-18343
US-08-804-227C-11

ALIGNMENTS

RESULT 1
US-08-159-339A-246
; Sequence 246, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Cellis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 246:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-246

Query Match 100.0%; Score 48; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
Db 1 VYDFAFRDL 9

RESULT 2

US-08-159-339A-564
; Sequence 564, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-Seq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 564:

SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-564

Query Match 100.0%; Score 48; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
Db 1 VYDFAFRDL 9

RESULT 3

US-07-909-122-4

; Sequence 4, Application US/07909122
; Patent No. 5415995
; GENERAL INFORMATION:
; APPLICANT: SCHOOLNIK, GARY K.
; APPLICANT: PALEFSKY, JOEL M.
; TITLE OF INVENTION: DIAGNOSTIC PEPTIDES OF HUMAN PAPILLOMA
; TITLE OF INVENTION: VIRUS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/909,122
FILING DATE: 19920706
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: BENZ, WILLIAM H.
REGISTRATION NUMBER: 25,952
REFERENCE/DOCKET NUMBER: 28600-20105.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-909-122-4

Query Match 100.0%; Score 48; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
Db 5 VYDFAFRDL 13

RESULT 4

US-09-980-523A-6
; Sequence 6, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: WO/91 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6

; LENGTH: 22
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-6

Query Match 100.0%; Score 48; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0097;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
| | | | | | | |
Db 4 VYDFAFRDL 12

RESULT 5

US-09-601-729-276
; Sequence 276, Application US/09601729
; Patent No. 6683052

GENERAL INFORMATION:

; APPLICANT: THIAM, KADER
; APPLICANT: AURIAULT, CLAUDE
; APPLICANT: GRAS-MASSE, HELENE
; APPLICANT: LOING, ESTELLE
; APPLICANT: VERAERDE, CLAUDE
; APPLICANT: GUILLET, JEAN GERARD
; TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES
; FILE REFERENCE: USB-97-AU-IN
; CURRENT APPLICATION NUMBER: US/09/601,729
; CURRENT FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: PCT/FR99/00259
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 98 01439
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 276
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-601-729-276

Query Match 100.0%; Score 48; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.01; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
| | | | | | | |
Db 5 VYDFAFRDL 13

RESULT 6

US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763

GENERAL INFORMATION:

; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; FILE REFERENCE: WO91 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012

; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 48; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.079;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
| | | | | | | |
Db 49 VYDFAFRDL 57

RESULT 7

US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5678509

GENERAL INFORMATION:

; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 100.0%; Score 48; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.081;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9
| | | | | | | |
Db 49 VYDFAFRDL 57

RESULT 8

US-08-316-239B-4

; Sequence 4, Application US/08316239B
; Patent No. 5679509

; GENERAL INFORMATION:

; APPLICANT: Wheeler, Cosette M.

; APPLICANT: Parmenter, Cheryl A.

; TITLE OF INVENTION: Methods and a Diagnostic Aid for

; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an

; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and

; TITLE OF INVENTION: Cervical Cancer

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jagtiani & Associates

; STREET: 6126 Rocky Way Court

; CITY: Centreville

; STATE: VA

; COUNTRY: USA

; ZIP: 20120-3400

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/316.239B

; FILING DATE: 30-SEP-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Jagtiani, Ajay A.

; REGISTRATION NUMBER: 35,205

; REFERENCE/DOCKET NUMBER: UNWE-0001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 817-9453

; TELEFAX: (703) 803-9387

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 162 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: not relevant

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

US-08-316-239B-4

Query Match 100.0%; Score 48; DB 1; Length 162;

Best Local Similarity 100.0%; Pred. No. 0.081;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9

Db 49 VYDFAFRDL 57

RESULT 9

US-08-860-165-14

; Sequence 14, Application US/08860165A

; Patent No. 6004557

; GENERAL INFORMATION:

; APPLICANT: EDWARDS, Stirling John

; APPLICANT: COX, John Cooper

; APPLICANT: WEBB, Elizabeth Ann

; APPLICANT: FRAZER, Ian

; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

; FILE REFERENCE: 17227/130

; CURRENT APPLICATION NUMBER: US/08/860.165A

; CURRENT FILING DATE: 1997-09-22

; EARLIER APPLICATION NUMBER: PCT/AU95/00868

; EARLIER FILING DATE: 1995-12-20

; EARLIER APPLICATION NUMBER: AU PN0157

; EARLIER FILING DATE: 1994-12-20

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14

; LENGTH: 172

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion

US-08-860-165-14

Query Match 100.0%; Score 48; DB 3; Length 172;

Best Local Similarity 100.0%; Pred. No. 0.087;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9

Db 118 VYDFAFRDL 126

RESULT 10

US-09-359-382-14

; Sequence 14, Application US/09359382

; Patent No. 6306397

; GENERAL INFORMATION:

; APPLICANT: EDWARDS, Stirling John

; APPLICANT: COX, John Cooper

; APPLICANT: WEBB, Elizabeth Ann

; APPLICANT: FRAZER, Ian

; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

; FILE REFERENCE: 017227/0148

; CURRENT APPLICATION NUMBER: US/09/359,382

; CURRENT FILING DATE: 1999-07-23

; EARLIER APPLICATION NUMBER: US 08/860,165

; EARLIER FILING DATE: 1997-09-22

; EARLIER APPLICATION NUMBER: PCT/AU95/00868

; EARLIER FILING DATE: 1995-12-20

; EARLIER APPLICATION NUMBER: AU PN0157/94

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14

; LENGTH: 172

; TYPE: PRT

; ORGANISM: Human papillomavirus type 16

US-09-359-382-14

Query Match 100.0%; Score 48; DB 3; Length 172;

Best Local Similarity 100.0%; Pred. No. 0.087;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VYDFAFRDL 9

Db 118 VYDFAFRDL 126

RESULT 11

US-08-117-083-10

; Sequence 10, Application US/08117083

; Patent No. 5719054

; GENERAL INFORMATION:

; APPLICANT: Boursnell, Michael E.

; APPLICANT: Inglis, Stephen C.

; APPLICANT: Munro, Alan J.

; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human

; TITLE OF INVENTION: Papilloma Virus Proteins

; NUMBER OF SEQUENCES: 70

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Walter H. Dreger

; STREET: 4 Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
; OTHER INFORMATION: /note= "Xaa refers to stop codon in
; the open reading frame."
US-08-117-083-10
```

```
Query Match 100.0%; Score 48; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.092;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 VYDFAFRDL 9
| | | | |
Db 50 VYDFAFRDL 58
```

```
RESULT 12
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10
```

```
Query Match 100.0%; Score 48; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 VYDFAFRDL 9
| | | | |
Db 49 VYDFAFRDL 57
```

```
RESULT 13
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10
```

```
Query Match 100.0%; Score 48; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 VYDFAFRDL 9
| | | | |
Db 49 VYDFAFRDL 57
```

```
RESULT 14
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1
```

```
Query Match 100.0%; Score 48; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 VYDFAFRDL 9
| | | | |
Db 49 VYDFAFRDL 57
```

```
RESULT 15
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
```

```
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match      100.0%; Score 48; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VYDFAFRDL 9
Db      155 VYDFAFRDL 163
```

Search completed: June 29, 2005, 01:44:24
Job time : 16.9126 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:32:21 ; Search time 11.2747 Seconds
(without alignments)
76.805 Million cell updates/sec

Title: US-08-170-344-66
Perfect score: 46
Sequence: 1 LLRREVYDF 9
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	158	1 W6WLS	protein E6 - human
2	36	78.3	299	2 C75514	conserved hypothetical
3	36	78.3	458	2 E95528	cobyrinic acid a,c
4	36	78.3	635	2 T27014	hypothetical prote
5	35	76.1	254	2 B81293	hypothetical prote
6	35	76.1	449	2 E86567	replicative DNA he
7	35	76.1	449	2 D72056	replicative DNA he
8	35	76.1	468	2 E81610	replicative DNA he
9	35	76.1	472	2 H81665	replicative DNA he
10	35	76.1	472	2 G71503	probable replicati
11	35	76.1	487	2 T05117	hypothetical prote
12	35	76.1	804	2 B48687	ribonucleoside-dip
13	35	76.1	847	2 A49412	ribonucleoside-dip
14	35	76.1	991	2 T01377	hypothetical prote
15	35	76.1	1117	2 C85018	hypothetical prote
16	34	73.9	149	1 W6WLS3	E6 protein - human
17	34	73.9	149	1 W6WLS3	E6 protein - human
18	34	73.9	149	1 W6WLS8	E6 protein - human
19	34	73.9	190	2 G70231	conserved hypothet
20	34	73.9	322	2 B81001	heptosyltransferas
21	34	73.9	461	2 JC4556	alcaligin synthesi
22	34	73.9	469	2 D70542	hypothetical prote
23	34	73.9	479	2 A71273	hypothetical prote
24	34	73.9	582	2 I50224	erythroid cell tra
25	34	73.9	660	2 T09537	xanthophyll epoxid
26	34	73.9	663	2 S69548	zeaxanthin epoxida
27	34	73.9	669	2 T07754	probable RNA helic
28	34	73.9	737	2 S63453	aconitate hydratase
29	34	73.9	778	2 S50387	aconitate hydratase

ALIGNMENTS

RESULT 1

W6WLS
Protein E6 - human papillomavirus type 16
C:Species: human papillomavirus type.16
C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C:Accession: A03682; T10427
R:Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
Virology 145, 181-185, 1985
A:Title: Human papillomavirus type 16 DNA sequence.
A:Reference number: A22355; MUID:85246220; PMID:2990099
A:Accession: A03682
A:Molecule type: DNA
A:Residues: 1-158 <SEE>
A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333033
R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level of transcriptional activation.
A:Reference number: Z17014; MUID:91162763; PMID:1848319
A:Accession: T10427
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-158 <KEN>
A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
C:Genetics:
A:Gene: E6
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:37-73/Region: zinc finger CCCC motif
F:110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 46; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. NO. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLRREVYDF 9
| | | | | | | |
Db 44 LLRREVYDF 52

RESULT 2

C75514
conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: C75514
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: C75514

```

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-299 <WHI>
A:Cross-references: UNIPROT:Q9RX35; GB:AE001907; GB:AE000513; NID:g6458162; PIDN:AAF1006
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0480
A:Map position: 1
C:Superfamily: conserved hypothetical protein MJ1157

Query Match      78.3%; Score 36; DB 2; Length 299;
Best Local Similarity 77.8%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLREYVDF 9
Db 256 LLRELYDF 264

RESULT 3
B69528
cobyrinic acid a,c-diamide synthase (cbiA) homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: E69528
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: E69528
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-458 <KLE>
A:Cross-references: UNIPROT:O28054; GB:AE000951; GB:AE000782; NID:g2689274; PIDN:AAB8902
C:Superfamily: cobyric acid a,c-diamide synthase

Query Match      78.3%; Score 36; DB 2; Length 458;
Best Local Similarity 75.0%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LRREYVDF 9
Db 317 LRNEIYDF 324

RESULT 4
T27014
hypothetical protein Y48E1B.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T27014
R:McMurray, A.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z20299
A:Accession: T27014
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-635 <WIL>
A:Cross-references: UNIPROT:O18199; EMBL:Z93393; PIDN:CAB07691.1; GSPDB:GN000020; CESP:Y4
A:Experimental source: clone Y48E1B
C:Genetics:
A:Gene: CESP:Y48E1B.5
A:Map position: 2
A:Introns: 77/3; 140/3; 183/2; 209/2; 236/2; 296/2; 413/3; 437/1; 473/3; 510/3; 525/1; 5
C:Superfamily: Caenorhabditis elegans hypothetical protein Y48E1B.5

Query Match      78.3%; Score 36; DB 2; Length 635;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 LLREYVDF 9
Db 413 LLNREIPDF 421

```

RESULT 5

```

B81293
hypothetical protein Cj1467 [imported] - Campylobacter jejuni (strain NCTC 11168)
C:Species: Campylobacter jejuni
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: B81293
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilli
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barre
Nature 403, 665-668, 2000
A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hy
A:Reference number: A81250; MUID:20150912; PMID:10688204
A:Accession: B81293
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-254 <PAR>
A:Cross-references: UNIPROT:Q9PMJ3; GB:AL139078; GB:AL111169; NID:g6968723; PIDN:CAB738
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: Cj1467

```

```

Query Match      76.1%; Score 35; DB 2; Length 254;
Best Local Similarity 55.6%; Pred. No. 15;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 LLREYVDF 9
Db 207 LLKKRIYDY 215

```

RESULT 6

```

E86567
replicative DNA helicase [imported] - Chlamydophila pneumoniae (strain J138)
C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E86567
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; I
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: E86567
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-449 <STO>
A:Cross-references: UNIPROT:Q9Z7T8; GB:BA000008; NID:g8978988; PIDN:BA098823.1; GSPDB:G
A:Experimental source: strain J138
C:Genetics:
A:Gene: dnaB
C:Superfamily: phage P22 gene 12 protein

```

```

Query Match      76.1%; Score 35; DB 2; Length 449;
Best Local Similarity 87.5%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 LLREYVD 8
Db 398 LLREYVD 405

```

RESULT 7

```

D72056
replicative DNA helicase - Chlamydophila pneumoniae (strain CWL029)
C:Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: D72056
R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.

```

A;Reference number: A72000; MUID:99206606; PMID:10192388

A;Accession: D72056

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-449 <ARN>

A;Cross-references: UNIPROT:Q9Z7T8; GB:AE001646; GB:AE001363; NID:G4376910; PIDN:AAI1875

A;Experimental source: strain CWL029

C;Genetics:

A;Gene: dnaB

C;Superfamily: phage P22 gene 12 protein

Query Match 76.1%; Score 35; DB 2; Length 449;

Best Local Similarity 87.5%; Pred. No. 28;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLREYVD 8

Db 398 LLREYVD 405

|||||

RESULT 8

E81610

replicative DNA helicase CP0131 [imported] - Chlamydophila pneumoniae (strain AR39)

C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C;Accession: E81610

R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,

C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,

Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: E81610

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-468 <REA>

A;Cross-references: UNIPROT:Q9K2D6; GB:AE002174; GB:AE002161; NID:G7189059; PIDN:AAF3801

A;Experimental source: strain AR39, HL cells

C;Genetics:

A;Gene: CP0131

C;Superfamily: phage P22 gene 12 protein

Query Match 76.1%; Score 35; DB 2; Length 468;

Best Local Similarity 87.5%; Pred. No. 29;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLREYVD 8

Db 417 LLREYVD 424

|||||

RESULT 9

H81665

replicative DNA helicase TC0784 [imported] - Chlamydia muridarum (strain Nigg)

C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C;Accession: H81665

R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heideberg, J.F.; White, O.; Hickey,

C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,

Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: H81665

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-472 <TET>

A;Cross-references: UNIPROT:Q9PJP4; GB:AE002346; GB:AE002160; NID:G7190805; PIDN:AAF3958

A;Experimental source: strain Nigg (MoPn)

C;Genetics:

A;Gene: TC0784

C;Superfamily: phage P22 gene 12 protein

Query Match 76.1%; Score 35; DB 2; Length 472;

Best Local Similarity 87.5%; Pred. No. 30;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLREYVD 8

Db 421 LLREYVD 428

|||||

RESULT 10

G71503

probable replicative DNA helicase - Chlamydia trachomatis (serotype D, strain UW3/Cx)

C;Species: Chlamydia trachomatis

C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004

C;Accession: G71503

R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,

Science 282, 754-759, 1998

A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra

A;Reference number: A71570; MUID:9900809; PMID:9784136

A;Accession: G71503

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-472 <ARN>

A;Cross-references: UNIPROT:O84505; GB:AE001323; GB:AE001273; NID:G3328931; PIDN:AAC680

A;Experimental source: serotype D, strain UN-3/Cx

C;Genetics:

A;Gene: dnaB

C;Superfamily: phage P22 gene 12 protein

Query Match 76.1%; Score 35; DB 2; Length 472;

Best Local Similarity 87.5%; Pred. No. 30;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLREYVD 8

Db 421 LLREYVD 428

|||||

RESULT 11

T05117

hypothetical protein F7H19.40 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C;Accession: T05117

R;Bavan, M.; Peters, S.A.; van Staveren, M.; Dirks, W.; Stiekema, W.; Bancroft, I.; Me

submitted to the Protein Sequence Database, July 1998

A;Reference number: Z15399

A;Accession: T05117

A;Molecule type: DNA

A;Residues: 1-487 <BEV>

A;Cross-references: UNIPROT:O82736; EMBL:AL031018

A;Experimental source: cultivar Columbia; BAC clone F7H19

C;Genetics:

A;Map position: 4

A;Introns: 59/1; 112/1; 141/1; 185/2; 222/3; 239/3; 272/2; 297/3; 318/3; 343/3; 363/2;

A;Note: F7H19.40

Query Match 76.1%; Score 35; DB 2; Length 487;

Best Local Similarity 87.5%; Pred. No. 31;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLREYVD 8

Db 65 LLREYVD 72

|||||

RESULT 12

B48687

ribonucleoside-diphosphate reductase (EC 1.17.4.1) large chain - malaria parasite (Plas

C;Species: Plasmodium falciparum

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004

C;Accession: B48687

R;Rubin, H.; Salem, J.S.; Li, L.S.; Yang, F.; Mama, S.; Wang, Z.; Fisher, A.; Hamann, C

Proc. Natl. Acad. Sci. U.S.A. 90, 9280-9284, 1993

A;Title: Cloning, sequence determination, and regulation of the ribonucleotide reductas

A;Reference number: A48687; MUID:94022359; PMID:8415692

A;Accession: B48687

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-804 <RUB>

A;Cross-references: UNIPROT:P50647; GB:L22057; NID:g349791; PIDN:AAA29755.1; PID:g349792

C;Superfamily: herpesvirus ribonucleoside-diphosphate reductase large chain

C;Keywords: deoxyribonucleoside biosynthesis; oxidoreductase; redox-active disulfide

F;1217-442,799-802/Disulfide bonds: redox-active #status predicted

F;425,429/Active site: Asn, Glu #status predicted

F;427/Active site: Cys (cysteine thiol radical intermediate) #status predicted

Query Match 76.1%; Score 35; DB 2; Length 804;

Best Local Similarity 66.7%; Pred. No. 53;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLREVDYDF 9

Db 114 LISKEVDYDF 122

RESULT 13

A49412 ribonucleoside-diphosphate reductase (EC 1.17.4.1) large chain - malaria parasite (Plasm

C;Species: Plasmodium falciparum

C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A49412

R;Chakrabarti, D.; Schuster, S.M.; Chakrabarti, R.

Proc. Natl. Acad. Sci. U.S.A. 90, 12020-12024, 1993

A;Title: Cloning and characterization of subunit genes of ribonucleotide reductase, a ce

A;Reference number: A49412; MUID:94089761; PMID:8265664

A;Accession: A49412

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-847 <CHA>

A;Cross-references: UNIPROT:Q8IL94

A;Experimental source: HB3, Dd2

A;Note: sequence extracted from NCBI backbone (NCBIP:141048)

C;Superfamily: herpesvirus ribonucleoside-diphosphate reductase large chain

C;Keywords: oxidoreductase

Query Match

Best Local Similarity 76.1%; Score 35; DB 2; Length 847;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LLREVDYDF 9

Db 154 LISKEVDYDF 162

RESULT 14

T01377

hypothetical protein F3D13.1 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004

C;Accession: T01377

R;Cordeiro, M.; Wollam, C.; Pape, K.

submitted to the EMBL Data Library, May 1998

A;Description: The sequence of A. thaliana F3D13.

A;Reference number: Z14309

A;Accession: T01377

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-991 <COR>

A;Cross-references: UNIPROT:Q81330; EMBL:AF069300; NID:g3193305; PID:g3193306

A;Experimental source: cultivar Columbia

C;Genetics:

A;Map position: 4

A;introns: 450/1

A;Note: F3D13.1

Query Match

Best Local Similarity 76.1%; Score 35; DB 2; Length 991;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2005, 23:28:22 ; Search time 54.2473 Seconds
(without alignments)
84.958 Million cell updates/sec

Title: US-08-170-344-66
Perfect score: 46
Sequence: 1 LLREVVYDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues 1612378
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	99	2 Q919B2	Q919B2 human papil
2	46	100.0	130	2 Q919B4	Q919B4 human papil
3	46	100.0	130	2 Q919B8	Q919B8 human papil
4	46	100.0	130	2 Q919C0	Q919C0 human papil
5	46	100.0	130	2 Q919C2	Q919C2 human papil
6	46	100.0	130	2 Q919C8	Q919C8 human papil
7	46	100.0	138	2 Q919D2	Q919D2 human papil
8	46	100.0	143	2 Q919B6	Q919B6 human papil
9	46	100.0	143	2 Q919C4	Q919C4 human papil
10	46	100.0	151	2 Q12335	Q12335 human papil
11	46	100.0	151	2 Q12336	Q12336 human papil
12	46	100.0	151	2 Q76TS0	Q76TS0 human papil
13	46	100.0	151	2 Q77816	Q77816 human papil
14	46	100.0	151	2 Q77816	Q77816 human papil
15	46	100.0	151	2 Q77JC7	Q77JC7 human papil
16	46	100.0	151	2 Q77ZJ5	Q77ZJ5 human papil
17	46	100.0	151	2 Q80963	Q80963 human papil
18	46	100.0	151	2 Q80966	Q80966 human papil
19	46	100.0	151	2 Q89640	Q89640 human papil
20	46	100.0	151	2 Q89648	Q89648 human papil
21	46	100.0	151	2 Q89708	Q89708 human papil
22	46	100.0	151	2 Q89755	Q89755 human papil
23	46	100.0	151	2 Q89852	Q89852 human papil
24	46	100.0	151	2 Q89887	Q89887 human papil
25	46	100.0	151	2 Q8B564	Q8B564 human papil
26	46	100.0	151	2 Q8BB19	Q8BB19 human papil
27	46	100.0	151	2 Q8BB20	Q8BB20 human papil
28	46	100.0	151	2 Q8BB21	Q8BB21 human papil
29	46	100.0	151	2 Q8WC3	Q8WC3 human papil
30	46	100.0	151	2 Q9W931	Q9W931 human papil
31	46	100.0	151	2 Q9WMP2	Q9WMP2 human papil

32 46 100.0 151 2 Q9WMP3 human papil
33 46 100.0 151 2 Q9WMP4 human papil
34 46 100.0 151 2 Q9WMP5 human papil
35 46 100.0 158 1 VE6_HPV16 human papil
36 46 100.0 158 2 Q8JMU8 human papil
37 46 100.0 158 2 Q8QHNO human papil
38 46 100.0 158 2 Q8QHP5 human papil
39 46 100.0 158 2 Q8QHT0 human papil
40 46 100.0 158 2 Q8QRD5 human papil
41 46 100.0 158 2 Q8QRD6 human papil
42 46 100.0 158 2 Q8QRD7 human papil
43 46 100.0 158 2 Q8QRD8 human papil
44 46 100.0 158 2 Q8QRD9 human papil
45 46 100.0 158 2 Q8QRE0 human papil

ALIGNMENTS

RESULT 1

Q919B2 PRELIMINARY; PRT; 99 AA.
AC Q919B2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL: AF404704; AL01365.1; -
DR GO: GO:0042025; C:host cell nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR Pfam: PF00518; B6; 1.
DR NON TER 1 1
FT NON TER 99 99
SQ SEQUENCE 99 AA; 12005 MW; C2B96025EC370E38 CRC64;
Query Match 100.0%; Score 46; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLREVVYDF 9
Db 13 LLREVVYDF 21

RESULT 2

Q919B4 PRELIMINARY; PRT; 130 AA.
AC Q919B4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";

RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404703; AAL01363.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227EBDDC CRC64;
 Query Match 100.0%; Score 46; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LLRREYDF 9
 Db 16 LLRREYDF 24
 RESULT 3
 ID Q91988 PRELIMINARY; PRT; 130 AA.
 AC Q91988;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404701; AAL01359.1; -.
 DR Int. J. Cancer 97:868-874(2002).
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 130 AA; 15775 MW; 92D3C07BF96B092F CRC64;
 Query Match 100.0%; Score 46; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LLRREYDF 9
 Db 16 LLRREYDF 24
 RESULT 4
 ID Q919C0 PRELIMINARY; PRT; 130 AA.
 AC Q919C0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404700; AAL01357.1; -.
 DR Int. J. Cancer 97:868-874(2002).
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
 Query Match 100.0%; Score 46; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LLRREYDF 9
 Db 16 LLRREYDF 24
 RESULT 5
 ID Q919C2 PRELIMINARY; PRT; 130 AA.
 AC Q919C2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404699; AAL01355.1; -.
 DR Int. J. Cancer 97:868-874(2002).
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
 Query Match 100.0%; Score 46; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LLRREYDF 9
 Db 16 LLRREYDF 24
 RESULT 6
 ID Q919C8 PRELIMINARY; PRT; 130 AA.
 AC Q919C8;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404696; AAL01349.1; -.
 DR Int. J. Cancer 97:868-874(2002).
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
 Query Match 100.0%; Score 46; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LLRREYDF 9
 Db 16 LLRREYDF 24
 RESULT 7
 ID Q919C9 PRELIMINARY; PRT; 130 AA.
 AC Q919C9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404702; AAL01356.1; -.
 DR Int. J. Cancer 97:868-874(2002).
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
 Query Match 100.0%; Score 46; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LLRREYDF 9
 Db 16 LLRREYDF 24
 RESULT 8
 ID Q919D0 PRELIMINARY; PRT; 130 AA.
 AC Q919D0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404704; AAL01358.1; -.
 DR Int. J. Cancer 97:868-874(2002).
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
 Query Match 100.0%; Score 46; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LLR

SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;

Query Match 100.0%; Score 46; DB 2; Length 130;

Best Local Similarity 100.0%; Pred. No. 0.2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLREVVDF 9
Db 16 LLREVVDF 24

RESULT 7

Q19D2 ID Q19D2 PRELIMINARY; PRT; 138 AA.
AC Q19D2; 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF04694; AAL01345.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 138 AA; 16596 MW; 481E5A9A90895FC2 CRC64;

Query Match 100.0%; Score 46; DB 2; Length 138;

Best Local Similarity 100.0%; Pred. No. 0.21; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLREVVDF 9
Db 24 LLREVVDF 32

RESULT 8

Q19B6 ID Q19B6 PRELIMINARY; PRT; 143 AA.
AC Q19B6; 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF04702; AAL01361.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 143 AA; 17272 MW; 071F14BE3E6BE2AC CRC64;

Query Match 100.0%; Score 46; DB 2; Length 143;

Best Local Similarity 100.0%; Pred. No. 0.22; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLREVVDF 9
Db 29 LLREVVDF 37

RESULT 9

Q19C4 ID Q19C4 PRELIMINARY; PRT; 143 AA.
AC Q19C4; 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF04698; AAL01353.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;

Query Match 100.0%; Score 46; DB 2; Length 143;

Best Local Similarity 100.0%; Pred. No. 0.22; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLREVVDF 9
Db 29 LLREVVDF 37

RESULT 10

O12335 ID O12335 PRELIMINARY; PRT; 151 AA.
AC O12335; 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003015; AAB70732.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 151 AA; 18238 MW; BEF32A8B016CC88B CRC64;

Query Match 100.0%; Score 46; DB 2; Length 151;

Best Local Similarity 100.0%; Pred. No. 0.24; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 LLREVVDF 9
Db 37 LLREVVDF 45

RESULT 11
O12336 PRELIMINARY; PRT; 151 AA.
AC O12336;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tonnesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RL type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003016; AAB70733.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;

Query Match 100.0%; Score 46; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLREVVDF 9
Db 37 LLREVVDF 45

RESULT 12
Q76TS0 PRELIMINARY; PRT; 151 AA.
AC Q76TS0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34114; AAA91661.1; -.
DR EMBL; U34125; AAA91672.1; -.
DR EMBL; U34130; AAA91677.1; -.
DR EMBL; U34131; AAA91678.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.

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DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;

Query Match 100.0%; Score 46; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLREVVDF 9
Db 37 LLREVVDF 45

RESULT 13
Q778I6 PRELIMINARY; PRT; 151 AA.
AC Q778I6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388056; CAB45104.1; -.
DR EMBL; AJ388061; CAB45114.1; -.
DR EMBL; AJ388066; CAB45124.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18334 MW; FF8F2A2FCEBA6C02 CRC64;

Query Match 100.0%; Score 46; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLREVVDF 9
Db 37 LLREVVDF 45

RESULT 14
Q77E16 PRELIMINARY; PRT; 151 AA.
AC Q77E16;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 oncoprotein (E6 protein).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to

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RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AF469197; AAO15691.1; -.
DR EMBL; AJ388063; CAB45118.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CF1F CRC64;

Query Match 100.0%; Score 46; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLREVDYDF 9
| | | | |
Db 37 LLREVDYDF 45

RESULT 15

Q77JC7 PRELIMINARY; PRT; 151 AA.
AC Q77JC7;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Early transforming protein E6 variant (Transforming protein E6).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Xinjiang;
RA Ma Z., Qian D., Ma J., Lin R., Ming W., Zhong Z., Zhang Q., Zhang F.;
RT "Cloning and Sequencing of HPV16 E6 gene from Cervical Carcinoma
Biopsies in Xinjiang.";
RL Sheng Wu Hua Xue Yu Sheng Wu Li Jin Zhan 0:0-0(2001).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE=22242222; PubMed=12355268; DOI=10.1007/s00239-002-2344-y;
RA DeFillippis V.R., Ayala F.J., Villarreal L.P.;
RT "Evidence of diversifying selection in human papillomavirus type 16 E6
but not E7 oncogenes.";
RL J. Mol. Evol. 55:491-499(2002).
RN [4]
RN SEQUENCE FROM N.A.
RA Cruz M., Cerqueira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,
RA Martins C.R.F.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RN SEQUENCE FROM N.A.
RA Cruz M.R., Martins C.R.F.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF327851; AAG45940.1; -.
DR EMBL; AJ388057; CAB45106.1; -.
DR EMBL; AJ388089; CAB45130.1; -.
DR EMBL; AY089951; AAM11875.1; -.
DR EMBL; AY089954; AAM11881.1; -.
DR EMBL; AY112663; AAM51854.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18320 MW; 617D2A2FDB4F8C17 CRC64;

Query Match 100.0%; Score 46; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LLREVDYDF 9
| | | | |
Db 37 LLREVDYDF 45

Search completed: June 29, 2005, 01:34:47
Job time : 54.2473 secs

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OM protein - protein search, using sw model

Run on: June 29, 2005, 05:18:25 ; Search time 53.8517 Seconds
(without alignments)
64.268 Million cell updates/sec

Title: US-08-170-344-66
Perfect score: 46
Sequence: 1 LLREVVDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
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18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	9	17	US-10-751-845-82
2	46	100.0	15	16	US-10-476-570-28
3	46	100.0	23	17	US-10-484-063-4
4	46	100.0	23	16	US-10-476-570-27
5	46	100.0	24	17	US-10-751-845-65
6	46	100.0	117	17	US-10-751-845-126
7	46	100.0	151	14	US-10-177-390-6
8	46	100.0	151	17	US-10-484-063-20
9	46	100.0	151	17	US-10-484-063-27
10	46	100.0	158	17	US-10-858-384-2
11	46	100.0	158	17	US-10-367-057-16

12	46	100.0	171	16	US-10-472-724-2	Sequence 2, Appli
13	46	100.0	236	17	US-10-751-845-157	Sequence 157, App
14	46	100.0	237	17	US-10-751-845-158	Sequence 158, App
15	46	100.0	261	17	US-10-751-845-160	Sequence 160, App
16	46	100.0	265	9	US-09-367-309A-1	Sequence 1, Appli
17	46	100.0	273	13	US-10-000-903-4	Sequence 4, Appli
18	46	100.0	273	17	US-10-899-771-4	Sequence 4, Appli
19	46	100.0	292	13	US-10-000-903-10	Sequence 10, Appl
20	46	100.0	292	17	US-10-899-771-10	Sequence 10, Appl
21	46	100.0	371	13	US-10-000-903-6	Sequence 6, Appli
22	46	100.0	371	17	US-10-899-771-6	Sequence 6, Appli
23	46	100.0	390	13	US-10-000-903-14	Sequence 14, Appl
24	46	100.0	390	17	US-10-899-771-14	Sequence 14, Appl
25	46	100.0	536	15	US-10-367-095-10	Sequence 10, Appl
26	46	100.0	536	15	US-10-368-046-10	Sequence 10, Appl
27	46	100.0	536	16	US-10-367-367-10	Sequence 10, Appl
28	46	100.0	536	17	US-10-318-337-10	Sequence 10, Appl
29	42	91.3	22	16	US-10-476-570-26	Sequence 26, Appl
30	38	82.6	9	17	US-10-751-845-72	Sequence 72, Appl
31	38	82.6	21	16	US-10-476-570-54	Sequence 54, Appl
32	38	82.6	22	17	US-10-858-384-6	Sequence 6, Appli
33	37	80.4	99	17	US-10-508-622-28	Sequence 28, Appl
34	36	78.3	620	15	US-10-108-260A-4145	Sequence 4145, Ap
35	35	76.1	77	15	US-10-424-599-242846	Sequence 242846,
36	35	76.1	234	16	US-10-767-701-31810	Sequence 31810, A
37	35	76.1	287	14	US-10-270-875-48	Sequence 48, Appl
38	35	76.1	287	14	US-10-270-878-48	Sequence 48, Appl
39	35	76.1	287	14	US-10-270-786-48	Sequence 48, Appl
40	35	76.1	287	14	US-10-270-710-48	Sequence 48, Appl
41	35	76.1	287	14	US-10-270-859-48	Sequence 48, Appl
42	35	76.1	287	14	US-10-270-846-48	Sequence 48, Appl
43	35	76.1	377	15	US-10-289-762-654	Sequence 654, App
44	35	76.1	468	15	US-10-282-122A-54740	Sequence 54740, A
45	35	76.1	472	15	US-10-282-122A-55283	Sequence 55283, A

ALIGNMENTS

RESULT 1
US-10-751-845-82
; Sequence 82, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Robert M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10751.845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-82

Query Match 100.0%; Score 46; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LLREVVDF 9
Db 1 LLREVVDF 9

RESULT 2
US-10-476-570-28
; Sequence 28, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 42-56
US-10-476-570-28

Query Match 100.0%; Score 46; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLRREVYDF 9
Db 3 LLRREVYDF 11

RESULT 3
US-10-484-063-4
; Sequence 4, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-4

Query Match 100.0%; Score 46; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLRREVYDF 9
Db 2 LLRREVYDF 10

RESULT 4
US-10-476-570-27
; Sequence 27, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 23
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 44-67
US-10-476-570-27

Query Match 100.0%; Score 46; DB 16; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLRREVYDF 9
Db 1 LLRREVYDF 9

RESULT 5
US-10-751-845-65
; Sequence 65, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-65

Query Match 100.0%; Score 46; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.095;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLRREVYDF 9
Db 1 LLRREVYDF 9


```

; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-20

Query Match      100.0%; Score 46; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLREVVYDF 9
Db 37 LLREVVYDF 45

RESULT 9
US-10-484-063-27
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-484-063-27

Query Match      100.0%; Score 46; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLREVVYDF 9
Db 37 LLREVVYDF 45

RESULT 10
US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE

```

```

; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-126

Query Match      100.0%; Score 46; DB 17; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLREVVYDF 9
Db 21 LLREVVYDF 29

RESULT 7
US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerp Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021503wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6

Query Match      100.0%; Score 46; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLREVVYDF 9
Db 37 LLREVVYDF 45

RESULT 8
US-10-484-063-20
; Sequence 20, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:

```

```
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2
```

```
Query Match 100.0%; Score 46; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 LLREVDYDF 9
Db 44 LLREVDYDF 52
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RESULT 11

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US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16
```

```
Query Match 100.0%; Score 46; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 LLREVDYDF 9
Db 44 LLREVDYDF 52
```

RESULT 12

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US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
```

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2
```

```
Query Match 100.0%; Score 46; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 LLREVDYDF 9
Db 49 LLREVDYDF 57
```

RESULT 13

```
US-10-751-845-157
; Sequence 157, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-157
```

```
Query Match 100.0%; Score 46; DB 17; Length 236;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 LLREVDYDF 9
Db 21 LLREVDYDF 29
```

RESULT 14

```
US-10-751-845-158
; Sequence 158, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
```

```
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-158
```

```
Query Match      100.0%; Score 46; DB 17; Length 237;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 LLRREVDYDF 9
    |||||
Db 22 LLRREVDYDF 30
```

RESULT 15

```
US-10-751-845-160
; Sequence 160, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-160
```

```
Query Match      100.0%; Score 46; DB 17; Length 261;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 1 LLRREVDYDF 9
    |||||
Db 46 LLRREVDYDF 54
```

Search completed: June 29, 2005, 05:48:13
Job time : 54.8517 secs

File Blank (uspto)

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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:37:59 ; Search time 16.8626 Seconds
(without alignments)
39.842 Million cell updates/sec

Title: US-08-170-344-66

Perfect score: 46

Sequence: 1 LLREVDF 9

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	9	3	US-08-159-339A-252
2	46	100.0	158	4	US-09-980-523A-2
3	46	100.0	162	1	US-08-316-239B-3
4	46	100.0	162	1	US-08-316-239B-4
5	46	100.0	172	3	US-08-860-165-14
6	46	100.0	172	3	US-09-359-382-14
7	46	100.0	182	1	US-08-117-083-10
8	46	100.0	266	3	US-08-860-165-10
9	46	100.0	266	3	US-09-359-382-10
10	46	100.0	266	4	US-09-367-309A-1
11	46	100.0	273	3	US-09-485-885-4
12	46	100.0	292	3	US-09-485-885-10
13	46	100.0	371	3	US-09-485-885-6
14	46	100.0	390	3	US-09-485-885-14
15	42	91.3	14	1	US-07-909-122-4
16	42	91.3	23	4	US-09-601-729-276
17	38	82.6	22	4	US-09-980-523A-6
18	35	76.1	20	2	US-08-934-915-160
19	35	76.1	287	4	US-09-585-858-48
20	35	76.1	287	4	US-10-270-878-48
21	35	76.1	377	4	US-09-198-452A-654
22	35	76.1	478	4	US-09-438-185A-618
23	35	76.1	811	1	US-08-136-743B-4
24	34	73.9	9	3	US-08-159-339A-135
25	34	73.9	426	4	US-09-248-796A-17266
26	34	73.9	445	4	US-09-328-352-4631
27	34	73.9	495	4	US-09-691-270A-24

Sequence 16475, A
Sequence 388, App
Sequence 4919, Ap
Sequence 23606, A
Sequence 5211, Ap
Sequence 7725, Ap
Sequence 1109, Ap
Sequence 19185, A
Sequence 5, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 214, App
Sequence 214, App
Sequence 3517, Ap
Sequence 21634, A
Sequence 14339, A

28 34 73.9 792 4 US-09-902-540-16475
29 33 71.7 264 4 US-09-710-279-388
30 33 71.7 269 3 US-09-134-001C-4919
31 32 69.6 85 4 US-09-248-796A-23606
32 32 69.6 169 4 US-09-107-532A-5211
33 32 69.6 362 4 US-09-949-016-7725
34 32 69.6 376 4 US-09-538-082-1109
35 32 69.6 457 4 US-09-248-796A-19185
36 32 69.6 473 4 US-09-790-838-5
37 32 69.6 474 4 US-09-790-838-4
38 32 69.6 487 4 US-09-790-838-2
39 32 69.6 4866 4 US-09-424-783-2
40 32 69.6 4872 4 US-09-424-783-3
41 31 67.4 208 3 US-08-961-083-214
42 31 67.4 208 3 US-09-536-784-214
43 31 67.4 271 4 US-09-583-110-3517
44 31 67.4 273 4 US-09-252-991A-21634
45 31 67.4 274 4 US-09-489-039A-14339

ALIGNMENTS

RESULT 1
US-08-159-339A-252
; Sequence 252, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Cellis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-252

Query Match 100.0%; Score 46; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLREVVYDF 9
| | | | | | | | | |
Db 1 LLREVVYDF 9

RESULT 2

US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO81 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 46; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLREVVYDF 9
| | | | | | | | | |
Db 44 LLREVVYDF 52

RESULT 3

US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 100.0%; Score 46; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLREVVYDF 9
| | | | | | | | | |
Db 44 LLREVVYDF 52

RESULT 4

US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 100.0%; Score 46; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLRREVYDF 9
Db 44 LLRREVYDF 52

RESULT 5
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14

Query Match 100.0%; Score 46; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLRREVYDF 9
Db 113 LLRREVYDF 121

RESULT 6
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; EARLIER FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match 100.0%; Score 46; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLRREVYDF 9
Db 113 LLRREVYDF 121

RESULT 7
US-08-117-083-10
; Sequence 10, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Boursnell, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
; OTHER INFORMATION: /note= "xaa refers to stop codon in
; the open reading frame."
US-08-117-083-10

Query Match 100.0%; Score 46; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLRREVYDF 9
Db 45 LLRREVYDF 53

RESULT 8
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John

; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 46; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLREVDYDF 9
Db 44 LLREVDYDF 52

RESULT 9
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 46; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLREVDYDF 9
Db 44 LLREVDYDF 52

RESULT 10
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM

; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 46; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLREVDYDF 9
Db 44 LLREVDYDF 52

RESULT 11
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match 100.0%; Score 46; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LLREVDYDF 9
Db 150 LLREVDYDF 158

RESULT 12
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885

; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10

Query Match 100.0%; Score 46; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.21; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 LLREVDYDF 9
Db 169 LLREVDYDF 177

RESULT 13
US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6

Query Match 100.0%; Score 46; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.27; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 LLREVDYDF 9
Db 150 LLREVDYDF 158

RESULT 14
US-09-485-885-14
; Sequence 14, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17

; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-14

Query Match 100.0%; Score 46; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 0.28; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 LLREVDYDF 9
Db 169 LLREVDYDF 177

RESULT 15
US-07-909-122-4
; Sequence 4, Application US/07909122
; Patent No. 5415995
; GENERAL INFORMATION:
; APPLICANT: SCHOOLNIK, GARY K.
; APPLICANT: PALEFSKY, JOEL M.
; TITLE OF INVENTION: DIAGNOSTIC PEPTIDES OF HUMAN PAPILLOMA
; TITLE OF INVENTION: VIRUS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESS: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/909,122
; FILING DATE: 19920706
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: BENZ, WILLIAM H.
; REGISTRATION NUMBER: 25,952
; REFERENCE/DOCKET NUMBER: 28600-20105.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-909-122-4

Query Match 91.3%; Score 42; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.05; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

Qy 2 LLREVDYDF 9
Db 1 LLREVDYDF 8

Search completed: June 29, 2005, 01:44:24
Job time : 17.9126 secs

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RP SEQUENCE FROM N.A.
RL Terai M., Ma Z., Burk R.D.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Cruz M.R., Cerqueira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,
RA Martins C.R.F.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF486314; AAL96619.1; -
DR EMBL; AF472509; AAO15705.1; -
DR EMBL; AF486324; AAL96629.1; -
DR EMBL; AV098918; AAM29166.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19157 MW; F140F509DAC794F6 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHQKRTAMF 9
DB |||||
1 MHQKRTAMF 9

RESULT 4
Q8QHP5 PRELIMINARY; PRT; 158 AA.
ID Q8QHP5
AC Q8QHP5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE B6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E-G276T, and E-G276G442T;
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RA "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486315; AAL96620.1; -
DR EMBL; AF486323; AAL96628.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19160 MW; AFF015533FC7FAF7 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHQKRTAMF 9
DB |||||
1 MHQKRTAMF 9

RESULT 5
Q8QHT0 PRELIMINARY; PRT; 158 AA.
ID Q8QHT0
AC Q8QHT0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative transforming protein E6.

```

OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=As-P, As-C193, and As-A178;
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Terai M., Fu L., Ma Z., Burk R.D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF486239; AAL96604.1; -
DR EMBL; AF486300; AAL96605.1; -
DR EMBL; AF486301; AAL96606.1; -
DR EMBL; AF486302; AAL96607.1; -
DR EMBL; AF486306; AAL96611.1; -
DR EMBL; AF486308; AAL96613.1; -
DR EMBL; AF534061; AAL10403.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19201 MW; 004EF5ADCE6B375B CRC64;

Query Match 100.0%; Score 48; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHQKRTAMF 9
|||
Db 1 MHQKRTAMF 9

RESULT 6

OS Q8QRD5 PRELIMINARY; PRT; 158 AA.
AC Q8QRD5;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Transforming protein E6.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NAl;
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Terai M., Burk R.D.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Cruz M.R., Cerqueira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,
RA Martins C.R.F.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Cruz Mr., Cerqueira D.M., Camara G.N.L., Silva E.O., Carvalho L.G.S.,
RA Martins C.R.F.;

RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Cruz M.R., Martins C.R.F.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF486325; AAL96630.1; -
DR EMBL; AF402678; AAO85408.1; -
DR EMBL; AY098923; AAM29171.1; -
DR EMBL; AY112662; AAM51853.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19208 MW; B8E47F57F22EC2E1 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHQKRTAMF 9
|||
Db 1 MHQKRTAMF 9

RESULT 7

OS Q8QRD6 PRELIMINARY; PRT; 158 AA.
AC Q8QRD6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E-T360T;
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486319; AAL96624.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19246 MW; 01FEF70F45F137EB CRC64;

Query Match 100.0%; Score 48; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHQKRTAMF 9
|||
Db 1 MHQKRTAMF 9

RESULT 8

OS Q8QRD7 PRELIMINARY; PRT; 158 AA.
AC Q8QRD7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;

```

RN  SEQUENCE FROM N.A.
RP  STRAIN=E-C442T;
RX  MEDLINE=22182962; PubMed=12195358;
RA  Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA  Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT  "Human papillomavirus type 16 intratypic variant infection and risk
RT  for cervical neoplasia in southern China.";
RL  J. Infect. Dis. 186:696-700(2002).
DR  EMBL; AF486318; AAL96623.1; -.
DR  GO; GO:0042025; C:host cell nucleus; IEA.
DR  GO; GO:0003677; F:DNA binding; IEA.
DR  InterPro; IPR001334; E6.
DR  Pfam; PF00518; E6; 1.
SQ  SEQUENCE 158 AA; 19173 MW; 14BF5BDCFB3640 CRC64;

Query Match      100.0%; Score 48; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 MHQKRTAMF 9
Db  |||||
    1 MHQKRTAMF 9

RESULT 9
Q8QRD8 ID Q8QRD8 PRELIMINARY; PRT; 158 AA.
AC Q8QRD8;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=E-G449T;
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486316; AAL96621.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 158 AA; 19188 MW; 01FEF5B1D21AF7EB CRC64;

Query Match      100.0%; Score 48; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 MHQKRTAMF 9
Db  |||||
    1 MHQKRTAMF 9

RESULT 10
Q8QRD9 ID Q8QRD9 PRELIMINARY; PRT; 158 AA.
AC Q8QRD9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.

```

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OX  NCBI_TaxID=10581;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  STRAIN=As-A267;
RX MEDLINE=22182962; PubMed=12195358;
RA  Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA  Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT  "Human papillomavirus type 16 intratypic variant infection and risk
RT  for cervical neoplasia in southern China.";
RL  J. Infect. Dis. 186:696-700(2002).
DR  EMBL; AF486309; AAL96614.1; -.
DR  GO; GO:0042025; C:host cell nucleus; IEA.
DR  GO; GO:0003677; F:DNA binding; IEA.
DR  InterPro; IPR001334; E6.
DR  Pfam; PF00518; E6; 1.
SQ  SEQUENCE 158 AA; 19173 MW; 161AD3EFAA4D636B CRC64;

Query Match      100.0%; Score 48; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 MHQKRTAMF 9
Db  |||||
    1 MHQKRTAMF 9

RESULT 11
Q8QRE0 ID Q8QRE0 PRELIMINARY; PRT; 158 AA.
AC Q8QRE0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=As-G137;
RX MEDLINE=22182962; PubMed=12195358;
RA  Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA  Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT  "Human papillomavirus type 16 intratypic variant infection and risk
RT  for cervical neoplasia in southern China.";
RL  J. Infect. Dis. 186:696-700(2002).
DR  EMBL; AF486307; AAL96612.1; -.
DR  GO; GO:0042025; C:host cell nucleus; IEA.
DR  GO; GO:0003677; F:DNA binding; IEA.
DR  InterPro; IPR001334; E6.
DR  Pfam; PF00518; E6; 1.
SQ  SEQUENCE 158 AA; 19187 MW; 005E2FC1E617C55B CRC64;

Query Match      100.0%; Score 48; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 MHQKRTAMF 9
Db  |||||
    1 MHQKRTAMF 9

RESULT 12
Q8QRE1 ID Q8QRE1 PRELIMINARY; PRT; 158 AA.
AC Q8QRE1;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

```

OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB-C131;
 RX MEDLINE=22182962; PubMed=12195358;
 RA Chan P.K.S., Lam C.W., Cheng T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
 RT "Human papillomavirus type 16 intratypic variant infection and risk
 RT for cervical neoplasia in southern China."; J. Infect. Dis. 186:696-700(2002).
 RL EMBL: AF486303; AAL96608.1; -
 DR GO: 0042025; C:host cell nucleus; IEA.
 DR GO: 0003677; F:DNA binding; IEA.
 DR InterPro: IPR001334; E6.
 DR Pfam: PF00518; E6; 1.
 SQ SEQUENCE 158 AA; 19146 MW; CB6EF5A91548727C CRC64;

Query Match 100.0%; Score 48; DB 2; Length 158;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHQKRTAMF 9
 |||||
 Db 1 MHQKRTAMF 9

RESULT 13

Q71B17 ID Q71B17 PRELIMINARY; PRT; 158 AA.

AC Q71B17; 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Putative transforming protein E6.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Terai M., Fu L., Ma Z., Burk R.D.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF536179; AAQ10712.1; -
 DR GO: 0042025; C:host cell nucleus; IEA.
 DR GO: 0003677; F:DNA binding; IEA.
 DR InterPro: IPR001334; E6.
 DR Pfam: PF00518; E6; 1.
 SQ SEQUENCE 158 AA; 19074 MW; 9BFCF5B6DB95D75E CRC64;

Query Match 100.0%; Score 48; DB 2; Length 158;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHQKRTAMF 9
 |||||
 Db 1 MHQKRTAMF 9

RESULT 14

Q9QDH3 ID Q9QDH3 PRELIMINARY; PRT; 158 AA.

AC Q9QDH3; 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF187869; AAF13398.1; -
 DR GO: 0042025; C:host cell nucleus; IEA.
 DR GO: 0003677; F:DNA binding; IEA.
 DR InterPro: IPR001334; E6.
 DR Pfam: PF00518; E6; 1.
 SQ SEQUENCE 158 AA; 19210 MW; 004EF5ADD6FABESB CRC64;

Query Match 100.0%; Score 48; DB 2; Length 158;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHQKRTAMF 9
 |||||
 Db 1 MHQKRTAMF 9

RESULT 15

Q9QDH5 ID Q9QDH5 PRELIMINARY; PRT; 158 AA.

AC Q9QDH5; 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF187868; AAF13396.1; -
 DR GO: 0042025; C:host cell nucleus; IEA.
 DR GO: 0003677; F:DNA binding; IEA.
 DR InterPro: IPR001334; E6.
 DR Pfam: PF00518; E6; 1.
 SQ SEQUENCE 158 AA; 19195 MW; 00564E1A8994CB0B CRC64;

Query Match 100.0%; Score 48; DB 2; Length 158;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHQKRTAMF 9
 |||||
 Db 1 MHQKRTAMF 9

Search completed: June 29, 2005, 01:34:47
 Job time : 56.2473 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:32:21 ; Search time 11.2747 Seconds
(without alignments)
76.805 Million cell updates/sec

Title: US-08-170-344-65

Perfect score: 48

Sequence: 1 MHQKRTAMP 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:**

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	158	1 W6WLHS	protein E6 - human
2	33	68.8	506	2 C81704	monooxygenase-rela
3	32	66.7	245	2 AF2911	transcription regu
4	32	66.7	267	2 D97886	ahl receptor (AF33
5	31	64.6	406	1 A48495	linalool 8-monooxy
6	31	64.6	423	2 T20233	hypothetical prote
7	31	64.6	424	2 S63583	tetrahydrofolylpol
8	31	64.6	424	2 B81936	tetrahydrofolylpol
9	31	64.6	424	2 C81170	folylpolyglutamate
10	31	64.6	571	2 T40911	probable PHD-type
11	30	62.5	80	1 OSHU7B	cytochrome-c oxida
12	30	62.5	181	2 G98140	dtldp-6-deoxy-1-man
13	30	62.5	210	2 B82522	hypothetical prote
14	30	62.5	215	2 I64035	hypothetical prote
15	30	62.5	219	2 A10886	Deda-family integr
16	30	62.5	219	2 E91115	hypothetical prote
17	30	62.5	219	2 G65087	hypothetical 24.1
18	30	62.5	219	2 E85267	hypothetical prote
19	30	62.5	251	2 T02277	hypothetical prote
20	30	62.5	274	2 D83425	conserved hypotet
21	30	62.5	275	1 WZBB88	gene 26 protein -
22	30	62.5	302	2 H82045	conserved hypotet
23	30	62.5	349	2 T49843	hypothetical prote
24	30	62.5	434	2 S11967	module-specific hy
25	30	62.5	461	2 T35151	hypothetical prote
26	30	62.5	469	2 C71336	hypothetical prote
27	30	62.5	492	2 T28025	hypothetical prote
28	30	62.5	521	2 T41621	hypothetical prote
29	30	62.5	891	2 H36790	hypothetical prote

RESULT 1
W6WLHS
C;Species: human papillomavirus type 16
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C;Accession: A03682; T10427
R;Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
Virology 145, 181-185, 1985
A;Title: Human papillomavirus type 16 DNA sequence.
A;Reference number: A22355; MUID:85246220; PMID:2990099
A;Accession: A03682
A;Molecule type: DNA
A;Residues: 1-158 <SEE>
A;Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G33303
R;Kennedy, I.M.; Hadow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A;Title: A negative element in the human poapillomavirus type 16 genome acts at the lev
A;Reference number: Z17014; MUID:91162763; PMID:1848319
A;Accession: T10427
A;Status: preliminary; translated from GB/EMBL/DBD
A;Molecule type: DNA
A;Residues: 1-158 <KEN>
A;Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
C;Gene: E6
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;37-73/Region: zinc finger CCCC motif
F;110-146/Region: zinc finger CCCC motif
Query Match 100.0%; Score 48; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.0029;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHQKRTAMP 9
|||||||
DB 1 MHQKRTAMP 9

RESULT 2

C81704
monooxygenase-related protein TC0425 [imported] - Chlamydia muridarum (strain Nigg)
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: C81704
A;Status: preliminary

hypothetical prote
hypothetical prote
cytochrome-c oxida
ferredoxin (import
ferredoxin II (AF2
hypothetical prote
hypothetical prote
hypothetical prote
glucose-inhibited
glucose-inhibited
hypothetical prote
conserved hypotet
endothelial cell p
hypothetical prote
hypothetical prote
probable deOR-fami

A:Molecule type: DNA

A:Residues: 1-506 <TET>

A:Cross-references: UNIPROT:Q9PKP0; GB:AB002309; GB:AB002160; NID:g7190464; PIDN:AAF3928

A:Experimental source: strain Nigg (MoPn)

C:Genetics:

A:Gene: TC0425

Query Match 68.8%; Score 33; DB 2; Length 506;

Best Local Similarity 85.7%; Pred. No. 22;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHQKRTA 7

DB 338 VHQRRTA 344

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|||||

RESULT 3

AF2911

transcription regulator, LuxR family Atu2727 [imported] - Agrobacterium tumefaciens (str

C:Species: Agrobacterium tumefaciens

C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C:Accession: AF2911

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I

erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell

; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.

A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A:Reference number: AB2577; MUID:21608550; PMID:11743193

A:Accession: AF2911

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-245 <KUR>

A:Cross-references: UNIPROT:Q8UBX2; GB:AB008688; PIDN:AAL43708.1; PID:g17741237; GSPDB:C

A:Experimental source: strain C58 (Dupont)

C:Genetics:

A:Gene: Atu2727

A:Map position: circular chromosome

Query Match 66.7%; Score 32; DB 2; Length 245;

Best Local Similarity 55.6%; Pred. No. 17;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MHQKRTAMP 9

DB 100 MHRKRASVP 108

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RESULT 4

D97686

ahl receptor (AF330023) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)

C:Species: Agrobacterium tumefaciens

C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004

C:Accession: D97686

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qureshi, B.; Goldman,

A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A:Reference number: A97359; MUID:21608551; PMID:11743194

A:Accession: D97686

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-267 <KUR>

A:Cross-references: UNIPROT:Q8UBX2; GB:AB007869; PIDN:AAK88445.1; PID:g15157942; GSPDB:C

C:Genetics:

A:Gene: AGR_C_4942

A:Map position: circular chromosome

Query Match 66.7%; Score 32; DB 2; Length 267;

Best Local Similarity 55.6%; Pred. No. 19;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MHQKRTAMP 9

DB 122 MHRKRASVP 130

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|||||

RESULT 5

A48495

linalool 8-monooxygenase (EC 1.14.99.28) - Pseudomonas incognita

C:Species: Pseudomonas incognita

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: A48495

R;Ropp, J.D.; Gunsalus, I.C.; Sligar, S.G.

J. Bacteriol. 175, 6028-6037, 1993

A:Title: Cloning and expression of a member of a new cytochrome P-450 family: cytochrome

A:Reference number: A48495; MUID:93388536; PMID:8376348

A:Accession: A48495

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-406 <ROP>

A:Cross-references: UNIPROT:Q59723; GB:I23310; NID:g405542; PIDN:AAA25810.1; PID:g40554

C:Superfamily: Bacillus cytochrome P450 CYP106; cytochrome P450 homology

C:Keywords: oxidoreductase

F;242-377/Domain: cytochrome P450 homology <CYP>

Query Match 64.6%; Score 31; DB 1; Length 406;

Best Local Similarity 62.5%; Pred. No. 49;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MHQKRTAM 8

DB 293 LHMRTAM 300

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RESULT 6

T20233

hypothetical protein C54G4.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T20233

R;Wilkinson, J.

submitted to the EMBL Data Library, June 1996

A:Reference number: Z19241

A:Accession: T20233

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-423 <WIL>

A:Cross-references: UNIPROT:Q18847; EMBL:Z75533; PIDN:CAA99815.1; GSPDB:GN00019; CESP:C

A:Experimental source: clone C54G4

C:Genetics:

A:Gene: CESP:C54G4.2

A:Map position: 1

A:Introns: 76/3; 172/3; 272/2; 312/1; 367/3

C:Superfamily: Caenorhabditis elegans hypothetical protein C54G4.2

Query Match 64.6%; Score 31; DB 2; Length 423;

Best Local Similarity 62.5%; Pred. No. 51;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MHQKRTAM 8

DB 1 MHQKKTIV 8

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RESULT 7

S63583

tetrahydrofolylpolyglutamate synthase (EC 6.3.2.17) / dihydrofolate synthase (EC 6.3.2.1

C:Species: Neisseria gonorrhoeae

A:Variety: strain MS11

C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C:Accession: S63583

R;Fussneger, M.; Meyer, T.F.

Mol. Gen. Genet. 250, 277-285, 1996

A:Title: Cloning and characterization of the Neisseria gonorrhoeae MS11 folC gene.

A;Reference number: S63582; MUID:96180644; PMID:8602142
A;Accession: S63583
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-424 <FUS>
A;Cross-references: UNIPROT:Q50990; GB:Z68205; NID:gl237075; PIDN:CAA92428.1; PID:gl2370
C;Superfamily: folsylpolyglutamate synthase
C;Keywords: ligase

Query Match 64.6%; Score 31; DB 2; Length 424;
Best Local Similarity 85.7%; Pred. No. 51;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QKRTAMF 9
Db 329 QKRTAVF 335

RESULT 8

B81936
tetrahydrofolsylpolyglutamate synthase (EC 6.3.2.17) / dihydrofolate synthase (EC 6.3.2.1
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: B81936
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: B81936
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-424 <PAR>
A;Cross-references: UNIPROT:Q9JVC6; GB:AL162754; GB:AL157959; NID:g7379424; PIDN:CAB8417
A;Superfamily: folsylpolyglutamate synthase
C;Genetics:
A;Gene: folC; NMA0896
C;Superfamily: folsylpolyglutamate synthase
C;Keywords: ligase

Query Match 64.6%; Score 31; DB 2; Length 424;
Best Local Similarity 85.7%; Pred. No. 51;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QKRTAMF 9
Db 329 QKRTAVF 335

RESULT 9

C81170
folsylpolyglutamate synthase/dihydrofolate synthase NMB0693 [imported] - Neisseria mening
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: C81170
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: C81170
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-424 <TET>
A;Cross-references: UNIPROT:Q9K0C1; GB:AB002423; GB:AB002098; NID:g7225913; PIDN:AAF4111
A;Superfamily: folsylpolyglutamate synthase
C;Genetics:
A;Gene: NMB0693
C;Superfamily: folsylpolyglutamate synthase

Query Match 64.6%; Score 31; DB 2; Length 424;

Best Local Similarity 85.7%; Pred. No. 51;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 3 QKRTAMF 9
Db 329 QKRTAVF 335

RESULT 10

T40911
probable PHD-type zinc finger - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T40911
R;Murphy, L.; Harris, D.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, December 1998
A;Reference number: Z21956
A;Accession: T40911
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-571 <MUR>
A;Cross-references: UNIPROT:O94400; EMBL:AL034490; PIDN:CAA22476.1; GSPDB:GN00068; SPDF
A;Experimental source: strain 972h-; cosmid c126
C;Genetics:
A;Gene: SPDB:SPCC126.07c
A;Map position: 3

Query Match 64.6%; Score 31; DB 2; Length 571;
Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHQKRTA 7
Db 475 MHQKRTS 481

RESULT 11

OSHU7B
cytochrome-c oxidase (EC 1.9.3.1) chain VIIb precursor - human
C;Species: Homo sapiens (man)
C;Date: 08-Dec-1993 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: S29856
R;Sadlock, J.B.; Lightowers, R.N.; Capaldi, R.A.; Schon, E.A.
Biochim. Biophys. Acta 1172, 223-225, 1993
A;Title: Isolation of a cDNA specifying subunit VIIb of human cytochrome c oxidase.
A;Reference number: S29856; MUID:93176819; PMID:8382530
A;Accession: S29856
A;Molecule type: mRNA
A;Residues: 1-80 <SAD>
A;Cross-references: UNIPROT:P24311; EMBL:Z14244; NID:g30150; PIDN:CAA78613.1; PID:g3015
C;Genetics:
A;Gene: GDB:COX7B
A;Cross-references: GDB:I138315
A;Map position: 14pter-14qter
C;Complex: part of a 13 chain complex spanning the inner mitochondrial membrane and con
m dimers within the mitochondrial inner-membrane
C;Function:
A;Description: the cytochrome-c oxidase complex catalyzes the oxidation of four molecu
ns from the mitochondrial matrix producing two molecules of water and lowering the conc
A;Pathway: oxidative phosphorylation; respiratory chain
A;Note: the role of chain VIIb is not clear
C;Superfamily: cytochrome-c oxidase chain VIIb
C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membran
F;1-23/Domain: transit peptide (mitochondrion) #status predicted <TMP>
F;24-80/Product: cytochrome-c oxidase chain VIIb #status predicted <MAP>
F;33-59/Domain: transmembrane helix #status predicted <TR01>

Query Match 62.5%; Score 30; DB 1; Length 80;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 HQKRTAMF 9

Db 26 HQKRTDPF 33
|||||
|
RESULT 12
G98140
ctdp-6-deoxy-1-mannose-dehydrogenase [imported] - Agrobacterium tumefaciens (strain C58,
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: G98140
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, P.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: G98140
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-181 <KUR>
A;Cross-references: UNIPROT:Q8U6K8; GB:AE007870; PIDN:AAK88649.1; PID:gl5158372; GSPDB:G
C;Genetics:
A;Gene: AGR_L166
A;Map position: linear chromosome
C;Superfamily: dtdp-4-dehydroxamnose 3,5-epimerase

Query Match 62.5%; Score 30; DB 2; Length 181;
Best Local Similarity 55.6%; Pred. No. 36;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MHQKRTAMF 9
|||||
|
Db 1 MHQERRMLF 9

RESULT 13
B82522
hypothetical protein XF2740 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: B82522
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: B82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: B82522
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-210 <SIM>
A;Cross-references: UNIPROT:Q9P9Y0; GB:AE004080; GB:AE003849; NID:g9107971; PIDN:AAF8552
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorfi, H.; Facincani, A.P.; Ferreira, J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krueger, J.E.; Kuramae, E.E.; Laig
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
C;Genetics:
A;Contents: annotation
A;Gene: XF2740

Query Match 62.5%; Score 30; DB 2; Length 210;
Best Local Similarity 62.5%; Pred. No. 42;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MHQKRTAM 8

Db 137 MHURTAIV 144
|||||
|

RESULT 14
I64035
hypothetical protein HI1552 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: I64035
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage,
C;Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman,
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.B.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: I64035
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-215 <TIGR>
A;Cross-references: UNIPROT:P44251; GB:U02830; GB:I42023; NID:gl574389; PIDN:AAK23210.1
C;Superfamily: Haemophilus influenzae hypothetical protein HI1552

Query Match 62.5%; Score 30; DB 2; Length 215;
Best Local Similarity 55.6%; Pred. No. 43;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MHQKRTAMF 9
|||||
|
Db 144 IHQELTALF 152

RESULT 15
AI0886
DedA-family integral membrane protein [imported] - Salmonella enterica subsp. enterica
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AI0886
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AI0886
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-219 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD02993.1; PID:gl5504240; GSPDB:GN00176
C;Genetics:
A;Gene: STV3334
C;Superfamily: dedA protein

Query Match 62.5%; Score 30; DB 2; Length 219;
Best Local Similarity 62.5%; Pred. No. 44;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 HOKRTAMF 9
|||||
|
Db 111 HQRATCMF 118

Search completed: June 29, 2005, 01:38:41
Job time : 13.2747 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 05:18:25 ; Search time 53.8517 Seconds
(without alignments)
64.268 Million cell updates/sec

Title: US-08-170-344-65

Perfect score: 48

Sequence: 1 MHQRTAMF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	22	16	US-10-476-570-59
2	48	100.0	158	17	US-10-858-384-2
3	48	100.0	158	17	US-10-367-057-16
4	48	100.0	266	9	US-09-367-309A-1
5	48	100.0	536	15	US-10-367-095-10
6	48	100.0	536	15	US-10-368-046-10
7	48	100.0	536	15	US-10-367-367-10
8	48	100.0	536	17	US-10-918-337-10
9	43	89.6	171	16	US-10-472-724-2
10	34	70.8	51	14	US-10-029-386-32092
11	33	68.8	73	15	US-10-424-599-154256

12	33	68.8	190	15	US-10-424-599-263544
13	33	68.8	436	15	US-10-038-854-130
14	32	66.7	66	15	US-10-424-599-159338
15	32	66.7	94	15	US-10-425-114-47963
16	32	66.7	112	15	US-10-424-599-178972
17	32	66.7	174	15	US-10-424-599-168961
18	32	66.7	481	15	US-10-203-319A-20
19	32	66.7	504	15	US-10-424-599-168323
20	32	66.7	743	17	US-10-965-017-9
21	32	66.7	759	17	US-10-965-017-3
22	32	66.7	1104	9	US-09-982-610-36
23	32	66.7	2771	16	US-10-437-963-195406
24	32	66.7	2882	16	US-10-437-963-195412
25	31	64.6	63	14	US-10-029-386-31107
26	31	64.6	67	16	US-10-425-115-300764
27	31	64.6	153	16	US-10-425-115-206745
28	31	64.6	311	16	US-10-786-720-57
29	31	64.6	311	17	US-10-774-355A-1447
30	31	64.6	4455	15	US-10-287-226-304
31	30	62.5	33	15	US-10-424-599-241203
32	30	62.5	58	16	US-10-425-115-307508
33	30	62.5	62	15	US-10-424-599-262525
34	30	62.5	72	15	US-10-424-599-250945
35	30	62.5	73	16	US-10-767-701-42125
36	30	62.5	75	16	US-10-425-115-238277
37	30	62.5	80	15	US-10-424-599-255598
38	30	62.5	80	15	US-10-363-616-348
39	30	62.5	80	16	US-10-408-765A-400
40	30	62.5	81	16	US-10-425-115-205781
41	30	62.5	87	14	US-10-083-357-905
42	30	62.5	138	14	US-10-156-761-12705
43	30	62.5	145	16	US-10-767-701-52503
44	30	62.5	171	14	US-10-017-161-1490
45	30	62.5	171	15	US-10-292-798-1196

ALIGNMENTS

RESULT 1

US-10-476-570-59
; Sequence 59, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 22
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 1-22

Query Match 100.0%; Score 48; DB 16; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHQKRTAMF 9
| | | | | | | |
Db 1 MHQKRTAMF 9

RESULT 2

US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match 100.0%; Score 48; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHQKRTAMF 9
| | | | | | | |
Db 1 MHQKRTAMF 9

RESULT 3

US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match 100.0%; Score 48; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHQKRTAMF 9
| | | | | | | |
Db 1 MHQKRTAMF 9

RESULT 4

Query Match 100.0%; Score 48; DB 15; Length 536;

US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 48; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.076;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHQKRTAMF 9
| | | | | | | |
Db 1 MHQKRTAMF 9

RESULT 5

US-10-367-095-10
; Sequence 10, Application US/10367095
; Publication No. US20030228696A1
; GENERAL INFORMATION:
; APPLICANT: Robin A. Robinson
; TITLE OF INVENTION: No. US20030228696A1 Insect Cell Line
; FILE REFERENCE: 44149-1US1
; CURRENT APPLICATION NUMBER: US/10/367,095
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 60/356,119
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,161
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,118
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,133
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,157
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,156
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,123
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,113
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,154
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,135
; PRIOR FILING DATE: 2002-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HPV-16 L2/E6 fusion protein
US-10-367-095-10

Query Match

Best Local Similarity 100.0%; Pred. No. 0.15; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHQKRTAMF 9
Db 471 MHQKRTAMF 479

RESULT 6
US-10-368-046-10
; Sequence 10, Application US/10368046
; Publication No. US20040063188A1
; GENERAL INFORMATION:
; APPLICANT: Robin A. Robinson
; TITLE OF INVENTION: Method for Isolation and Purification of
; FILE REFERENCE: 44149-3US1
; CURRENT APPLICATION NUMBER: US/10/368,046
; CURRENT FILING DATE: 2003-02-15
; PRIOR APPLICATION NUMBER: US 60/356,119
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,161
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,118
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,133
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,157
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,156
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,135
; PRIOR FILING DATE: 2002-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HPV-16 L2/E6 fusion protein
US-10-368-046-10

Query Match 100.0%; Score 48; DB 15; Length 536;
Best Local Similarity 100.0%; Pred. No. 0.15; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHQKRTAMF 9
Db 471 MHQKRTAMF 479

RESULT 7
US-10-367-367-10
; Sequence 10, Application US/10367367
; Publication No. US20040121465A1
; GENERAL INFORMATION:
; APPLICANT: Robin A. Robinson
; TITLE OF INVENTION: Optimization of Gene Sequences of
; FILE REFERENCE: 44149-2US1
; CURRENT APPLICATION NUMBER: US/10/367,367
; CURRENT FILING DATE: 2003-02-15
; PRIOR APPLICATION NUMBER: US 60/356,119
; PRIOR FILING DATE: 2002-02-14

; PRIOR APPLICATION NUMBER: US 60/356,161
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,118
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,133
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,157
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,156
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HPV-16 L2/E6 fusion protein
US-10-367-367-10

Query Match 100.0%; Score 48; DB 16; Length 536;
Best Local Similarity 100.0%; Pred. No. 0.15; Mismatches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHQKRTAMF 9
Db 471 MHQKRTAMF 479

RESULT 8
US-10-918-337-10
; Sequence 10, Application US/10918337
; Publication No. US20050118191A1
; GENERAL INFORMATION:
; APPLICANT: NOVAVAX, INC., et al.
; TITLE OF INVENTION: Optimization of Gene Sequences of
; FILE REFERENCE: 19065/2132
; CURRENT APPLICATION NUMBER: US/10/918,337
; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: PCT/US03/04473
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 60/356,119
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,161
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,118
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,133
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,157
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,156
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,123
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,113
; PRIOR FILING DATE: 2002-02-14
; PRIOR APPLICATION NUMBER: US 60/356,154
; PRIOR FILING DATE: 2002-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HPV-16 L2/E6 fusion protein
US-10-918-337-10

Query Match 100.0%; Score 48; DB 17; Length 536;
Best Local Similarity 100.0%; Pred. No. 0.15;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHQKRTAMF 9
| | | | | | | | | |
Db 471 MHQKRTAMF 479

RESULT 9
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match 89.6%; Score 43; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HOKRTAMF 9
| | | | | | | | | |
Db 7 HOKRTAMF 14

RESULT 10
US-10-029-386-32092
; Sequence 32092, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 32092
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL022067.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.35
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.6
; OTHER INFORMATION: SWISSPROT HIT: P39768, EVALU 4.30e-01
US-10-029-386-32092

Query Match 70.8%; Score 34; DB 14; Length 51;

Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HOKRTAM 8
| | | | | | | | | |
Db 17 HOKRTSM 23

RESULT 11
US-10-424-599-154256
; Sequence 154256, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 154256
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_110314C.1.pep
US-10-424-599-154256

Query Match 68.8%; Score 33; DB 15; Length 73;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 HOKRTAMF 9
| | | | | | | | | |
Db 39 HWKKTAMF 46

RESULT 12
US-10-424-599-263544
; Sequence 263544, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 263544
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_7C.1.pep
US-10-424-599-263544

Query Match 68.8%; Score 33; DB 15; Length 190;
Best Local Similarity 85.7%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 HOKETAM 8
| | | | | | | | | |
Db 94 HOKETCM 100

RESULT 13

US-10-038-854-130
; Sequence 130, Application US/10038854
; Publication No. US20040022781A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Li, Li
; APPLICANT: Wolenc, Adam R
; APPLICANT: Vernet, Corine
; APPLICANT: Eisen, Andrew J
; APPLICANT: Liu, Xiaohong
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Shimkets, Richard A
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spaderna, Steven K
; APPLICANT: Gorman, Linda
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Gangolli, Esha A
; APPLICANT: Guo, Xiaojia S
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Rastelli, Luca
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc
; APPLICANT: Burgess, Catherine E
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gunther, Erik
; APPLICANT: Smithson, Glenna
; APPLICANT: Millet, Isabelle
; APPLICANT: MacDougall, John R
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-230
; CURRENT APPLICATION NUMBER: US/10/038,854
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/258,928
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: 60/259,415
; PRIOR FILING DATE: 2001-01-02
; PRIOR APPLICATION NUMBER: 60/259,785
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: 60/269,814
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/279,832
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,833
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/279,863
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/283,889
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,447
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/286,683
; PRIOR FILING DATE: 2001-04-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 411
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 130
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-038-854-130

Query Match 68.8%; Score 33; DB 15; Length 436;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 HOKRTAMF 9
|||:|
Db 41 HOKRTAVF 48

RESULT 14
US-10-424-599-159338
; Sequence 159338, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 159338
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_114902C.1.pap
US-10-424-599-159338

Query Match 66.7%; Score 32; DB 15; Length 66;
Best Local Similarity 75.0%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 HOKRTAMF 9
|||:|
Db 31 HOKRTCPF 38

RESULT 15
US-10-425-114-47963
; Sequence 47963, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 47963
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700553710_FLI.pap
US-10-425-114-47963

Query Match 66.7%; Score 32; DB 15; Length 94;
Best Local Similarity 75.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 HOKRTAMF 9
|||:|
Db 85 HOKNEAMF 92

Search completed: June 29, 2005, 05:48:12
Job time : 53.8517 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:37:59 ; Search time 16.8626 Seconds
(without alignments)
39.842 Million cell updates/sec

Title: US-08-170-344-65

Perfect score: 48

Sequence: 1 MHQKRTAMF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*

2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*

3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*

4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*

5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*

6: /cgn2_6/ptodata/1/iaa/backfiles.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	9	3	US-08-159-339A-250
2	48	100.0	23	1	US-08-363-586-3
3	48	100.0	158	4	US-09-980-523A-2
4	48	100.0	162	1	US-08-316-239B-3
5	48	100.0	162	1	US-08-316-239B-4
6	48	100.0	172	3	US-08-860-165-14
7	48	100.0	172	3	US-09-359-382-14
8	48	100.0	266	3	US-08-860-165-10
9	48	100.0	266	3	US-09-359-382-10
10	48	100.0	266	4	US-09-367-309A-1
11	43	89.6	20	2	US-08-934-915-158
12	39	81.2	182	1	US-08-117-083-10
13	33	68.8	249	4	US-09-270-767-34874
14	33	68.8	249	4	US-09-270-767-50091
15	32	66.7	225	4	US-09-489-039A-10152
16	32	66.7	520	4	US-09-270-767-43468
17	32	66.7	635	4	US-09-270-767-44609
18	32	66.7	1104	1	US-08-222-616-36
19	32	66.7	1104	3	US-08-446-648-36
20	32	66.7	1104	4	US-09-982-610-36
21	32	66.7	1104	5	PCT-US95-04228-36
22	31	64.6	193	4	US-09-107-532A-7122
23	31	64.6	274	4	US-09-540-236-2944
24	31	64.6	281	4	US-09-252-991A-21873
25	31	64.6	892	4	US-09-949-016-10407
26	31	64.6	1005	4	US-09-949-016-6391
27	30	62.5	47	2	US-08-637-759B-263

Sequence 263, App
Sequence 263, App
Sequence 9242, Ap
Sequence 6713, Ap
Sequence 24480, A
Sequence 43484, A
Sequence 25314, A
Sequence 37468, A
Sequence 52685, A
Sequence 8579, Ap
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 6725, Ap
Sequence 4947, Ap
Sequence 10136, A

28 30 62.5 47 3 US-08-871-355A-263
29 30 62.5 47 3 US-09-201-945-263
30 30 62.5 229 4 US-09-489-039A-9242
31 30 62.5 249 4 US-09-134-000C-6713
32 30 62.5 559 4 US-09-252-991A-24480
33 30 62.5 595 4 US-09-270-767-43484
34 30 62.5 655 4 US-09-252-991A-25314
35 29 60.4 46 4 US-09-270-767-37468
36 29 60.4 46 4 US-09-270-767-52685
37 29 60.4 198 4 US-09-489-039A-8579
38 29 60.4 238 1 US-08-289-699A-2
39 29 60.4 238 1 US-08-884-203-2
40 29 60.4 238 2 US-08-878-283-2
41 29 60.4 238 3 US-09-082-021-2
42 29 60.4 238 3 US-09-182-616-2
43 29 60.4 238 4 US-09-949-016-6725
44 29 60.4 239 4 US-09-134-000C-4947
45 29 60.4 246 4 US-09-949-016-10136

ALIGNMENTS

RESULT 1

US-08-159-339A-250
; Sequence 250, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 250:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-250

Query Match 100.0%; Score 48; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHQKRTAMF 9
Db 1 MHQKRTAMF 9

RESULT 2

US-08-363-586-3
; Sequence 3, Application US/08363586
; Patent No. 5629161
; GENERAL INFORMATION:
; APPLICANT: Mueller, Martin
; APPLICANT: Gissmann, Lutz
; TITLE OF INVENTION: Use of HPV-16 E6 and E7-Gene Derived
; TITLE OF INVENTION: Peptides for the Diagnostic Purpose
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363.586
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/909,296
; FILING DATE: 09-JUL-1992
; APPLICATION NUMBER: EP 91111720.8
; FILING DATE: 13-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Wadler, Linda A.
; REGISTRATION NUMBER: 33,218
; REFERENCE/DOCKET NUMBER: 02481-1195-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400

INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-363-586-3

Query Match 100.0%; Score 48; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHQKRTAMF 9
Db 1 MHQKRTAMF 9

RESULT 3

US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE

; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO/1 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 48; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHQKRTAMF 9
Db 1 MHQKRTAMF 9

RESULT 4

US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:

; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/316,239B
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein

; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 100.0%; Score 48; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHQKRTAMP 9
| | | | |
Db 1 MHQKRTAMP 9

RESULT 5

US-08-316-239B-4
; Sequence 4, Application US/08316239B

; Patent No. 5679509

; GENERAL INFORMATION:

; APPLICANT: Wheeler, Cosette M.

; ATTORNEY: Parmenter, Cheryl A.

; TITLE OF INVENTION: Methods and a Diagnostic Aid for

; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an

; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and

; TITLE OF INVENTION: Cervical Cancer

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jagtiani & Associates

; STREET: 6126 Rocky Way Court

; CITY: Centreville

; STATE: VA

; COUNTRY: USA

; ZIP: 20120-3400

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/316,239B

; FILING DATE: 30-SEP-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Jagtiani, Ajay A.

; REGISTRATION NUMBER: 35,205

; REFERENCE/DOCKET NUMBER: UNME-0001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 817-9453

; TELEFAX: (703) 803-9387

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 162 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: not relevant

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

US-08-316-239B-4

Query Match 100.0%; Score 48; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHQKRTAMP 9
| | | | |
Db 1 MHQKRTAMP 9

RESULT 6

US-08-860-165-14

; Sequence 14, Application US/08860165A

; Patent No. 6004557

; GENERAL INFORMATION:

; APPLICANT: EDWARDS, Stirling John

; APPLICANT: COX, John Cooper

; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130

; CURRENT APPLICATION NUMBER: US/08/860,165A

; CURRENT FILING DATE: 1997-09-22

; EARLIER APPLICATION NUMBER: PCT/AU95/00868

; EARLIER FILING DATE: 1995-12-20

; EARLIER APPLICATION NUMBER: AU PN0157

; EARLIER FILING DATE: 1994-12-20

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14

; LENGTH: 172

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion

US-08-860-165-14

Query Match 100.0%; Score 48; DB 3; Length 172;

Best Local Similarity 100.0%; Pred. No. 0.017;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHQKRTAMP 9
| | | | |
Db 70 MHQKRTAMP 78

RESULT 7

US-09-359-382-14

; Sequence 14, Application US/09359382

; Patent No. 6306397

; GENERAL INFORMATION:

; APPLICANT: EDWARDS, Stirling John

; APPLICANT: COX, John Cooper

; APPLICANT: WEBB, Elizabeth Ann

; APPLICANT: FRAZER, Ian

; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

; FILE REFERENCE: 01727/0148

; CURRENT APPLICATION NUMBER: US/09/359,382

; CURRENT FILING DATE: 1999-07-23

; EARLIER APPLICATION NUMBER: US 08/860,165

; EARLIER FILING DATE: 1997-09-22

; EARLIER APPLICATION NUMBER: PCT/AU95/00868

; EARLIER FILING DATE: 1995-12-20

; EARLIER APPLICATION NUMBER: AU PN0157/94

; EARLIER FILING DATE: 1994-12-20

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14

; LENGTH: 172

; TYPE: PRT

; ORGANISM: Human papillomavirus type 16

US-09-359-382-14

Query Match 100.0%; Score 48; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHQKRTAMP 9
| | | | |
Db 70 MHQKRTAMP 78

RESULT 8

US-08-860-165-10

; Sequence 10, Application US/08860165A

; Patent No. 6004557

; GENERAL INFORMATION:

; APPLICANT: EDWARDS, Stirling John

; APPLICANT: COX, John Cooper

; APPLICANT: WEBB, Elizabeth Ann

```

; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCI/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match          100.0%; Score 48; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. NO. 0.026;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 |||||

Db 1 MHOQRTAMP 9

RESULT 11

US-08-934-915-158

; Sequence 158, Application US/08934915

APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836

ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. FOUTCH
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820

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; ;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-934-915-158
Query Match      89.6%;   Score 43;   DB 2;   Length 20;
Best Local Similarity 100.0%; Pred. No. 0.022;
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 HQKRTAMF 9
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Db 1 HQKRTAMF 8

RESULT 12
US-08-117-083-10
; Sequence 10, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Bourns, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
; OTHER INFORMATION: /note= "Xaa refers to stop codon in
; OTHER INFORMATION: the open reading frame."
US-08-117-083-10

Query Match 81.2%; Score 39; DB 1; Length 182;
Best Local Similarity 88.9%; Pred. No. 1.3; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0;

Qy 1 MHQKRTAMF 9
   |||||
Db 2 MDQKRTAMF 10

RESULT 13
US-09-270-767-34874
; Sequence 34874, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
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; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34874
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-34874

Query Match 68.8%; Score 33; DB 4; Length 249;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MHQKRTAMF 9
   :|||
Db 215 IHKRTAMY 223

RESULT 14
US-09-270-767-50091
; Sequence 50091, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50091
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-50091

Query Match 68.8%; Score 33; DB 4; Length 249;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MHQKRTAMF 9
   :|||
Db 215 IHKRTAMY 223

RESULT 15
US-09-489-039A-10152
; Sequence 10152, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10152
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10152

Query Match 66.7%; Score 32; DB 4; Length 225;
Best Local Similarity 85.7%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 2 HOKETAM 8
| | | | |
Db 5 HOKKRAM 11

Search completed: June 29, 2005, 01:44:23
Job time : 17.9126 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2005, 23:28:22 ; Search time 54.2473 Seconds
(without alignments)
84.958 Million cell updates/sec

Title: US-08-170-344-64
Perfect score: 54
Sequence: 1 VCPICSQKP 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	26	Q84267	Q84267 human papil
2	54	100.0	98	1 VET_HPV16	P03129 human papil
3	54	100.0	98	O11650	O11650 human papil
4	54	100.0	98	O12337	O12337 human papil
5	54	100.0	98	O12338	O12338 human papil
6	54	100.0	98	Q8QD2	Q8QD2 human papil
7	54	100.0	98	Q8QD3	Q8QD3 human papil
8	54	100.0	98	Q8QD4	Q8QD4 human papil
9	54	100.0	98	Q778H3	Q778H3 human papil
10	54	100.0	98	Q778H5	Q778H5 human papil
11	50	92.6	98	Q8V1J0	Q8V1J0 human papil
12	49	90.7	95	Q8T797	Q8T797 methanosarc
13	45	83.3	98	1 VET_HPV11	P04020 human papil
14	44	81.5	565	2 Q8TF36	Q8TF36 homo sapien
15	44	81.5	678	2 Q643S1	Q643S1 gallus gall
16	44	81.5	685	1 BMER_HUMAN	Q8n8u9 homo sapien
17	44	81.5	685	1 BMER_MOUSE	Q8cj69 mus musculu
18	43	79.6	104	2 Q8Q8B0	Q8Q8B0 homo sapien
19	43	79.6	171	2 Q781V7	Q781V7 mus musculu
20	43	79.6	349	2 Q8CQ04	Q8CQ04 m mus muscu
21	43	79.6	1496	1 CA25_HUMAN	P05997 homo sapien
22	42	77.8	128	2 Q86DM0	Q86dm0 homo sapien
23	42	77.8	185	2 Q8KK54	Q8KK54 proteus vul
24	42	77.8	227	2 Q4C20	Q4C20 arabidopsis
25	42	77.8	237	2 Q96A37	Q96a37 homo sapien
26	42	77.8	237	2 Q6J1I7	Q6j1i7 rattus norv
27	42	77.8	249	2 Q8ZGP6	Q8zgp6 oryza sativ
28	42	77.8	371	2 Q7QSL9	Q7qsl9 giardia lam
29	41	75.9	56	2 Q37902	Q37902 xanthomonas
30	41	75.9	74	2 Q73989	Q73989 pyrococcus
31	41	75.9	95	2 Q8PW93	Q8pw93 methanosarc

32	41	75.9	95	2	Q9UZ74	Q9uz74 pyrococcus
33	41	75.9	96	2	Q8U3F8	Q8u3f8 pyrococcus
34	41	75.9	250	2	Q805A6	Q805a6 gallus gall
35	41	75.9	279	2	Q7Q8X6	Q7q8x6 anopheles g
36	41	75.9	512	2	Q7P249	Q7p249 chromobacte
37	41	75.9	1000	2	Q7QXM4	Q7qxm4 giardia lam
38	40	74.1	88	2	Q7RSQ3	Q7rsq3 giardia lam
39	40	74.1	126	2	Q66IR3	Q66ir3 xenopus lae
40	40	74.1	220	2	Q6JON0	Q6jon0 oryzias lat
41	40	74.1	221	2	Q6AXJ1	Q6axj1 brachydanio
42	40	74.1	221	2	Q6JON1	Q6jon1 brachydanio
43	40	74.1	223	2	Q6IZ49	Q6iz49 xenopus tro
44	40	74.1	225	2	Q6J2I1	Q6j2i1 gallus gall
45	40	74.1	226	2	Q6J2U7	Q6j2u7 xenopus lae

ALIGNMENTS

RESULT 1

Q84267 ID Q84267 PRELIMINARY; PRT; 26 AA.
AC Q84267;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E7 ORF (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89095007; PubMed=2536104;
RA Choo K.-B., Cheung W.-F., Liew L.-N., Lee H.-H., Han S.-H.;
RT "Presence of Caenacted Human Papillomavirus Type 16 Episomes in a
RT Cervical Carcinoma Cell Line."
RL J. Virol. 63:782-789 (1989).
DR EMBL; M24215; AAA46944.1; -
DR InterPro: IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON_TER
SQ SEQUENCE 26 AA; 2799 MW; 91C16F1D34D18B34 CRC64;

Query Match 100.0%; Score 54; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
Db 18 VCPICSQKP 26

RESULT 2

VE7_HPV16 ID VE7_HPV16 STANDARD; PRT; 98 AA.
AC P03129;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE E7 protein.
OS Name=E7;
GN Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85246220; PubMed=2990099;
RA Seedorf K., Kramer G., Durst M., Suhai S., Rowekamp W.G.;
RT "Human papillomavirus type 16 DNA sequence."
RL Virology 145:181-185 (1985).

```
RP SEQUENCE FROM N.A.
RX MEDLINE=90218027; PubMed=2157796;
RA Schneider-Maunoury S., Pehau-Arnautet G., Breitburd F., Orth G.;
RT "Expression of the human papillomavirus type 16 genome in SK-v cells,
RL a line derived from a vulvar intraepithelial neoplasia.";
RN J. Gen. Virol. 71:809-817(1990).
[3]
RP SEQUENCE FROM N.A.
RA Song Y.-S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Lee H.P.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Girardo E., Giraldo G.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
[5]
RP FUNCTION.
RX MEDLINE=88223347; PubMed=2836062;
RA Phelps W.C., Yee C.L., Mungler K., Howley P.M.;
RT "The human papillomavirus type 16 E7 gene encodes transactivation and
RL transformation functions similar to those of adenovirus E1A.";
CC Cell 53:539-547(1988).
CC -!- FUNCTION: E7 protein has both transforming and trans-activating
CC activities.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL; K02718; AAA46940.1; -
DR EMBL; D00735; BAA00633.1; -
DR EMBL; U76411; AAB18962.1; -
DR EMBL; U76412; AAB18963.1; -
DR EMBL; U76413; AAB18964.1; -
DR EMBL; AF003020; AAB70737.1; -
DR EMBL; AF003023; AAB70740.1; -
DR EMBL; AF003024; AAB70741.1; -
DR EMBL; AF003025; AAB70742.1; -
DR EMBL; AF003026; AAB70743.1; -
DR PIR; A03688; W7WLHS.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
KW DNA-binding; Early protein; Oncogene; Trans-acting factor;
KW Transcription regulation.
FT SITE 58 61 C-XX-C motif-1.
FT SITE 91 94 C-XX-C motif-2.
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 100.0%; Score 54; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
Db 90 VCPICSQKP 98

RESULT 3
ID O11650 PRELIMINARY; PRT; 98 AA.
AC O11650;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative transforming protein E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
```

```
RP SEQUENCE FROM N.A.
RX MEDLINE=97407827; PubMed=9264576; DOI=10.1006/gyno.1997.4756;
RA Song Y.-S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Chang W.H.,
RA Lee H.P.;
RT "Major sequence variants in E7 gene of human papillomavirus type 16
RL from cervical cancerous and noncancerous lesions of Korean women.";
RN Gynecol. Oncol. 66:275-281(1997).
[2]
RP SEQUENCE FROM N.A.
RA Song Y.-S., Kee S.-H., Kim J.-W., Park N.-H., Kang S.-B., Chang W.-H.,
RA Lee H.-P.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Terai M., Ma Z., Burk R.D.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.-S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RL for cervical neoplasia in southern China.";
RN J. Infect. Dis. 186:696-700(2002).
[5]
RP SEQUENCE FROM N.A.
RA Terai M., Fu L., Ma Z., Burk R.D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U76404; AAC58243.1; -
DR EMBL; AF472509; AA015706.1; -
DR EMBL; AF486326; AAL96631.1; -
DR EMBL; AF486327; AAL96632.1; -
DR EMBL; AF486330; AAL96635.1; -
DR EMBL; AF486331; AAL96636.1; -
DR EMBL; AF486332; AAL96637.1; -
DR EMBL; AF486333; AAL96638.1; -
DR EMBL; AF486334; AAL96639.1; -
DR EMBL; AF486336; AAL96641.1; -
DR EMBL; AF486338; AAL96643.1; -
DR EMBL; AF486346; AAL96651.1; -
DR EMBL; AF486350; AAL96655.1; -
DR EMBL; AF486351; AAL96656.1; -
DR EMBL; AF534061; AAQ10404.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 100.0%; Score 54; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
Db 90 VCPICSQKP 98

RESULT 4
ID O12337 PRELIMINARY; PRT; 98 AA.
AC O12337;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
```

RA Beth-Giraldo E., Giraldo G.;
 RT "Sequence variations and viral genomic state of human papillomavirus
 type 16 in penile carcinomas from Ugandan patients.";
 RL J. Gen. Virol. 78:2199-2208(1997).
 DR EMBL; AF003021; AAB70738.1; -.
 DR InterPro: IPR000148; Papvi_E7.
 DR Pfam: PF00527; E7; 1.
 SQ SEQUENCE 98 AA; 11056 MW; 19DEB8F14CD2C705 CRC64;

Query Match 100.0%; Score 54; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.096;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
 |||||
 Db 90 VCPICSQKP 98

RESULT 5

OL2338
 ID OI2338 PRELIMINARY; PRT; 98 AA.
 AC OI2338;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE E7 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97437474; PubMed=9292007;
 RA Tonnesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
 RA Beth-Giraldo E., Giraldo G.;
 RT "Sequence variations and viral genomic state of human papillomavirus
 type 16 in penile carcinomas from Ugandan patients.";
 RL J. Gen. Virol. 78:2199-2208(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Jinhu X., Xinxing W., Yun T.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF003022; AAB70739.1; -.
 DR EMBL; AF477385; AAM03025.1; -.
 DR InterPro: IPR000148; Papvi_E7.
 DR Pfam: PF00527; E7; 1.
 SQ SEQUENCE 98 AA; 10969 MW; 9BD6125334CCEA59B CRC64;

Query Match 100.0%; Score 54; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.096;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
 |||||
 Db 90 VCPICSQKP 98

RESULT 6

Q8QRD2
 ID Q8QRD2 PRELIMINARY; PRT; 98 AA.
 AC Q8QRD2;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE E7 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22182962; PubMed=12195358;
 RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,

RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
 RT "Human papillomavirus type 16 intratypic variant infection and risk
 for cervical neoplasia in southern China.";
 RL J. Infect. Dis. 186:696-700(2002).
 DR EMBL; AF486345; AAL96650.1; -.
 DR InterPro: IPR000148; Papvi_E7.
 DR Pfam: PF00527; E7; 1.
 SQ SEQUENCE 98 AA; 11045 MW; 9C4F8C534CD76C4B CRC64;

Query Match 100.0%; Score 54; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.096;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
 |||||
 Db 90 VCPICSQKP 98

RESULT 7

Q8QRD3
 ID Q8QRD3 PRELIMINARY; PRT; 98 AA.
 AC Q8QRD3;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE E7 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22182962; PubMed=12195358;
 RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
 RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
 RT "Human papillomavirus type 16 intratypic variant infection and risk
 for cervical neoplasia in southern China.";
 RL J. Infect. Dis. 186:696-700(2002).
 DR EMBL; AF486344; AAL96649.1; -.
 DR InterPro: IPR000148; Papvi_E7.
 DR Pfam: PF00527; E7; 1.
 SQ SEQUENCE 98 AA; 11021 MW; 9BD6125946D2C3E1 CRC64;

Query Match 100.0%; Score 54; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.096;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
 |||||
 Db 90 VCPICSQKP 98

RESULT 8

Q8QRD4
 ID Q8QRD4 PRELIMINARY; PRT; 98 AA.
 AC Q8QRD4;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE E7 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22182962; PubMed=12195358;
 RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
 RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
 RT "Human papillomavirus type 16 intratypic variant infection and risk
 for cervical neoplasia in southern China.";
 RL J. Infect. Dis. 186:696-700(2002).
 DR EMBL; AF486329; AAL96634.1; -.
 DR

DR InterPro: IPR000148; Papvi_E7.

DR Pfam: PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11025 MW; 86E24B234CC3281B CRC64;

Query Match 100.0%; Score 54; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
| | | | | | | | | |
Db 90 VCPICSQKP 98

RESULT 9

ID Q778H3 PRELIMINARY; PRT; 98 AA.
AC Q778H3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388063; CAB45119.1; -.
DR InterPro: IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 98
SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 100.0%; Score 54; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
| | | | | | | | | |
Db 90 VCPICSQKP 98

RESULT 10

ID Q778H5 PRELIMINARY; PRT; 98 AA.
AC Q778H5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388062; CAB45117.1; -.
DR InterPro: IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 98
SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 100.0%; Score 54; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
| | | | | | | | | |
Db 90 VCPICSQKP 98

RESULT 11

ID Q8V1J0 PRELIMINARY; PRT; 98 AA.
AC Q8V1J0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Jinhu X., Xinxiang W., Yun T.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF461264; AAL66736.1; -.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10997 MW; 98D610834CCEA59B CRC64;

Query Match 92.6%; Score 50; DB 2; Length 98;
Best Local Similarity 88.9%; Pred. No. 0.46;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VCPICSQKP 9
| | | | | | | | | |
Db 90 VCPICSRKP 98

RESULT 12

ID Q8TT97 PRELIMINARY; PRT; 95 AA.
AC Q8TT97;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein MA0540.
GN OrderedLocusNames=MA0540;
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=1932760; PubMed=11932239; DOI=10.1101/gr.223902;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atncor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hederich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.P., Jing H., Macario A.J.L., Paulsen I.T.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542(2002).
DR EMBL; AE010714; AAM03984.1; -.
DR Pfam; PF03819; MazG; 1.
DR PIRSF; PIRSF006690; UCP006690_pph; 1.

```
KW Complete proteome.
SQ SEQUENCE 95 AA; 10875 MW; 8A68E2F4EFA616BA CRC64;

Query Match
Best Local Similarity 90.7%; Score 49; DB 2; Length 95;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 VCPICSQKP 9
Db 82 VCPTCSQKP 90

RESULT 13
VE7 HPV11 STANDARD; PRT; 98 AA.
AC P04020;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE E7 protein.
GN Name=E7;
OS Human papillomavirus type 11.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10580;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86181601; PubMed=3008427;
RA Dartmann K., Schwarz E., Glassmann L., Zur Hausen H.;
RT "The nucleotide sequence and genome organization of human papilloma
virus type 11."
RL Virology 151:124-130 (1986).
RN [2]
RP SEQUENCE FROM N.A.
RA Fife K.H., Fan L., Pritch M.H., Bryan J., Brown D.R.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: E7 protein has both transforming and trans-activating
activities.
CC -----
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CC -----
DR EMBL; M14119; AAA46928.1; -
DR EMBL; L36108; AAA21704.1; -
DR PIR; A03690; W7ML11.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
KW DNA-binding; Early protein; Oncogene; Trans-acting factor;
KW Transcription regulation.
FT SITE 58 61 C-XX-C motif-1.
FT SITE 91 94 C-XX-C motif-2.
FT SITE 91 94
SQ SEQUENCE 98 AA; 10889 MW; AAC9A60C933E1F6 CRC64;

Query Match
Best Local Similarity 83.3%; Score 45; DB 1; Length 98;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 VCPICSQKP 9
Db 90 VCPCAPKP 98

RESULT 14
Q8TF36 PRELIMINARY; PRT; 565 AA.
AC Q8TF36;
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
```

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DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE KIAA1965 protein (Fragment).
GN Name=KIAA1965;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
EX MEDLINE=21842142; PubMed=11853319;
RA Negase T., Kikuno R., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XXII.
RT The complete sequences of 50 new cDNA clones which code for large
RT proteins."
RL DNA Res. 8:319-327 (2001).
DR EMBL; AB075845; BAB85551.1; -
DR InterPro; IPR002919; Cyrich_TIL.
DR InterPro; IPR009041; PMP_SGCI.
DR InterPro; IPR000294; VitK_dep_GLA.
DR InterPro; IPR001007; VWF_C.
DR InterPro; IPR001846; VWF_D.
DR Pfam; PF01826; TIL; 1.
DR Pfam; PF00093; VWC; 3.
DR Pfam; PF00094; VMD; 1.
DR SMART; SM00214; VWC; 1.
DR SMART; SM00216; VMD; 1.
DR PROSITE; PS00011; GLA_1; UNKNOWN_1.
DR PROSITE; PS01208; VWF_1; UNKNOWN_2.
DR PROSITE; PS0184; VWF_2; 2.
FT NON TER 1
SQ SEQUENCE 565 AA; 62934 MW; 1F7A15206F2B9D45 CRC64;

Query Match
Best Local Similarity 81.5%; Score 44; DB 2; Length 565;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 2 CPICSQKP 9
Db 234 CPICTEKP 241

RESULT 15
Q643S1 PRELIMINARY; PRT; 678 AA.
AC Q643S1;
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Crossveinless-2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Coles E.G., Christiansen J.H., Economou A., Bronner-Fraser M.,
RA Wilkinson D.G.;
RT "A vertebrate crossveinless-2 homolog modulates BMP activity and
RT neural crest cell migration."
RL Development 0:0-0 (2004).
DR EMBL; AY731507; AAU34017.1; -
DR SEQUENCE 678 AA; 75031 MW; B4EF49FAEDCCCB CRC64;

Query Match
Best Local Similarity 81.5%; Score 44; DB 2; Length 678;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Oy 2 CPICSQKP 9
Db 347 CPICTEKP 354
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Search completed: June 29, 2005, 01:34:45
Job time : 56.2473 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:28:22 ; Search time 54.2473 Seconds
(without alignments)
84.958 Million cell updates/sec

Title: US-08-170-344-63
Perfect score: 57
Sequence: 1 TGRMCCR 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	103	2 Q919D6	Q919D6 human papil
2	57	100.0	130	2 Q919B4	Q919B4 human papil
3	57	100.0	130	2 Q919B8	Q919B8 human papil
4	57	100.0	130	2 Q919C0	Q919C0 human papil
5	57	100.0	130	2 Q919C2	Q919C2 human papil
6	57	100.0	130	2 Q919C8	Q919C8 human papil
7	57	100.0	130	2 Q919D0	Q919D0 human papil
8	57	100.0	138	2 Q919D2	Q919D2 human papil
9	57	100.0	143	2 Q919B6	Q919B6 human papil
10	57	100.0	143	2 Q919C4	Q919C4 human papil
11	57	100.0	151	2 Q12335	Q12335 human papil
12	57	100.0	151	2 Q12336	Q12336 human papil
13	57	100.0	151	2 Q76TS0	Q76TS0 human papil
14	57	100.0	151	2 Q77E16	Q77E16 human papil
15	57	100.0	151	2 Q77E16	Q77E16 human papil
16	57	100.0	151	2 Q77JC7	Q77JC7 human papil
17	57	100.0	151	2 Q77ZJ5	Q77ZJ5 human papil
18	57	100.0	151	2 Q80963	Q80963 human papil
19	57	100.0	151	2 Q80966	Q80966 human papil
20	57	100.0	151	2 Q89640	Q89640 human papil
21	57	100.0	151	2 Q89648	Q89648 human papil
22	57	100.0	151	2 Q89708	Q89708 human papil
23	57	100.0	151	2 Q89755	Q89755 human papil
24	57	100.0	151	2 Q89852	Q89852 human papil
25	57	100.0	151	2 Q89887	Q89887 human papil
26	57	100.0	151	2 Q8B564	Q8B564 human papil
27	57	100.0	151	2 Q8BB19	Q8BB19 human papil
28	57	100.0	151	2 Q8BB20	Q8BB20 human papil
29	57	100.0	151	2 Q8BB21	Q8BB21 human papil
30	57	100.0	151	2 Q9W8C3	Q9W8C3 human papil
31	57	100.0	151	2 Q9W931	Q9W931 human papil

32	57	100.0	151	2 Q9WMP2	Q9WMP2 human papil
33	57	100.0	151	2 Q9WMP3	Q9WMP3 human papil
34	57	100.0	151	2 Q9WMP4	Q9WMP4 human papil
35	57	100.0	151	2 Q9WMP5	Q9WMP5 human papil
36	57	100.0	158	1 VE6 HPV16	P03126 human papil
37	57	100.0	158	2 Q8JMU8	Q8JMU8 human papil
38	57	100.0	158	2 Q8QHN0	Q8QHN0 human papil
39	57	100.0	158	2 Q8QHP5	Q8QHP5 human papil
40	57	100.0	158	2 Q8QHT0	Q8QHT0 human papil
41	57	100.0	158	2 Q8QRT5	Q8QRT5 human papil
42	57	100.0	158	2 Q8QRD6	Q8QRD6 human papil
43	57	100.0	158	2 Q8QRD7	Q8QRD7 human papil
44	57	100.0	158	2 Q8QRD8	Q8QRD8 human papil
45	57	100.0	158	2 Q8QRD9	Q8QRD9 human papil

ALIGNMENTS

RESULT 1

Q919D6 PRELIMINARY; PRT; 103 AA.
AC Q919D6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=1846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF0404692; AAL01342.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1 1
SQ SEQUENCE 103 AA; 12422 MW; 6F90CBAF1F25449B CRC64;

Query Match 100.0%; Score 57; DB 2; Length 103;

Best Local Similarity 100.0%; Pred. No. 0.22; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRMCCR 9

Db 85 TGRMCCR 93

RESULT 2

Q919B4 PRELIMINARY; PRT; 130 AA.
AC Q919B4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=1846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).

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DR EMBL; AF404703; AAL01363.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227BEDDC CRC64;

Query Match 100.0%; Score 57; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRCMSCCR 9
Db 112 TGRCMSCCR 120

RESULT 3
Q919B8 ID Q919B8 PRELIMINARY; PRT; 130 AA.
AC Q919B8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404703; AAL01359.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15775 MW; 92D3C07BF96B092F CRC64;

Query Match 100.0%; Score 57; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRCMSCCR 9
Db 112 TGRCMSCCR 120

RESULT 4
Q919C0 ID Q919C0 PRELIMINARY; PRT; 130 AA.
AC Q919C0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404700; AAL01357.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;

DR EMBL; AF404703; AAL01363.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRCMSCCR 9
Db 112 TGRCMSCCR 120

RESULT 5
Q919C2 ID Q919C2 PRELIMINARY; PRT; 130 AA.
AC Q919C2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404699; AAL01355.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRCMSCCR 9
Db 112 TGRCMSCCR 120

RESULT 6
Q919C8 ID Q919C8 PRELIMINARY; PRT; 130 AA.
AC Q919C8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404696; AAL01349.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;

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Query Match 100.0%; Score 57; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRCMSCCR 9
Db 112 TGRCMSCCR 120

RESULT 7

Q919D0 PRELIMINARY; PRT; 130 AA.
AC Q919D0; (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404694; AAL01347.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR PFam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15735 MW; 9EPB30EEDCA21AF3 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRCMSCCR 9
Db 112 TGRCMSCCR 120

RESULT 8

Q919D2 PRELIMINARY; PRT; 138 AA.
AC Q919D2; (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404694; AAL01345.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR PFam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 138 AA; 16696 MW; 481E5AEA90895FC2 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.28;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TGRCMSCCR 9
Db 120 TGRCMSCCR 128

RESULT 9

Q919B6 PRELIMINARY; PRT; 143 AA.
AC Q919B6; (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404702; AAL01361.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR PFam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;

Query Match 100.0%; Score 57; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRCMSCCR 9
Db 125 TGRCMSCCR 133

RESULT 10

Q919C4 PRELIMINARY; PRT; 143 AA.
AC Q919C4; (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404698; AAL01353.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR PFam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRCMSCCR 9

Db 125 TGRCSOCCR 133
|||||

RESULT 11

O12335 PRELIMINARY; PRT; 151 AA.
AC O12335
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Beth-Girardo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003015; AAB70732.1; --
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18238 MW; BEF32A8B016CC88B CRC64;

Query Match 100.0%; Score 57; DB 2; Length 151;

Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGRCSOCCR 9
|||||
Db 133 TGRCSOCCR 141

RESULT 12

O12336 PRELIMINARY; PRT; 151 AA.
AC O12336
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Beth-Girardo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003016; AAB70733.1; --
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;

Query Match 100.0%; Score 57; DB 2; Length 151;

Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGRCSOCCR 9
|||||

Db 133 TGRCSOCCR 141

RESULT 13

Q76TSO PRELIMINARY; PRT; 151 AA.
AC Q76TSO
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
populations characterized by nucleotide sequence analysis of the E6,
L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34114; AAA91661.1; --
DR EMBL; U34125; AAA91672.1; --
DR EMBL; U34130; AAA91677.1; --
DR EMBL; U34131; AAA91678.1; --
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;

Query Match 100.0%; Score 57; DB 2; Length 151;

Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGRCSOCCR 9
|||||
Db 133 TGRCSOCCR 141

RESULT 14

Q778I6 PRELIMINARY; PRT; 151 AA.
AC Q778I6
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders F.J., Vossen M.T., Klaassen E., Voorhorst F.,
Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388056; CAB45104.1; --
DR EMBL; AJ388061; CAB45114.1; --
DR EMBL; AJ388066; CAB45124.1; --
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.

DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18334 MW; FF8F2A2FCBBA6C02 CRC64;
Query Match 100.0%; Score 57; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.3; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGRCMSCCR 9
| | | | | | | | |
Db 133 TGRCMSCCR 141

RESULT 15
Q77E16 PRELIMINARY; PRT; 151 AA.
AC Q77E16;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE E6 oncoprotein (E6 protein).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteswoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
EL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AF469197; AAC15691.1; -;
DR EMBL; AJ388063; CAB45118.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CFLF CRC64;

Query Match 100.0%; Score 57; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.3; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGRCMSCCR 9
| | | | | | | | |
Db 133 TGRCMSCCR 141

Search completed: June 29, 2005, 01:34:43
Job time : 55.2473 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:32:21 ; Search time 11.2747 Seconds
(without alignments)
76.805 Million cell updates/sec

Title: US-08-170-344-63

Perfect score: 57

Sequence: 1 TGRMSSCCR 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	158	1 W6WLHS	protein E6 - human
2	43	75.4	149	1 W6WL35	E6 protein - human
3	42	73.7	137	1 W6WLEB	E6 protein - bovin
4	42	73.7	139	1 W6WL82	muscarinic acetylcholine receptor
5	41	71.9	460	2 A31897	muscarinic acetylcholine receptor
6	41	71.9	460	2 I51837	muscarinic acetylcholine receptor
7	41	71.9	460	2 S09508	muscarinic acetylcholine receptor
8	41	71.9	460	2 A24325	muscarinic acetylcholine receptor
9	41	71.9	460	2 A29514	muscarinic acetylcholine receptor
10	40	70.2	222	2 E84560	hypothetical protein
11	40	70.2	280	2 G84839	late embryogenesis
12	40	70.2	355	1 H71363	conserved hypothetical protein
13	40	70.2	369	2 E84542	hypothetical protein
14	40	70.2	6420	2 T30283	polyketide synthase
15	39	68.4	149	1 W6WL31	E6 protein - human
16	39	68.4	174	1 JQ1625	small hydrophobic
17	39	68.4	305	2 T20906	hypothetical protein
18	38.5	67.5	305	2 B84274	heme biosynthesis
19	38	66.7	101	2 JQ0877	cycO2 protein precursor
20	38	66.7	143	2 A72759	hypothetical protein
21	38	66.7	191	1 W6WL81	collagen - nematode
22	38	66.7	295	2 A44984	hypothetical protein
23	38	66.7	310	2 T17980	hypothetical protein
24	38	66.7	591	2 C71460	hypothetical protein
25	38	66.7	747	2 T33488	hypothetical protein
26	38	66.7	911	2 S28098	guanine-nucleotide
27	37	64.9	152	2 T18975	hypothetical protein
28	37	64.9	164	2 T24272	hypothetical protein
29	37	64.9	188	2 T15651	hypothetical protein

ALIGNMENTS

RESULT 1

W6WLHS

protein E6 - human papillomavirus type 16

C:Species: human papillomavirus type 16

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03682; T10427

R:Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virolgy 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03682

A:Molecule type: DNA

A:Residues: 1-158 <SEE>

A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333033

R:Kennedy, I.M.; Haddock, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human papillomavirus type 16 genome acts at the level of transcription

A:Reference number: Z17014; MUID:91162763; PMID:1848319

A:Accession: T10427

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-158 <KEN>

A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

C:Genetics:

A:Gene: E6

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:37-73/Region: zinc finger CCCC motif

F:110-146/Region: zinc finger CCCC motif

Query Match

Best Local Similarity 100.0%; Score 57; DB 1; Length 158;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

1 TGRMSSCCR 9

|||||||

Db 140 TGRMSSCCR 148

RESULT 2

W6WL35

E6 protein - human papillomavirus type 35

C:Species: human papillomavirus type 35

A:Note: host Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C:Accession: E40824; S36521

R:Marich, J.E.; Pontele, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.

Virolgy 186, 770-776, 1992

A:Title: The phylogenetic relationship and complete nucleotide sequence of human papilloma virus type 35

A:Reference number: A40824; MUID:92124753; PMID:1310198

A:Accession: E40824

A:Status: translation not shown

A:Molecule type: DNA
A:Residues: 1-149 <MAR>
A:Cross-references: UNIPROT:P27228; GB:M74117; NID:G333050; PIDN:AAA46966.1; PID:G333051
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36521
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-149
A:Cross-references: EMBL:X74477; NID:G396997; PIDN:CAA52561.1; PID:G396998
A:Experimental source: strain 35H
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match 75.4%; Score 43; DB 1; Length 149;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRCMSC 7
|||||
Db 133 TGRCMSC 139

RESULT 3
W6WLEB
E6 protein - bovine papillomavirus type 1
C:Species: bovine papillomavirus type 1
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: C18151
R:Chen, E.Y.; Howley, P.M.; Levinson, A.D.; Seeburg, P.H.
Nature 299, 529-534, 1982
A:Title: The primary structure and genetic organization of the bovine papillomavirus type 1
A:Reference number: A93289; MUID:83012974; PMID:6289124
A:Accession: C18151
A:Molecule type: DNA
A:Residues: 1-137 <CHE>
A:Cross-references: UNIPROT:P06931; GB:X02346; GB:J02044; GB:M24622; GB:X00473; NID:G609
R:Danon, O.; Engel, L.W.; Chen, E.Y.; Yaniv, M.; Howley, P.M.
J. Virol. 46, 557-566, 1983
A:Title: Comparative analysis of the human type 1a and bovine type 1 papillomavirus genes
A:Reference number: A92993; MUID:83189357; PMID:6302319
A:Contents: annotation
R:Androphy, E.J.; Schiller, J.T.; Lowy, D.R.
Science 230, 442-445, 1985
A:Title: Identification of the protein encoded by the E6 transforming gene of bovine papillomavirus type 1
A:Reference number: A94282; MUID:86018841; PMID:2996134
A:Contents: annotation; identification of the protein
C:Comment: This protein is present in the cell nucleus and the cellular membrane.
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; transforming protein; zinc finger

Query Match 73.7%; Score 42; DB 1; Length 137;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GRCMSCCR 9
|||||
Db 122 GRCYDCCR 129

RESULT 4
W6WLEB
E6 protein - bovine papillomavirus type 2
C:Species: bovine papillomavirus type 2
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C:Accession: H31169
R:Groff, D.E.; Mitra, R.; Lancaster, W.D.
submitted to GenBank, May 1988
A:Reference number: A94519

A:Accession: H31169
A:Molecule type: DNA
A:Residues: 1-139 <GRO>
A:Cross-references: UNIPROT:P11302; GB:M20219; GB:M19551; NID:G332996
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:17-55/Region: zinc finger CCCC motif
F:90-129/Region: zinc finger CCCC motif

Query Match 73.7%; Score 42; DB 1; Length 139;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GRCMSCCR 9
|||||
Db 124 GRCYDCCR 131

RESULT 5
A31897
muscarinic acetylcholine receptor M1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 24-Nov-1999
C:Accession: A31897
R:Shapiro, R.A.; Scherer, N.M.; Habecker, B.A.; Subers, E.M.; Nathanson, N.M.
J. Biol. Chem. 263, 18397-18403, 1988
A:Title: Isolation, sequence, and functional expression of the mouse M1 muscarinic acetylcholine receptor
A:Reference number: A92694; MUID:89054021; PMID:2848036
A:Accession: A31897
A:Molecule type: DNA
A:Residues: 1-460 <SHA>
A:Note: the authors translated the codon ATC for residue 119 as Thr
R:Shapiro, R.A.; Scherer, N.M.; Habecker, B.A.; Subers, E.M.; Nathanson, N.M.
J. Biol. Chem. 264, 6596, 1989
A:Reference number: A92742
A:Contents: annotation; erratum, correct translation of residue 119
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phosphatase
F:23-50/Domain: transmembrane #status predicted <TM1>
F:62-93/Domain: transmembrane #status predicted <TM2>
F:100-121/Domain: transmembrane #status predicted <TM3>
F:142-168/Domain: transmembrane #status predicted <TM4>
F:187-209/Domain: transmembrane #status predicted <TM5>
F:367-387/Domain: transmembrane #status predicted <TM6>
F:402-420/Domain: transmembrane #status predicted <TM7>

Query Match 71.9%; Score 41; DB 2; Length 460;
Best Local Similarity 75.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GRCMSCCR 9
|||||
Db 257 GRCRCRCC 264

RESULT 6
151837
muscarinic receptor - rat
C:Species: Rattus sp. (rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 24-Nov-1999
C:Accession: I51837
R:Iwai, J.; Smith, T.L.; Mei, L.; Ikeda, M.; Fujiwara, Y.; Gomez, J.; Halonen, M.; Roesske, J.R.
Adv. Exp. Med. Biol. 287, 313-330, 1991
A:Title: The molecular properties of the M1 muscarinic receptor and its regulation of calcium release from the sarcoplasmic reticulum
A:Reference number: I51837; MUID:92101806; PMID:1759615
A:Accession: I51837
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-460 <RGS>
A:Cross-references: GB:S73971; NID:G241253; PIDN:AAB20705.1; PID:G241254
C:Genetics:
A:Gene: ml
C:Superfamily: vertebrate rhodopsin

A:Molecule type: mRNA
A:Residues: 1-460 <KUR>
A:Cross-references: UNIPROT:P04761; GB:X04413; NID:g1863; PIDN:CAA28003.1; PID:g1866
C:Superfamily: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho
F:25-50/Domain: transmembrane #status predicted <TM1>
F:62-93/Domain: transmembrane #status predicted <TM2>
F:100-121/Domain: transmembrane #status predicted <TM3>
F:142-168/Domain: transmembrane #status predicted <TM4>
F:187-209/Domain: transmembrane #status predicted <TM5>
F:367-387/Domain: transmembrane #status predicted <TM6>
F:402-420/Domain: transmembrane #status predicted <TM7>

Query Match 71.9%; Score 41; DB 2; Length 460;
Best Local Similarity 75.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GRCMSCCR 9
Db 257 GRCRCRCC 264

RESULT 9
A29514
muscarinic acetylcholine receptor M1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1989 #sequence revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: A94518; A94293; A37121; A29514
R:Bonner, T.I
submitted to GenBank, July 1987
A:Reference number: A94518
A:Accession: A94518
A:Molecule type: mRNA
A:Residues: 1-460 <BO1>
A:Cross-references: UNIPROT:P08482
R:Bonner, T.I.; Buckley, N.J.; Young, A.C.; Brann, M.R.
Science 237, 527-532, 1987
A:Title: Identification of a family of muscarinic acetylcholine receptor genes.
A:Reference number: A94293; MUID:87263421; PMID:3037705
A:Accession: A94293
A:Molecule type: mRNA
A:Residues: 1-227;338-460 <BO2>
A:Experimental source: cerebral cortex
A:Note: only a part of the protein translation is given; none of the nucleotide sequen-
R:Kurténbach, E.; Curtis, C.A.M.; Pedder, E.K.; Aitken, A.; Harris, A.C.M.; Hulme, E.C
J. Biol. Chem. 265, 13702-13708, 1990
A:Title: Muscarinic acetylcholine receptors. Peptide sequencing identifies residues in-
A:Reference number: A37121; MUID:90337982; PMID:2380182
A:Accession: A37121
A:Status: preliminary
A:Molecule type: protein
A:Residues: 62-124 <KUR>
C:Superfamily: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho
F:25-50/Domain: transmembrane #status predicted <TM1>
F:62-93/Domain: transmembrane #status predicted <TM2>
F:100-121/Domain: transmembrane #status predicted <TM3>
F:142-168/Domain: transmembrane #status predicted <TM4>
F:187-209/Domain: transmembrane #status predicted <TM5>
F:367-387/Domain: transmembrane #status predicted <TM6>
F:402-420/Domain: transmembrane #status predicted <TM7>
F:2,12/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 71.9%; Score 41; DB 2; Length 460;
Best Local Similarity 75.0%; Pred. No. 86;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GRCMSCCR 9
Db 257 GRCRCRCC 264

RESULT 10

E84560
 hypothetical protein At2g18120 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: E84560
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: E84560
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-222 <STO>
 A:Cross-references: UNIPROT:Q9S119; GB:AE002093; NID:g4874291; PIDN:AAD31354.1; GSPDB:GN
 C:Genetics:
 A:Gene: At2g18120
 A:Map position: 2

Query Match 70.2%; Score 40; DB 2; Length 222;
 Best Local Similarity 62.5%; Pred. No. 76;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GRCMSCCR 9
 ||| :||:
 Db 86 GRCRTCK 93

RESULT 11
 G84839
 late embryogenesis abundant M17 protein [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: G84839
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: G84839
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-280 <STO>
 A:Cross-references: UNIPROT:Q9S7S3; GB:AE002093; NID:g3894196; PIDN:AACT78545.1; GSPDB:GN
 C:Genetics:
 A:Gene: At2g41260
 A:Map position: 2

Query Match 70.2%; Score 40; DB 2; Length 280;
 Best Local Similarity 75.0%; Pred. No. 88;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GRCMSCCR 9
 ||| ||||
 Db 89 GRCRYCCR 96

RESULT 12
 H71363
 conserved hypothetical protein TP0121 - syphilis spirochete
 C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: H71363
 R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
 rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McD
 they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
 Science 281, 375-388, 1998
 A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
 A:Reference number: A71250; MUID:98332770; PMID:9665876
 A:Accession: H71363
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
 A:Residues: 1-355 <COL>
 A:Cross-references: UNIPROT:O83158; GB:AE001197; GB:AE000520; NID:g3322382; PIDN:AAAC651
 A:Experimental source: strain Nichols
 C:Genetics:
 A:Gene: TP0121
 C:Superfamily: conserved hypothetical protein yodo

Query Match 70.2%; Score 40; DB 1; Length 355;
 Best Local Similarity 77.8%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGRCMSCCR 9
 ||||| ||||
 Db 105 TGRCFSHCR 113

RESULT 13
 E84542
 hypothetical protein At2g16650 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: E84542
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: E84542
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-369 <STO>
 A:Cross-references: UNIPROT:Q9SLF2; GB:AE002093; NID:g4581132; PIDN:AAD24622.1; GSPDB:GN
 C:Genetics:
 A:Gene: At2g16650
 A:Map position: 2

Query Match 70.2%; Score 40; DB 2; Length 369;
 Best Local Similarity 85.7%; Pred. No. 1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRCMSC 7
 ||||| ||||
 Db 261 TGRCLSC 267

RESULT 14
 T30283
 polyketide synthase - Streptomyces sp. (strain MA6548)
 C:Species: Streptomyces sp.
 A:Variety: strain MA6548
 C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-May-2004
 C:Accession: T30283
 R:Motamedi, H.; Cai, S.J.; Shafiee, S.J.; Elliston, K.O.
 Eur. J. Biochem. 244, 74-80, 1997
 A:Title: Structural organization of a multifunctional polyketide synthase involved in
 A:Reference number: Z20806; MUID:97217427; PMID:9063448
 A:Accession: T30283
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-6420 <MOT>
 A:Cross-references: EMBL:Y10438; NID:e1014806; PID:e290681; PIDN:CAA71463.1
 C:Genetics:
 A:Note: fKBA
 C:Keywords: carrier protein
 F:51-433/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS1>
 F:1930-2325/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS2>
 F:3391-3462/Domain: acyl carrier protein homology <ACPI>
 F:3395-3900/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS3>
 F:3393-4254/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT1>
 F:5307-5378/Domain: acyl carrier protein homology <ACP2>
 F:5431-5831/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <OAS4>

F:5932-6206/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT2>
F:6293-6364/Domain: acyl carrier protein homology <ACP3>

Query Match 70.2%; Score 40; DB 2; Length 6420;
Best Local Similarity 71.4%; Pred. No. 5.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRCMSCC 8
DB 5845 GRCLGCC 5851

RESULT 15

W6WL31

E6 protein - human papillomavirus type 31

C:Species: human papillomavirus type 31

A:Note: host Homo sapiens (man)

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004

C:Accession: A32444

R:Goldborough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.

Virology 171, 306-311, 1989

A:Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associated

A:Reference number: A94398; MUID:89299478; PMID:2545036

A:Accession: A32444

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-149 <GOL>

A:Cross-references: UNIPROT:P17386; GB:J04353; NID:G333048; PIDN:AAA46950.1; PID:9459916

C:Comment: This protein may be involved in the oncogenic potential of this virus.

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:30-66/Region: zinc finger CCCC motif

F:103-139/Region: zinc finger CCCC motif

Query Match 68.4%; Score 39; DB 1; Length 149;
Best Local Similarity 66.7%; Pred. No. 82;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGRCMSCCR 9
DB 133 TGRCIACWR 141

Search completed: June 29, 2005, 01:38:37
Job time : 12.2747 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 05:18:25 ; Search time 53.8517 Seconds
(without alignments)
64.268 Million cell updates/sec

Title: US-08-170-344-63

Perfect score: 57

Sequence: 1 TGRMCCR 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	16	17	US-10-484-063-9
2	57	100.0	20	16	Sequence 9, Appli
3	57	100.0	24	16	Sequence 513, App
4	57	100.0	151	14	US-10-476-570-44
5	57	100.0	151	17	US-10-177-390-6
6	57	100.0	151	17	US-10-484-063-20
7	57	100.0	158	17	US-10-484-063-27
8	57	100.0	158	17	US-10-858-384-2
9	57	100.0	158	17	US-10-367-057-16
10	57	100.0	266	9	US-10-472-724-2
11	57	100.0	273	13	US-09-367-309A-1
					Sequence 4, Appli

Sequence 4, Appli	273	17	US-10-899-771-4	57	100.0
Sequence 10, Appl	292	13	US-10-000-903-10	57	100.0
Sequence 10, Appl	292	17	US-10-899-771-10	57	100.0
Sequence 6, Appli	371	13	US-10-000-903-6	57	100.0
Sequence 6, Appli	371	17	US-10-899-771-6	57	100.0
Sequence 14, Appl	390	13	US-10-000-903-14	57	100.0
Sequence 10, Appl	390	17	US-10-899-771-14	57	100.0
Sequence 10, Appl	390	17	US-10-484-063-10	52	91.2
Sequence 214017,	43	16	US-10-425-115-214017	45	78.9
Sequence 3195, Ap	573	15	US-10-094-749-3195	21	75.4
Sequence 197255,	42	73.7	US-10-437-963-197255	22	71.9
Sequence 286658,	56	16	US-10-425-115-286658	41	71.9
Sequence 155, App	89	9	US-09-984-245-155	41	71.9
Sequence 155, App	89	10	US-09-366-262-155	41	71.9
Sequence 155, App	89	10	US-09-983-966-155	26	71.9
Sequence 724, App	89	11	US-09-978-360A-724	27	71.9
Sequence 155, App	89	14	US-10-059-395-155	28	71.9
Sequence 155, App	89	14	US-10-143-090-155	29	71.9
Sequence 118, App	89	14	US-10-319-763-118	30	71.9
Sequence 212, App	89	14	US-10-319-763-212	31	71.9
Sequence 155, App	89	17	US-10-960-251-155	32	71.9
Sequence 357248,	113	16	US-10-425-115-357248	33	71.9
Sequence 11071, A	377	16	US-10-739-930-11071	34	71.9
Sequence 82, Appli	460	9	US-03-782-980-82	35	71.9
Sequence 6, Appli	460	9	US-09-884-430-6	36	71.9
Sequence 513, App	460	10	US-09-826-509-513	37	71.9
Sequence 188, App	460	14	US-10-225-567A-188	38	71.9
Sequence 6, Appli	460	14	US-10-336-489-6	39	71.9
Sequence 93, Appl	460	15	US-10-423-543-93	40	71.9
Sequence 82, Appl	460	16	US-10-806-018-82	41	71.9
Sequence 513, App	460	17	US-10-525-095-513	42	71.9
Sequence 10, Appl	478	13	US-10-029-009-10	43	71.9
Sequence 22, Appl	498	13	US-10-029-009-22	44	71.9
Sequence 36259, A	61	9	US-09-864-761-36259	45	70.2

ALIGNMENTS

RESULT 1
US-10-484-063-9
; Sequence 9, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-9

Query Match 100.0%; Score 57; DB 17; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TGRMCCR 9
Db 3 TGRMCCR 11

Query Match 100.0%; Score 57; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRWMSCCR 9
Db 133 TGRWMSCCR 141

RESULT 6
US-10-484-063-27
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTS-560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; PRIOR FILING DATE: 2004-01-15
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-484-063-27

Query Match 100.0%; Score 57; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRWMSCCR 9
Db 133 TGRWMSCCR 141

RESULT 7
US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: BOUPPIN, JEANNINE
; APPLICANT: BOURGALT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match 100.0%; Score 57; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRWMSCCR 9
Db 140 TGRWMSCCR 148

RESULT 8
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match 100.0%; Score 57; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRWMSCCR 9
Db 140 TGRWMSCCR 148

RESULT 9
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match 100.0%; Score 57; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRWMSCCR 9
Db 145 TGRWMSCCR 153

RESULT 10

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US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match      100.0%; Score 57; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRCMSCCR 9
Db 140 TGRCMSCCR 148

RESULT 11
US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4

Query Match      100.0%; Score 57; DB 13; Length 273;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRCMSCCR 9
Db 246 TGRCMSCCR 254

RESULT 12
US-10-899-771-4
; Sequence 4, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine

```

```

; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; FILE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-4

Query Match      100.0%; Score 57; DB 17; Length 273;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRCMSCCR 9
Db 246 TGRCMSCCR 254

RESULT 13
US-10-000-903-10
; Sequence 10, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-10

Query Match      100.0%; Score 57; DB 13; Length 292;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRCMSCCR 9
Db 265 TGRCMSCCR 273

RESULT 14
US-10-899-771-10
; Sequence 10, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.

```

; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein (Clyta from Streptococcus
; OTHER INFORMATION: pneumoniae and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-10

Query Match 100.0%; Score 57; DB 17; Length 292;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGRCMSCCR 9
| | | | | | | | | |
Db 265 TGRCMSCCR 273

RESULT 15

US-10-000-903-6
; Sequence 6, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-6

Query Match 100.0%; Score 57; DB 13; Length 371;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGRCMSCCR 9
| | | | | | | | | |
Db 246 TGRCMSCCR 254

Search completed: June 29, 2005, 05:48:12
Job time : 54.8517 secs

22 drunk (uspto)

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:28:22 ; Search time 54.2473 Seconds
(without alignments)
84.958 Million cell updates/sec

Title: US-08-170-344-62
Perfect score: 51
Sequence: 1 KCDSTLRIC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	77	2 QB5P5	QB5P5 human papil
2	51	100.0	93	2 Q9QDH2	Q9QDH2 human papil
3	51	100.0	93	2 Q9QDH4	Q9QDH4 human papil
4	51	100.0	93	2 Q9QDH6	Q9QDH6 human papil
5	51	100.0	93	2 Q9QDH8	Q9QDH8 human papil
6	51	100.0	94	2 QB5P6	QB5P6 human papil
7	51	100.0	98	1 VE7_HPV16	P03129 human papil
8	51	100.0	98	2 O11650	O11650 human papil
9	51	100.0	98	2 O12337	O12337 human papil
10	51	100.0	98	2 O12338	O12338 human papil
11	51	100.0	98	2 Q9QD2	Q9QD2 human papil
12	51	100.0	98	2 Q9QD3	Q9QD3 human papil
13	51	100.0	98	2 Q9V1J0	Q9V1J0 human papil
14	51	100.0	98	2 Q778H3	Q778H3 human papil
15	51	100.0	98	2 Q778H5	Q778H5 human papil
16	46	90.2	99	1 VE7_HPV52	P36831 human papil
17	44	86.3	99	1 VE7_HPV35	P27230 human papil
18	44	86.3	99	2 Q76WP2	Q76WP2 human papil
19	43	84.3	98	2 Q9QD4	Q9QD4 human papil
20	43	84.3	98	2 Q6T377	Q6T377 human papil
21	40	78.4	98	1 VE7_HPV31	P17387 human papil
22	40	78.4	98	2 Q9QD21	Q9QD21 human papil
23	39	76.5	510	2 Q7XIE6	Q7XIE6 oryza sativ
24	39	76.5	606	2 Q8LHW4	Q8LHW4 oryza sativ
25	38	74.5	130	2 Q84GQ6	Q84GQ6 myxococcus
26	38	74.5	676	2 Q8SZQ6	Q8SZQ6 drosophila
27	38	74.5	974	2 Q9VDE8	Q9VDE8 drosophila
28	37	72.5	99	2 Q90724	Q90724 human papil
29	37	72.5	252	2 Q90113	Q90113 bombyx mori
30	37	72.5	252	2 Q90114	Q90114 bombyx mori
31	37	72.5	353	2 Q69R12	Q69R12 oryza sativ

32	37	72.5	414	2 Q7XIB4	Q7XIE4 oryza sativ
33	37	72.5	507	2 Q8LHX1	Q8LHX1 oryza sativ
34	37	72.5	507	2 Q6Z4S9	Q6Z4S9 oryza sativ
35	37	72.5	512	2 Q8LHX2	Q8LHX2 oryza sativ
36	37	72.5	513	2 Q6Z4S8	Q6Z4S8 oryza sativ
37	37	72.5	599	2 Q7X6E9	Q7X6E9 oryza sativ
38	37	72.5	4190	2 Q6K796	Q6K796 oryza sativ
39	36	70.6	57	1 GRN2_CYP6A	P81014 cyprinus ca
40	36	70.6	90	2 O56947	O56947 human papil
41	36	70.6	247	2 O29955	O29955 archaeoglob
42	36	70.6	1227	2 Q9GP60	Q9GP60 drosophila
43	36	70.6	1893	2 Q7R5N9	Q7R5N9 giardia lam
44	35	68.6	97	1 VE7_HPV33	P06429 human papil
45	35	68.6	281	2 Q7V307	Q7V307 prochloroc

ALIGNMENTS

RESULT 1

Q8B5P5 PRELIMINARY; PRT; 77 AA.
AC Q8B5P5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewootacharn K.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF469198; A015694.1; -;
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 77
SQ SEQUENCE 77 AA; 8782 MW; C5DE3A7E546AC31B CRC64;

Query Match 100.0%; Score 51; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRIC 9
Db 60 KCDSTLRIC 68

RESULT 2

Q9QDH2 PRELIMINARY; PRT; 93 AA.
AC Q9QDH2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187869; AAF13399.1; -;
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;
Query Match 100.0%; Score 51; DB 2; Length 93;

Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
| | | | |
Db 60 KCDSTLRLC 68

RESULT 3

Q9QDH4 PRELIMINARY; PRT; 93 AA.
AC Q9QDH4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187868; AAF13397.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 51; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
| | | | |
Db 60 KCDSTLRLC 68

RESULT 4

Q9QDH6 PRELIMINARY; PRT; 93 AA.
AC Q9QDH6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187867; AAF13395.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10513 MW; 92C7054341326A1F CRC64;

Query Match 100.0%; Score 51; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
| | | | |
Db 60 KCDSTLRLC 68

RESULT 5

Q9QDH8 PRELIMINARY; PRT; 93 AA.

Q9QDH8;
AC 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187866; AAF13393.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 51; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
| | | | |
Db 60 KCDSTLRLC 68

RESULT 6

Q8B5P6 PRELIMINARY; PRT; 94 AA.
AC Q8B5P6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE E7 oncoprotein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF469197; AAQ15692.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 94
SQ SEQUENCE 94 AA; 10555 MW; 7CC3281BB2AE2C8A CRC64;

Query Match 100.0%; Score 51; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
| | | | |
Db 60 KCDSTLRLC 68

RESULT 7

VE7_HPV16 STANDARD; PRT; 98 AA.
AC P03129;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE E7 protein.
GN Name=E7;
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]


```

OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RL type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003021; AAB70738.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR SEQUENCE 98 AA; 11056 MW; 19DEB8F14CD2C705 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
Db 60 KCDSTLRLC 68

RESULT 10
Q12338
ID O12338 PRELIMINARY; PRT; 98 AA.
AC O12338;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RL type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003022; AAB70739.1; -.
DR EMBL; AF477385; AAM03025.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR SEQUENCE 98 AA; 10969 MW; 9BD612534CCEA59B CRC64;

Query Match 100.0%; Score 51; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
Db 60 KCDSTLRLC 68

RESULT 11
Q8QRD2
ID Q8QRD2 PRELIMINARY; PRT; 98 AA.
AC Q8QRD2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

```

```

OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RL for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486345; AAL96650.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR SEQUENCE 98 AA; 11045 MW; 9C4F8C534CD76C4B CRC64;

Query Match 100.0%; Score 51; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
Db 60 KCDSTLRLC 68

RESULT 12
Q8QRD3
ID Q8QRD3 PRELIMINARY; PRT; 98 AA.
AC Q8QRD3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RL for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486344; AAL96649.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR SEQUENCE 98 AA; 11021 MW; 9BD6125946D2C3E1 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
Db 60 KCDSTLRLC 68

RESULT 13
Q8VLJ0
ID Q8VLJ0 PRELIMINARY; PRT; 98 AA.
AC Q8VLJ0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Jinhu X., Xinxiang W., Yun T.;

```

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF461264; AAL66736.1; -

DR Pfam; PF00527; E7; 1.

SQ SEQUENCE 98 AA; 10997 MW; 9BD610834CCEA59B CRC64;

Query Match 100.0%; Score 51; DB 2; Length 98;

Best Local Similarity 100.0%; Pred. No. 0.035;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCDSTLRLC 9

|||||

Db 60 KCDSTLRLC 68

RESULT 14

Q778H3

ID Q778H3 PRELIMINARY; PRT; 98 AA.

AC Q778H3;

DT 05-JUL-2004 (TREMELrel. 27, Created)

DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)

DE E7 protein (Fragment)

OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI_TaxID=10581;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20112892; PubMed=10644829;

RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,

RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;

RT "Analysis of human papillomavirus type 16 E6 variants in relation to

RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";

RL J. Gen. Virol. 81:317-325(2000).

DR EMBL; AJ388063; CAB45119.1; -

DR InterPro; IPR000148; Papvi_E7.

DR Pfam; PF00527; E7; 1.

DR NON_TER 98

SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 100.0%; Score 51; DB 2; Length 98;

Best Local Similarity 100.0%; Pred. No. 0.035;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCDSTLRLC 9

|||||

Db 60 KCDSTLRLC 68

RESULT 15

Q778H5

ID Q778H5 PRELIMINARY; PRT; 98 AA.

AC Q778H5;

DT 05-JUL-2004 (TREMELrel. 27, Created)

DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)

DE E7 protein (Fragment)

OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI_TaxID=10581;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20112892; PubMed=10644829;

RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,

RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;

RT "Analysis of human papillomavirus type 16 E6 variants in relation to

RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";

RL J. Gen. Virol. 81:317-325(2000).

DR EMBL; AJ388062; CAB45117.1; -

DR InterPro; IPR000148; Papvi_E7.

DR Pfam; PF00527; E7; 1.

DR NON_TER 98

SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 100.0%; Score 51; DB 2; Length 98;

Best Local Similarity 100.0%; Pred. No. 0.035;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCDSTLRLC 9

|||||

Db 60 KCDSTLRLC 68

Search completed: June 29, 2005, 01:34:42

Job time : 55.2473 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:37:59 ; Search time 16.8626 Seconds
(without alignments)
39.842 Million cell updates/sec

Title: US-08-170-344-63

Perfect score: 57

Sequence: 1 TGRMCCR 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	21	US-08-934-915-167	Sequence 167, Appl
2	57	100.0	158	US-09-980-523A-2	Sequence 2, Appli
3	57	100.0	162	US-08-316-239B-3	Sequence 3, Appli
4	57	100.0	162	US-08-316-239B-4	Sequence 4, Appli
5	57	100.0	172	US-08-860-165-12	Sequence 12, Appl
6	57	100.0	172	US-09-359-382-12	Sequence 12, Appl
7	57	100.0	266	US-08-860-165-10	Sequence 10, Appl
8	57	100.0	266	US-09-359-382-10	Sequence 10, Appl
9	57	100.0	266	US-09-367-309A-1	Sequence 1, Appli
10	57	100.0	273	US-09-485-885-4	Sequence 4, Appli
11	57	100.0	292	US-09-485-885-10	Sequence 10, Appl
12	57	100.0	371	US-09-485-885-6	Sequence 6, Appli
13	57	100.0	390	US-09-485-885-14	Sequence 14, Appl
14	42	73.7	261	US-09-949-016-9721	Sequence 7, Appli
15	41	71.9	89	US-09-663-600A-118	Sequence 118, App
16	41	71.9	89	US-09-663-600A-212	Sequence 212, App
17	41	71.9	460	US-09-826-509-513	Sequence 513, App
18	41	71.9	479	US-08-313-553-7	Sequence 7, Appli
19	41	71.9	479	US-08-767-933-7	Sequence 7, Appli
20	40	70.2	73	US-09-270-767-35372	Sequence 35372, A
21	40	70.2	73	US-09-270-767-50589	Sequence 50589, A
22	40	70.2	85	US-09-674-973A-189	Sequence 189, App
23	40	70.2	94	US-09-674-973A-191	Sequence 191, App
24	40	70.2	95	US-09-674-973A-192	Sequence 192, App
25	40	70.2	226	US-09-252-991A-23893	Sequence 23893, A
26	40	70.2	355	US-09-330-611-16	Sequence 16, Appl
27	39	68.4	163	US-09-354-129-12	Sequence 12, Appl

28	39	68.4	163	4	US-09-504-357-12	Sequence 12, Appl
29	39	68.4	266	4	US-09-252-991A-18776	Sequence 18776, A
30	38	66.7	84	4	US-09-198-452A-1276	Sequence 1276, Ap
31	38	66.7	87	4	US-09-252-991A-27237	Sequence 27237, A
32	38	66.7	911	3	US-09-356-952-6	Sequence 6, Appli
33	37	64.9	17	4	US-09-481-593-21	Sequence 21, Appl
34	37	64.9	24	3	US-08-900-230-24	Sequence 24, Appl
35	37	64.9	41	5	PCT-US96-01720-7	Sequence 7, Appli
36	37	64.9	45	3	US-08-900-230-39	Sequence 39, Appl
37	37	64.9	158	4	US-09-252-991A-25074	Sequence 25074, A
38	37	64.9	223	4	US-09-252-991A-25636	Sequence 25636, A
39	37	64.9	626	6	5268290-2	Patent No. 5268290
40	37	64.9	626	6	5268290-2	Patent No. 5268290
41	37	64.9	1461	4	US-10-142-231-86	Sequence 86, Appl
42	37	64.9	1917	4	US-09-627-650B-5	Sequence 5, Appli
43	37	64.9	1917	4	US-09-436-063C-5	Sequence 5, Appli
44	37	64.9	2211	3	US-09-738-884-1	Sequence 1, Appli
45	37	64.9	2211	4	US-10-036-961A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-934-915-167
; Sequence 167, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 167:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-167
Query Match 100.0%; Score 57; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.1;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRCMSCCR 9
| | | | | | | |
Db 3 TGRCMSCCR 11

RESULT 2

US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCES
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO/01 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 57; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.53; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRCMSCCR 9
| | | | | | | |
Db 140 TGRCMSCCR 148

RESULT 3

US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 100.0%; Score 57; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 100.0%; Score 57; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRCMSCCR 9
| | | | | | | |
Db 140 TGRCMSCCR 148

RESULT 4

US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Cancer
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 100.0%; Score 57; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRMSSCR 9
| | | | |
Db 140 TGRMSSCR 148

RESULT 5
US-08-860-165-12
; Sequence 12, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12

Query Match 100.0%; Score 57; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRMSSCR 9
| | | | |
Db 78 TGRMSSCR 86

RESULT 6
US-09-359-382-12
; Sequence 12, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-12

Query Match 100.0%; Score 57; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRMSSCR 9
| | | | |
Db 78 TGRMSSCR 86

RESULT 7
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 57; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRMSSCR 9
| | | | |
Db 140 TGRMSSCR 148

RESULT 8
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 57; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRMSSCR 9

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; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-10

Query Match      100.0%; Score 57; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.87; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRCMSCCR 9
Db 265 TGRCMSCCR 273

RESULT 12
US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-6

Query Match      100.0%; Score 57; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 1.1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRCMSCCR 9
Db 246 TGRCMSCCR 254

RESULT 13
US-09-485-885-14
; Sequence 14, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:

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; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JTM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; US-09-367-309A-1

Query Match      100.0%; Score 57; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.8; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRCMSCCR 9
Db 140 TGRCMSCCR 148

RESULT 10
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-4

Query Match      100.0%; Score 57; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.82; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRCMSCCR 9
Db 246 TGRCMSCCR 254

RESULT 11
US-09-485-885-10

```

APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Bernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 14
LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapien
US-09-485-885-14

Query Match 100.0%; Score 57; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGRMSCCR 9
Db 265 TGRMSCCR 273

RESULT 14

US-09-949-016-9721
Sequence 9721, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9721
LENGTH: 261
TYPE: PRT
ORGANISM: Human
US-09-949-016-9721

Query Match 73.7%; Score 42; DB 4; Length 261;
Best Local Similarity 75.0%; Pred. No. 79;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGRMSCCR 8
Db 147 TGRCPACC 154

RESULT 15

US-09-663-600A-118
Sequence 118, Application US/09663600A
Patent No. 6573068
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: EXTENDED CONAS FOR SECRETED PROTEINS

FILE REFERENCE: 31.US3.CIP
CURRENT APPLICATION NUMBER: US/09/663,600A
CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 118
LENGTH: 89
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: -16...-1
US-09-663-600A-118

Query Match 71.9%; Score 41; DB 4; Length 89;
Best Local Similarity 77.8%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGRMSCCR 9
Db 38 TGRMQCCR 46

Search completed: June 29, 2005, 01:44:22
Job time : 17.9126 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:32:21 ; Search time 11.2747 Seconds
(without alignments)
76.805 Million cell updates/sec

Title: US-08-170-344-62

Perfect score: 51

Sequence: 1 KCDSTLRLC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	98	1 W7WLS	E7 protein - human
2	46	90.2	99	2 S36574	E7 protein - human
3	44	86.3	99	1 W7WLS5	E7 protein - human
4	40	78.4	98	1 W7WLS1	E7 protein - human
5	36	70.6	57	2 B4654	growth modulatory
6	36	70.6	247	2 F69285	electron transfer
7	35	68.6	97	1 W7WLS3	E7 protein - human
8	35	68.6	1174	2 S57060	probable membrane
9	34	66.7	57	2 C4654	growth modulatory
10	34	66.7	89	2 A69513	hypothetical prote
11	34	66.7	249	2 T31837	hypothetical prote
12	34	66.7	315	2 A71288	probable methylene
13	34	66.7	429	2 T20326	hypothetical prote
14	34	66.7	439	2 E84985	hypothetical prote
15	34	66.7	578	2 D95988	probable esterase
16	34	66.7	798	2 T34248	hypothetical prote
17	34	66.7	952	2 D86179	hypothetical prote
18	33	64.7	57	2 F64324	DNA-directed RNA p
19	33	64.7	98	1 W7WLS8	E7 protein - human
20	33	64.7	201	2 T00944	hypothetical prote
21	33	64.7	214	2 E85086	hypothetical prote
22	33	64.7	281	2 AB1699	nicotinate-nucleot
23	33	64.7	287	2 A11072	conserved hypothet
24	33	64.7	300	2 S41171	transrepressor pro
25	33	64.7	363	2 H69393	iron-sulfur cluste
26	33	64.7	377	1 S01615	site-specific DNA-
27	33	64.7	420	2 A54759	cytochrome ba(3) c
28	33	64.7	428	2 T39773	hypothetical prote
29	33	64.7	458	2 C82386	probable extracell

ALIGNMENTS

RESULT 1

W7WLS

E7 protein - human papillomavirus type 16

C:Species: human papillomavirus type 16

C>Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03688; S12367; T10428

R:Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virolgy 145, 181-185, 1985

A>Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03688

A:Molecule type: DNA

A:Residues: 1-98 <SEE>

A:Cross-references: UNIPROT:P03129; GB:K02718; NID:g333031; PIDN:AAA46940.1; PID:g33303

R:Barbosa, M.S.; Edmonds, C.; Fisher, C.; Schiller, J.T.; Lowy, D.R.; Vousden, K.H.

EMBO J. 9, 153-160, 1990

A>Title: The region of the HPV E7 oncoprotein homologous to adenovirus E1a and SV40 la

A:Reference number: S12367; MUID:90107938; PMID:2153075

A:Accession: S12367

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-98 <BAR>

R:Kennedy, I.M.; Haddock, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A>Title: A negative element in the human papillomavirus type 16 genome acts at the le

A:Reference number: Z17014; MUID:91162763; PMID:11848319

A:Accession: T10428

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-98 <KEN>

A:Cross-references: EMBL:K02718; NID:g333031; PIDN:AAA46940.1; PID:g333033

C:Genetics:

A:Gene: E7

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation; zinc finger

F:58-94/Region: zinc finger CCCC motif

Query Match 100.0%; Score 51; DB 1; Length 98;

Best Local Similarity 100.0%; Pred. No. 0.016;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9

Db 60 KCDSTLRLC 68

RESULT 2

S36574

E7 protein - human papillomavirus type 52

C:Species: human papillomavirus type 52

C>Date: 08-May-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C:Accession: S36574

R;Delius, H.; Hofmann, B.
 submitted to the EMBL Data Library, August 1993
 A;Description: Primer-directed sequencing of human papillomavirus types.
 A;Reference number: S36469
 C;Superfamily: papillomavirus E7 protein
 A;Accession: S36574
 A;Molecule type: DNA
 A;Residues: 1-99
 A;Cross-references: UNIPROT:P36831; EMBL:X74481; NID:G397038; PIDN:CAA52586.1; PID:G3970
 C;Superfamily: papillomavirus E7 protein
 C;Keywords: DNA binding; early protein; transcription regulation

Query Match 90.2%; Score 46; DB 2; Length 99;
 Best Local Similarity 100.0%; Pred. No. 0.14; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0

Qy 2 CDSLTRLC 9
 :|||||
 Db 63 CDSLTRLC 70

RESULT 3
 W7WL35
 C;Species: human papillomavirus type 35
 A;Note: host Homo sapiens (man)
 C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C;Accession: F40824; S36522
 R;Marich, J.E.; Ponteler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
 Virolgy 186, 770-776, 1992
 A;Title: The phylogenetic relationship and complete nucleotide sequence of human papillo
 A;Reference number: A40824; MUID:92124753; PMID:1310198
 A;Accession: F40824
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-99 <MAR>
 A;Cross-references: UNIPROT:P27230; GB:M74117; NID:G333050; PIDN:AAA46967.1; PID:G333052
 R;Delius, H.; Hofmann, B.
 submitted to the EMBL Data Library, August 1993
 A;Description: Primer-directed sequencing of human papillomavirus types.
 A;Reference number: S36469
 A;Accession: S36522
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-99
 A;Cross-references: EMBL:X74477; NID:G396997; PIDN:CAA52562.1; PID:G396999
 A;Experimental source: strain 35H
 C;Superfamily: papillomavirus E7 protein
 C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
 F;59-95/Region: zinc finger CCCC motif

Query Match 86.3%; Score 44; DB 1; Length 99;
 Best Local Similarity 77.8%; Pred. No. 0.33;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
 :|||||
 Db 61 KCEATLRLC 69

RESULT 4
 W7WL31
 E7 protein - human papillomavirus type 31
 C;Species: human papillomavirus type 31
 A;Note: host Homo sapiens (man)
 C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
 C;Accession: B32444
 R;Goldsborough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.
 Virolgy 171, 306-311, 1989
 A;Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associ
 A;Reference number: A94398; MUID:89299478; PMID:2545036
 A;Accession: B32444
 A;Status: translation not shown
 A;Molecule type: DNA

A;Residues: 1-98 <GOL>
 A;Cross-references: UNIPROT:P17387; GB:J04353; NID:G333048; PIDN:AAA46951.1; PID:G45991
 C;Comment: This protein may be involved in the oncogenic potential of this virus.
 C;Superfamily: papillomavirus E7 protein
 C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
 F;58-94/Region: zinc finger CCCC motif

Query Match 78.4%; Score 40; DB 1; Length 98;
 Best Local Similarity 77.8%; Pred. No. 1.8;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
 :|||||
 Db 60 QCKSTLRLC 68

RESULT 5
 B46654
 growth modulatory factor granulin-2 - common carp
 C;Species: Cyprinus carpio (common carp)
 C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C;Accession: B46654; B40180
 R;Belcourt, D.R.; Lazure, C.; Bennett, H.P.
 J. Biol. Chem. 268, 9230-9237, 1993
 A;Title: Isolation and primary structure of the three major forms of granulin-like pep
 A;Reference number: A46654; MUID:93252783; PMID:8486624
 A;Accession: B46654
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-57 <BEL>
 A;Cross-references: UNIPROT:P81014
 A;Experimental source: spleen and head kidney
 A;Note: sequence extracted from NCBI backbone (NCBIP:131315)
 C;Keywords: disulfide bond; monomer

Query Match 70.6%; Score 36; DB 2; Length 57;
 Best Local Similarity 66.7%; Pred. No. 6.4;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
 :|||||
 Db 47 RCDSTSLC 55

RESULT 6
 F69285
 electron transfer flavoprotein, subunit beta (etfB) homolog - Archaeoglobus fulgidus
 C;Species: Archaeoglobus fulgidus
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C;Accession: F69285
 R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodso
 ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Attiach, P.; Kaine, B.P.; Sykes, S
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
 A;Reference number: A69250; MUID:98049343; PMID:9389475
 A;Accession: F69285
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-247 <KLE>
 A;Cross-references: UNIPROT:O29955; GB:AE001085; GB:AE000782; NID:G2689408; PIDN:AAB90C
 C;Superfamily: electron transfer flavoprotein, beta subunit

Query Match 70.6%; Score 36; DB 2; Length 247;
 Best Local Similarity 75.0%; Pred. No. 22;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CDSLTRLC 9
 :|||||
 Db 66 CDDTLRKC 73

```

RESULT 7
W7WL33
E7 protein - human papillomavirus type 33
C:Species: human papillomavirus type 33
C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: A03689; S23831; S23827
R:Coile, S.T.; Streeck, R.E.
J. Virol. 58, 991-995, 1986
A:Title: Genome organization and nucleotide sequence of human papillomavirus type 33, wh
A:Reference number: A93020; MUID:86200464; PMID:3009902
A:Accession: A03689
A:Molecule type: DNA
A:Residues: 1-97 <COL>
A:Cross-references: UNIPROT:P06429; GB:M12732; NID:G333049; PIDN:AAA46959.1; PID:G463178
R:Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; Me
submitted to the EMBL Data Library, January 1992
A:Description: HPV type 33 in a tonsillar carcinoma generates its putative E7 mRNA via t
A:Reference number: S19906
A:Accession: S23831
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-97 <SNI>
A:Cross-references: EMBL:X64085; NID:G60278; PIDN:CAA45434.1; PID:G60281; EMBL:X64084; N
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
F:58-94/Region: zinc finger CCCC motif

Query Match 68.6%; Score 35; DB 1; Length 97;
Best Local Similarity 62.5%; Pred. No. 15;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CDSLTRLC 9
|:|:|
Db 61 CNTVRLC 68

RESULT 8
S57060
probable membrane protein YJR041c - Yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein J1622
C:Species: Saccharomyces cerevisiae
C>Date: 08-Jul-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
C:Accession: S57060; S63765
R:Huang, M.E.; Chuat, J.C.; Galibert, F.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S57052
A:Accession: S57060
A:Molecule type: DNA
A:Residues: 1-1174 <MAN>
A:Cross-references: UNIPROT:P47108; EMBL:Z49541; NID:G1015692; PID:G1015693; MIPS:YJR041
R:Huang, M.E.; Chuat, J.C.; Galibert, F.
Yeast 11, 775-781, 1995
A:Title: Analysis of a 42.5 kb DNA sequence of chromosome X reveals three tRNA genes and
A:Reference number: S63757; MUID:95397595; PMID:7668047
A:Accession: S63765
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1174 <HUA>
A:Cross-references: EMBL:L36344; NID:G1197060; PIDN:AAA88743.1; PID:G1197069
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
C:Genetics:
A:Cross-references: SGD:S0003802
A:Map position: 10R
A:Note: YJR041c
C:Superfamily: Saccharomyces cerevisiae probable membrane protein YJR041c

Query Match 68.6%; Score 35; DB 2; Length 1174;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KCDSTRLC 9
|:|:|

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Db 878 KCDSALGFC 886
|:|:|

RESULT 9
C46654
growth modulatory factor granulin-3 - common carp
C:Species: Cyprinus carpio (common carp)
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: C46654; C40180
R:Belcourt, D.R.; Lazure, C.; Bennett, H.P.
J. Biol. Chem. 268, 9230-9237, 1993
A:Title: Isolation and primary structure of the three major forms of granulin-like pep.
A:Reference number: A46654; MUID:93252781; PMID:8486624
A:Accession: C46654
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-57 <BEL>
A:Cross-references: UNIPROT:P81015
A:Experimental source: spleen and head kidney
A:Note: sequence extracted from NCBI backbone (NCBIP:131316)

Query Match 66.7%; Score 34; DB 2; Length 57;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CDSLTRLC 9
|:|:|
Db 48 CDSSTSLC 55

RESULT 10
A69513
hypothetical protein AF2105 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Aug-2004
C:Accession: A69513
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archa
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: A69513
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-89 <KLE>
A:Cross-references: UNIPROT:O28175; GB:AB000958; GB:AE000782; NID:G2689281; PIDN:AAB891
C:Superfamily: Molybdopter in biosynthesis sulfur carrier protein
F:89/Modified site: 1-thioglycine (Gly) #status predicted

Query Match 66.7%; Score 34; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLR 7
|:|:|
Db 22 ECDSTLR 28

RESULT 11
T31837
hypothetical protein T0584.11 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T31837
R:Bradehaw, H.
submitted to the EMBL Data Library, July 1997
A:Description: The sequence of C. elegans cosmid T0584.
A:Reference number: Z21092
A:Accession: T31837

```

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-249 <BRA>
 A:Cross-references: UNIPROT:O16420; EMBL:AF016445; PIDN:AAC69060.1; GSPDB:GN00023; CESP:
 A:Experimental source: strain Bristol N2; clone T05B4
 C:Genetics:
 A:Gene: CESP:T05B4.11
 A:Map position: 5
 A:Introns: 34/3; 121/1
 C:Superfamily: Caenorhabditis elegans hypothetical protein C49G7.3

Query Match 66.7%; Score 34; DB 2; Length 249;
 Best Local Similarity 55.6%; Pred. No. 53;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KCDSTLRCL 9

Db 241 RCGSTCRIC 249

RESULT 12

A71288

probable methylenetetrahydrofolate dehydrogenase (fold) - syphilis spirochete
 C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
 C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004

C:Accession: A71288

R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin-
 rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo-
 they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
 Science 281, 375-388, 1998

A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
 A:Reference number: A71250; MUID:98332770; PMID:9665876

A:Accession: A71288

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA

A:Residues: 1-315 <COL>

A:Cross-references: UNIPROT:O83714; GB:AE001245; GB:AE000520; NID:g3323033; PIDN:AAC6570

A:Experimental source: strain Nichols

C:Genetics:

A:Gene: TP0732

C:Superfamily: methylenetetrahydrofolate dehydrogenase (NAD+); methylenetetrahydrofolate
 F:5-288/Domain: methylenetetrahydrofolate dehydrogenase (NAD+) homology <MtFD>

Query Match 66.7%; Score 34; DB 2; Length 315;
 Best Local Similarity 62.5%; Pred. No. 65;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CDSTLRCL 9

Db 184 CDATVTL 191

RESULT 13

T20326

hypothetical protein D1086.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T20326

R:Smyle, R.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19257

A:Accession: T20326

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-349 <WIL>

A:Cross-references: UNIPROT:O62125; EMBL:Z81491; PIDN:CAB04022.1; GSPDB:GN00023; CESP:D1

A:Experimental source: clone D1086

C:Genetics:

A:Gene: CESP:D1086.7

A:Map position: 5

A:Introns: 10/3; 108/3; 144/3; 160/2; 174/1; 247/3; 308/3

Query Match 66.7%; Score 34; DB 2; Length 349;

Best Local Similarity 66.7%; Pred. No. 71;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KCDSTLRCL 9

Db 248 KCYKTLQLC 256

RESULT 14

B84985

hypothetical protein clpX [imported] - Buchnera sp. (strain APS)

C:Species: Buchnera sp.

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001

C:Accession: B84985

R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.

Nature 407, 81-86, 2000

A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp.
 A:Reference number: A84930; MUID:20445173; PMID:10993077

A:Accession: B84985

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-429 <STO>

A:Cross-references: GB:AP000398; GSPDB:GN00144

A:Experimental source: strain APS

C:Genetics:

A:Gene: clpX; BU476

C:Superfamily: heat shock protein hslU; FtsH/SEC18/CDC48-type ATP-binding domain homolo

Query Match 66.7%; Score 34; DB 2; Length 429;
 Best Local Similarity 62.5%; Pred. No. 85;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CDSTLRCL 9

Db 37 CDECIRLC 44

RESULT 15

D95998

probable esterase or acylase protein [imported] - Sinorhizobium meliloti (strain 1021)
 C:Species: Sinorhizobium meliloti

C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004

C:Accession: D95998

R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmaster, J.; Chain, P.; Vorholter, F.J.; Herna

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing end
 A:Reference number: A95842; MUID:21396508; PMID:11481431

A:Accession: D95998

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-578 <KUR>

A:Cross-references: UNIPROT:Q92U85; GB:AL591985; PIDN:CAC49652.1; PID:gl5141139; GSPDB:

A:Experimental source: strain 1021, megaplasmid pSymB

R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,

Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.

Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelauro

hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, I

A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A:Reference number: A96039; MUID:21368234; PMID:11474104

A:Contents: annotation

C:Genetics:

A:Gene: SMD21424

A:Genome: plasmid

Query Match 66.7%; Score 34; DB 2; Length 578;
 Best Local Similarity 75.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CDSTLRCL 9

Db 456 CDWTARLC 463

Search completed: June 29, 2005, 01:38:36
Job time : 13.2747 secs

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; PRIOR APPLICATION NUMBER: US 60/041,726
; PRIOR FILING DATE: 1997-03-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: HPV 16 E7 PEPTIDE
US-10-668-400-9

Query Match 100.0%; Score 51; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
Db 1 KCDSTLRLC 9

RESULT 7

US-10-432-465-49
; Sequence 49, Application US/10432465
; Publication No. US20040091479A1
; GENERAL INFORMATION:
; APPLICANT: Kaufmann, John
; APPLICANT: Kaufmann, Andreas
; APPLICANT: Kather, Angela
; APPLICANT: Schinz, Manuela
; TITLE OF INVENTION: T-Cell Epitopes of the Papillomavirus L1
; TITLE OF INVENTION: Protein and E7 Protein and Their Use in Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/077001
; CURRENT APPLICATION NUMBER: US/10/432,465
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/14037
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: DE 10059631.2
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-432-465-49

Query Match 100.0%; Score 51; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
Db 5 KCDSTLRLC 13

RESULT 8

US-10-890-526-74
; Sequence 74, Application US/10890526
; Publication No. US20040258708A1
; GENERAL INFORMATION:
; APPLICANT: Jochmus, Ingrid
; APPLICANT: Nieland, John
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
; TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/036001
; CURRENT APPLICATION NUMBER: US/10/890,526
; CURRENT FILING DATE: 2004-07-13
; PRIOR APPLICATION NUMBER: US/09/980,177
; PRIOR FILING DATE: 2002-05-02

; PRIOR APPLICATION NUMBER: PCT/EP00/05006
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: DE 19925199.1
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-890-526-74

Query Match 100.0%; Score 51; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
Db 5 KCDSTLRLC 13

RESULT 9

US-09-728-466-1
; Sequence 1, Application US/09728466
; Patent No. US20010029022A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Christopher
; APPLICANT: He, Wanxia
; TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
; FILE REFERENCE: 28341/6216
; CURRENT APPLICATION NUMBER: US/09/728,466
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/382,616
; PRIOR FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Papillomavirus sylvilagi
US-09-728-466-1

Query Match 100.0%; Score 51; DB 9; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
Db 60 KCDSTLRLC 68

RESULT 10

US-09-820-765-4
; Sequence 4, Application US/09820765
; Publication No. US2002039584A1
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; APPLICANT: HALLEK, Michael
; TITLE OF INVENTION: PAPILOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/820,765
; FILING DATE: 30-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,896
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-820-765-4
Query Match 100.0%; Score 51; DB 9; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
Db 60 KCDSTLRLC 68

RESULT 11
US-09-824-017-4
; Sequence 4, Application US/09824017
; Publication No. US20020197668A1
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/824,017
; FILING DATE: 03-Apr-2001
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER: 09/026,896
; FILING DATE: 1998-02-20
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
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;
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-824-017-4
Query Match 100.0%; Score 51; DB 9; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
Db 60 KCDSTLRLC 68

RESULT 12
US-09-986-118A-4
; Sequence 4, Application US/09986118A
; Publication No. US20030021806A1
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/986,118A
; FILING DATE: 07-No. US20030021806A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,896
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-986-118A-4
Query Match 100.0%; Score 51; DB 10; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
Db 60 KCDSTLRLC 68

RESULT 13
US-10-267-311-8
; Sequence 8, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
```

; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-8

Query Match 100.0%; Score 51; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
|||
Db 60 KCDSTLRLC 68

RESULT 14

US-10-177-390-8
; Sequence 8, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold.
; APPLICANT: N.V. Antwerp Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: fragment of
; OTHER INFORMATION: human papilloma virus type 16 E7 gene
US-10-177-390-8

Query Match 100.0%; Score 51; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
|||
Db 60 KCDSTLRLC 68

RESULT 15

US-10-201-764-19
; Sequence 19, Application US/10201764
; Publication No. US20030166140A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, SI-YI AND ZHAOYANG, YOU
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTIGENS WHICH ELICIT AN
; TITLE OF INVENTION: IMMUNE RESPONSE
; FILE REFERENCE: TEA
; CURRENT APPLICATION NUMBER: US/10/201,764
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/566,420

; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,752
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 60/132,750
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Human papillomavirus type E7
US-10-201-764-19

Query Match 100.0%; Score 51; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
|||
Db 60 KCDSTLRLC 68

Search completed: June 29, 2005, 05:48:11
Job time : 53.8517 secs

Large Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:37:59 ; Search time 16.8626 Seconds
(without alignments)
39.842 Million cell updates/sec

Title: US-08-170-344-62

Perfect score: 51

Sequence: 1 KCDSTLRIC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/prodata/1/aaa/5B COMB.pep:*
- 3: /cgn2_6/prodata/1/aaa/6A COMB.pep:*
- 4: /cgn2_6/prodata/1/aaa/6B COMB.pep:*
- 5: /cgn2_6/prodata/1/aaa/6CTUS COMB.pep:*
- 6: /cgn2_6/prodata/1/aaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	19	3	US-08-075-541D-38
2	51	100.0	19	4	US-09-000-003A-8
3	51	100.0	19	4	US-09-405-986A-9
4	51	100.0	20	4	US-09-980-177A-74
5	51	100.0	25	3	US-08-075-541D-47
6	51	100.0	30	2	US-08-934-915-52
7	51	100.0	30	2	US-08-934-915-53
8	51	100.0	30	4	US-09-486-394-3
9	51	100.0	98	1	US-08-406-248-6
10	51	100.0	98	3	US-08-075-541D-42
11	51	100.0	98	3	US-09-382-616A-1
12	51	100.0	98	3	US-08-944-368A-4
13	51	100.0	98	3	US-09-820-764-4
14	51	100.0	98	4	US-09-613-303-8
15	51	100.0	98	4	US-09-566-420-19
16	51	100.0	98	4	US-09-986-118A-4
17	51	100.0	98	4	US-09-728-466-1
18	51	100.0	98	4	US-09-824-017-4
19	51	100.0	98	4	US-10-267-311-8
20	51	100.0	98	4	US-10-201-764-19
21	51	100.0	98	4	US-09-637-746-3
22	51	100.0	98	4	US-09-501-097A-7
23	51	100.0	98	4	US-09-980-523A-12
24	51	100.0	121	4	US-09-613-303-12
25	51	100.0	121	4	US-10-267-311-12
26	51	100.0	172	3	US-08-860-165-14
27	51	100.0	172	3	US-09-359-382-14

Query Match 100.0%; Score 51; DB 3; Length 19;

ALIGNMENTS

RESULT 1

US-08-075-541D-38
; Sequence 38, Application US/08075541D
; Patent No. 6183745

; GENERAL INFORMATION:

; APPLICANT: TINDLE, ROBERT

; APPLICANT: FERNANDO, GERMAIN

; APPLICANT: FRAZER, IAN

; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND

; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESS: PANITCH SCHWARZE JACOBS & NADEL, P. C.

; STREET: 1601 MARKET STREET, 36TH FLOOR

; CITY: PHILADELPHIA

; STATE: PENNSYLVANIA

; COUNTRY: USA

; ZIP: 19103-2398

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/075,541D

; FILING DATE: 10-JUN-1993

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: AU pk 3876

; FILING DATE: 12-DEC-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: pct/au91/00575

; FILING DATE: 12-DEC-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: NADEL, ALAN S

; REGISTRATION NUMBER: 27,363

; REFERENCE/DOCKET NUMBER: 8795-4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 215-567-2020

; TELEFAX: 215-567-2991

; INFORMATION FOR SEQ ID NO: 38:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 19 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-075-541D-38

Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
Db 7 KCDSTLRLC 15

RESULT 2
US-09-000-003A-8
; Sequence 8, Application US/090000003A
; Patent No. 6652850
; GENERAL INFORMATION:
; APPLICANT: Philip, Ramila
; APPLICANT: Ledkowski, Jane S.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRAL LIPOSOMES AND
; THEIR USE IN TRANSFECTING DENDRITIC CELLS TO STIMULATE
; SPECIFIC IMMUNITY
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Alexis Barron, Esq.
; STREET: Suite 2600 Aramark Tower, 1101 Market Street
; CITY: Philadelphia
; STATE: PA
; COUNTRY: United States of America
; ZIP: 19107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/000,003A
; FILING DATE: 15-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/12012
; FILING DATE: 19-JUN-1996
; APPLICATION NUMBER: US 60/001,312
; FILING DATE: 21-JUL-1995
; APPLICATION NUMBER: US 60/007,184
; FILING DATE: 01-NOV-1995
; APPLICATION NUMBER: US 08/566,286
; FILING DATE: 01-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Barron, Alexis
; REGISTRATION NUMBER: 22,702
; REFERENCE/DOCKET NUMBER: 20,846-K USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 923-4466
; TELEFAX: (215) 923-2189
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-000-003A-8

Query Match 100.0%; Score 51; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
Db 1 KCDSTLRLC 9

RESULT 3
US-09-405-986A-9
; Sequence 9, Application US/09405986A

Patent No. 6676946
; GENERAL INFORMATION:
; APPLICANT: Bay, Sylvie
; APPLICANT: Cantacuzene, Daniele
; APPLICANT: Leclerc, Claude
; APPLICANT: Lo-Man, Richard
; TITLE OF INVENTION: MULTIPLE ANTIGEN GLYCOPOLYMER CARBOHYDRATE.
; TITLE OF INVENTION: VACCINE COMPRISING THE SAME AND USE THEREOF
; FILE REFERENCE: 102.166A-1
; CURRENT APPLICATION NUMBER: US/09/405,986A
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 09/049,847
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/041,726
; PRIOR FILING DATE: 1997-03-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: HPV 16 E7 PEPTIDE
US-09-405-986A-9

Query Match 100.0%; Score 51; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
Db 1 KCDSTLRLC 9

RESULT 4
US-09-980-177A-74
; Sequence 74, Application US/09980177A
; Patent No. 6838084
; GENERAL INFORMATION:
; APPLICANT: Jochmus, Ingrid
; APPLICANT: Nieland, John
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
; TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/036001
; CURRENT APPLICATION NUMBER: US/09/980,177A
; CURRENT FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: PCT/EP00/05006
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: DE 19925199.1
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-980-177A-74

Query Match 100.0%; Score 51; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.012; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
Db 5 KCDSTLRLC 13

RESULT 5
US-08-075-541D-47
; Sequence 47, Application US/08075541D
; Patent No. 6183745

GENERAL INFORMATION:
APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERMAIN
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
NUMBER OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
CITY: PHILADELPHIA
STATE: PENNSYLVANIA
COUNTRY: USA
ZIP: 19103-2398

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876

FILING DATE: 12-DEC-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575

FILING DATE: 12-DEC-1991

ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S

REGISTRATION NUMBER: 27,363

REFERENCE/DOCKET NUMBER: 8795-4

TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020

TELEFAX: 215-567-2991

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-075-541D-47

Query Match 100.0%; Score 51; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCDSTLRLC 9

Db 11 KCDSTLRLC 19

RESULT 6

US-08-934-915-52

Sequence 52, Application US/08934915

Patent No. 5932412

GENERAL INFORMATION:

APPLICANT: DILLNER, JOAKIM

APPLICANT: DILLNER, LENA

APPLICANT: CHENG, HWE-MING

TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN

TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,

TITLE OF INVENTION: 11, 16, 31, 33 AND 56,

TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR

TITLE OF INVENTION: DIAGNOSTIC PURPOSES

NUMBER OF SEQUENCES: 193

CORRESPONDENCE ADDRESS:

ADDRESSEE: MASON & ASSOCIATES, P.A.

STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500

CITY: CLEARWATER

STATE: FLORIDA

COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: LOUISE A. FOUTCH

REGISTRATION NUMBER: 37,133

REFERENCE/DOCKET NUMBER: 1946.6

TELECOMMUNICATION INFORMATION:

TELEPHONE: 813-538-3800

TELEFAX: 813-538-3820

TELEX:

INFORMATION FOR SEQ ID NO: 52:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-934-915-52

Query Match 100.0%; Score 51; DB 2; Length 30;

Best Local Similarity 100.0%; Pred. No. 0.017;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCDSTLRLC 9

Db 17 KCDSTLRLC 25

RESULT 7

US-08-934-915-53

Sequence 53, Application US/08934915

Patent No. 5932412

GENERAL INFORMATION:

APPLICANT: DILLNER, JOAKIM

APPLICANT: DILLNER, LENA

APPLICANT: CHENG, HWE-MING

TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN

TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,

TITLE OF INVENTION: 11, 16, 31, 33 AND 56,

TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR

TITLE OF INVENTION: DIAGNOSTIC PURPOSES

NUMBER OF SEQUENCES: 193

CORRESPONDENCE ADDRESS:

ADDRESSEE: MASON & ASSOCIATES, P.A.

STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500

CITY: CLEARWATER

STATE: FLORIDA

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows 3.0

SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/934,915

FILING DATE: 22-SEP-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/949,836

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: LOUISE A. FOUTCH

REGISTRATION NUMBER: 37,133

; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEX: 813-538-3820
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-53

Query Match 100.0%; Score 51; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCDSTLRLC 9
DB 3 KCDSTLRLC 11

RESULT 8
US-09-486-394-3
; Sequence 3, Application US/09486394
; Patent No. 6478749
; GENERAL INFORMATION:
; APPLICANT: Hopf, Reinhard
; TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method
; FILE REFERENCE: 032929-001
; CURRENT APPLICATION NUMBER: US/09/486,394
; CURRENT FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/04773
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: DE 197 37 409.3
; PRIOR FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(30)
; OTHER INFORMATION: E7 peptide.
US-09-486-394-3

Query Match 100.0%; Score 51; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCDSTLRLC 9
DB 20 KCDSTLRLC 28

RESULT 9
US-08-406-248-6
; Sequence 6, Application US/08406248
; Patent No. 5736318
; GENERAL INFORMATION:
; APPLICANT: Munger, Karl
; APPLICANT: Jones, D. Leanne
; TITLE OF INVENTION: METHOD AND KIT FOR EVALUATING
; TITLE OF INVENTION: TRANSFORMED CELLS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ann-Louise Kerner, Ph.D., Lappin & Kusmer
; STREET: 200 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA

; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,248
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: MCDaniels, Patricia A.
; REGISTRATION NUMBER: 33,194
; REFERENCE/DOCKET NUMBER: HAZ-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-330-1300
; TELEFAX: 617-330-1311
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-406-248-6

Query Match 100.0%; Score 51; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCDSTLRLC 9
DB 60 KCDSTLRLC 68

RESULT 10
US-08-075-541D-42
; Sequence 42, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020

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/ TELEFAX: 215-567-2991
/ INFORMATION FOR SEQ ID NO: 42:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 98 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-075-541D-42

Query Match 100.0%; Score 51; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCDSTLRLC 9
Db 60 KCDSTLRLC 68

RESULT 11
US-09-382-616A-1
; Sequence 1, Application US/09382616A
; Patent No. 6200746
; GENERAL INFORMATION:
; APPLICANT: Fisher, Christopher
; APPLICANT: He, Wanxia
; TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
; FILE REFERENCE: 28341/6216
; CURRENT APPLICATION NUMBER: US/09/382,616A
; CURRENT FILING DATE: 1999-08-25
; PRIOR FILING DATE: 09/382,616
; PRIOR FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Papillomavirus sylvilagi
US-09-382-616A-1

Query Match 100.0%; Score 51; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCDSTLRLC 9
Db 60 KCDSTLRLC 68

RESULT 12
US-08-944-368A-4
; Sequence 4, Application US/08944368A
; Patent No. 6228368
; GENERAL INFORMATION:
; APPLICANT: Gissman, et al.
; TITLE OF INVENTION: Papilloma Virus Capsomere Vaccine
; TITLE OF INVENTION: Formulations and Methods of Use
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 233 South Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,368A
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/ FILING DATE:
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams Jr., Joseph A.
/ REGISTRATION NUMBER: 38,659
/ REFERENCE/DOCKET NUMBER: 27013/34028
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-474-6300
/ TELEFAX: 312-474-0448
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 98 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-944-368A-4

Query Match 100.0%; Score 51; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCDSTLRLC 9
Db 60 KCDSTLRLC 68

RESULT 13
US-09-820-764-4
; Sequence 4, Application US/09820764
; Patent No. 6352696
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; APPLICANT: HALLEK, Michael
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/820,764
; FILING DATE: 30-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,896
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-820-764-4

Query Match 100.0%; Score 51; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.054;
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Job time : 17.9126 secs

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
| | | | | | | |
Db 60 KCDSTLRLC 68

RESULT 14
US-09-613-303-8
; Sequence 8, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-09-613-303-8

Query Match 100.0%; Score 51; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
| | | | | | | |
Db 60 KCDSTLRLC 68

RESULT 15
US-09-566-420-19
; Sequence 19, Application US/09566420
; Patent No. 6500641
; GENERAL INFORMATION:
; APPLICANT: CHEN, SI-YI AND ZHAOYANG, YOU
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTIGENS WHICH ELICIT AN
; TITLE OF INVENTION: IMMUNE RESPONSE
; FILE REFERENCE: TBA
; CURRENT APPLICATION NUMBER: US/09/566,420
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/132,752
; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 60/132,750
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Human papillomavirus type E7
US-09-566-420-19

Query Match 100.0%; Score 51; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
| | | | | | | |
Db 60 KCDSTLRLC 68

Search completed: June 29, 2005, 01:44:21

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2005, 23:28:22 ; Search time 54.2473 Seconds
(without alignments)
84.958 Million cell updates/sec

Title: US-08-170-344-61

Perfect score: 56

Sequence: 1 CCKCDSTLR 9

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	77	2	Q8B5P5
2	56	100.0	93	2	Q9QDH2
3	56	100.0	93	2	Q9QDH4
4	56	100.0	93	2	Q9QDH6
5	56	100.0	93	2	Q9QDH8
6	56	100.0	94	2	Q8B5P6
7	56	100.0	98	1	VE7_HPV16
8	56	100.0	98	2	O11650
9	56	100.0	98	2	O12337
10	56	100.0	98	2	O12338
11	56	100.0	98	2	O8QRD2
12	56	100.0	98	2	Q8QRD3
13	56	100.0	98	2	O8V1J0
14	56	100.0	98	2	Q778H3
15	56	100.0	98	2	Q778H5
16	51	91.1	65	2	Q8B563
17	51	91.1	98	2	Q8QRD4
18	49	87.5	99	1	VE7_HPV35
19	49	87.5	99	2	Q76WP2
20	48	85.7	98	2	Q6T377
21	47	83.9	867	2	Q6BWH5
22	46	82.1	92	1	VE7_HPV57
23	45	80.4	64	2	Q6Q3F8
24	45	80.4	98	1	VE7_HPV31
25	45	80.4	131	2	P70637
26	45	80.4	247	2	Q61964
27	45	80.4	1168	1	LMB3 MOUSE
28	45	80.4	1168	2	Q91V90
29	44	78.6	109	1	VE7_HPV39
30	44	78.6	605	2	Q8IMS6
31	44	78.6	633	2	Q9VBP9

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32 43 76.8 109 1 VE7_HPV70 P50785 human papil
33 42 75.0 93 1 VE7_HPV15 P36820 human papil
34 42 75.0 266 2 Q7XL73 Q7XL73 oryza sativ
35 42 75.0 1172 1 LMB3 HUMAN Q13751 homo sapien
36 41 73.2 92 1 VE7_HPV2A P25485 human papil
37 41 73.2 98 1 VE7_HPV11 P04020 human papil
38 41 73.2 98 1 VE7_HPV6A Q84292 human papil
39 41 73.2 98 1 VE7_HPV6B P06464 human papil
40 41 73.2 98 2 Q9QLP4 Q9QLP4 human papil
41 41 73.2 108 2 Q9WHG1 Q9WHG1 human papil
42 41 73.2 391 2 Q86PQ9 Q86PQ9 cryptospori
43 41 73.2 814 2 Q23141 Q23141 caenorhabdi
44 40 71.4 61 2 Q6VRG0 Q6VRG0 melon necro
45 40 71.4 61 2 Q89846 Q89846 melon necro

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ALIGNMENTS

RESULT 1

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Q8B5P5 PRELIMINARY; PRT; 77 AA.
ID Q8B5P5
AC Q8B5P5;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF469198; AAC15694.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 77
SQ SEQUENCE 77 AA; 8782 MW; C5DE3A7E546AC31B CRC64;

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Query Match 100.0%; Score 56; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. NO. 0.09;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CCKCDSTLR 9
Db 58 CCKCDSTLR 66

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RESULT 2

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Q9QDH2 PRELIMINARY; PRT; 93 AA.
ID Q9QDH2
AC Q9QDH2;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187869; AAF13399.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

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Query Match 100.0%; Score 56; DB 2; Length 93;

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Best Local Similarity 100.0%; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 CCKCDSTLR 9
Db 58 CCKCDSTLR 66

RESULT 3
Q9QDH4 PRELIMINARY; PRT; 93 AA.
AC Q9QDH4;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187866; AAF13393.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 56; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 CCKCDSTLR 9
Db 58 CCKCDSTLR 66

RESULT 4
Q9QDH6 PRELIMINARY; PRT; 93 AA.
AC Q9QDH6;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187867; AAF13395.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10513 MW; 92C7054341326A1F CRC64;

Query Match 100.0%; Score 56; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 CCKCDSTLR 9
Db 58 CCKCDSTLR 66

RESULT 5
Q9QDH8 PRELIMINARY; PRT; 93 AA.
AC Q9QDH8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187866; AAF13393.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 56; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 CCKCDSTLR 9
Db 58 CCKCDSTLR 66

RESULT 6
Q8B5P6 PRELIMINARY; PRT; 94 AA.
AC Q8B5P6;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE E7 oncoprotein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglakitmongkol M., Vaeteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF465197; AAO15692.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 94
SQ SEQUENCE 94 AA; 10555 MW; 7CC3281BB2AE2C8A CRC64;

Query Match 100.0%; Score 56; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 CCKCDSTLR 9
Db 58 CCKCDSTLR 66

RESULT 7
VE7 HPV16 STANDARD; PRT; 98 AA.
AC P03129;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE E7 protein.
GN Name=E7;
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]

```

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AC Q9QDH8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187866; AAF13393.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 56; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 CCKCDSTLR 9
Db 58 CCKCDSTLR 66

RESULT 6
Q8B5P6 PRELIMINARY; PRT; 94 AA.
AC Q8B5P6;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE E7 oncoprotein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglakitmongkol M., Vaeteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF465197; AAO15692.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 94
SQ SEQUENCE 94 AA; 10555 MW; 7CC3281BB2AE2C8A CRC64;

Query Match 100.0%; Score 56; DB 2; Length 94;
Best Local Similarity 100.0%; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 CCKCDSTLR 9
Db 58 CCKCDSTLR 66

RESULT 7
VE7 HPV16 STANDARD; PRT; 98 AA.
AC P03129;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE E7 protein.
GN Name=E7;
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=85246220; PubMed=2990099;
RA Seedorf K., Kramer G., Durst M., Suhai S., Rowekamp W.G.;
RT "Human papillomavirus type 16 DNA sequence.";
RL Virology 145:181-185(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90218027; PubMed=2157796;
RA Schneider-Maunoury S., Pehau-Arnaut G., Breitburd F., Orth G.;
RT "Expression of the human papillomavirus type 16 genome in SK-v cells,
a line derived from a vulvar intraepithelial neoplasia.";
RL J. Gen. Virol. 71:809-817(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Lee H.P.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [5]
RP FUNCTION.
RX MEDLINE=88223347; PubMed=2836062;
RA Phelps W.C., Yee C.L., Munger K., Howley P.M.;
RT "The human papillomavirus type 16 E7 gene encodes transactivation and
transformation functions similar to those of adenovirus E1A.";
RL Cell 53:539-547(1988).
CC -!- FUNCTION: E7 protein has both transforming and trans-activating
CC activities.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K02718; AAA46940.1; -
DR EMBL; D00735; AAA00633.1; -
DR EMBL; U76411; AAB18962.1; -
DR EMBL; U76412; AAB18963.1; -
DR EMBL; U76413; AAB18964.1; -
DR EMBL; AF003020; AAB70737.1; -
DR EMBL; AF003023; AAB70740.1; -
DR EMBL; AF003024; AAB70741.1; -
DR EMBL; AF003025; AAB70742.1; -
DR EMBL; AF003026; AAB70743.1; -
DR FIR; A03688; W7WLHS.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
KW DNA-binding; Early protein; Oncogene; Trans-acting factor;
KW Transcription regulation.
FT SITE 58 61 C-XX-C motif-1.
FT SITE 91 94 C-XX-C motif-2.
SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 100.0%; Score 56; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
DB 58 CCKCDSTLR 66

RESULT 8
O11650 PRELIMINARY; PRT; 98 AA.
AC O11650;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

```

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DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative transforming protein E7.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97407827; PubMed=9264576; DOI=10.1006/gyno.1997.4756;
RA Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Chang W.H.,
RA Lee H.P.;
RT "Major sequence variants in E7 gene of human papillomavirus type 16
from cervical cancerous and noncancerous lesions of Korean women.";
RL Gynecol. Oncol. 66:275-281(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX Song Y.-S., Kee S.-H., Kim J.-W., Park N.-H., Kang S.-B., Chang W.-H.,
RA Lee H.-P.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX Terai M., Ma Z., Burk R.D.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
RN [5]
RP SEQUENCE FROM N.A.
RX Terai M., Fu L., Ma Z., Burk R.D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U76404; AAC58243.1; -
DR EMBL; AF472509; AAO15706.1; -
DR EMBL; AF486326; AAL96631.1; -
DR EMBL; AF486327; AAL96632.1; -
DR EMBL; AF486330; AAL96635.1; -
DR EMBL; AF486331; AAL96636.1; -
DR EMBL; AF486332; AAL96637.1; -
DR EMBL; AF486333; AAL96638.1; -
DR EMBL; AF486334; AAL96639.1; -
DR EMBL; AF486336; AAL96641.1; -
DR EMBL; AF486338; AAL96643.1; -
DR EMBL; AF486346; AAL96651.1; -
DR EMBL; AF486350; AAL96655.1; -
DR EMBL; AF486351; AAL96656.1; -
DR EMBL; AF534061; AAO10404.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 100.0%; Score 56; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
DB 58 CCKCDSTLR 66

RESULT 9
O12337 PRELIMINARY; PRT; 98 AA.
AC O12337;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

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OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RL type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003021; AAB70738.1; -.
DR InterPro; IPR000148; PapiV_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11056 MW; 19DEB8F14CD2C705 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
Db 58 CCKCDSTLR 66

RESULT 10
O12338
ID O12338 PRELIMINARY; PRT; 98 AA.
AC O12338;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RL type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003022; AAB70739.1; -.
DR EMBL; AF477385; AAM03025.1; -.
DR InterPro; IPR000148; PapiV_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10969 MW; 9BD612534CCEA59B CRC64;

Query Match 100.0%; Score 56; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
Db 58 CCKCDSTLR 66

RESULT 11
O8QRD2
ID O8QRD2 PRELIMINARY; PRT; 98 AA.
AC O8QRD2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

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OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486345; AAL96650.1; -.
DR InterPro; IPR000148; PapiV_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11045 MW; 9C4F8C534CD76C4B CRC64;

Query Match 100.0%; Score 56; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
Db 58 CCKCDSTLR 66

RESULT 12
O8QRD3
ID O8QRD3 PRELIMINARY; PRT; 98 AA.
AC O8QRD3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486344; AAL96649.1; -.
DR InterPro; IPR000148; PapiV_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 11021 MW; 9BD6125946D2C3E1 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
Db 58 CCKCDSTLR 66

RESULT 13
O8VLJ0
ID O8VLJ0 PRELIMINARY; PRT; 98 AA.
AC O8VLJ0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Jinhu X., Xinling W., Yun T.;

```


RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF461264; AAL66736.1; -

DR Pfam; PF00527; E7; 1.

SQ SEQUENCE 98 AA; 10997 MW; 9BD610834CCEA59B CRC64;

Query Match 100.0%; Score 56; DB 2; Length 98;

Best Local Similarity 100.0%; Pred. No. 0.11; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9

|||||

Db 58 CCKCDSTLR 66

RESULT 14

Q778H3

AC Q778H3 PRELIMINARY; PRT; 98 AA.

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE E7 protein (Fragment).

OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI_TaxID=10581;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20112892; PubMed=10644829;

RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,

RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;

RT "Analysis of human papillomavirus type 16 E6 variants in relation to

RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";

RL J. Gen. Virol. 81:317-325(2000).

DR EMBL; AJ388063; CAB45119.1; -

DR InterPro; IPR000148; Papvi_E7.

DR Pfam; PF00527; E7; 1.

FT NON_TER 98

SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match

Best Local Similarity 100.0%; Score 56; DB 2; Length 98;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9

|||||

Db 58 CCKCDSTLR 66

RESULT 15

Q778H5

AC Q778H5 PRELIMINARY; PRT; 98 AA.

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE E7 protein (Fragment).

OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI_TaxID=10581;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20112892; PubMed=10644829;

RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,

RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;

RT "Analysis of human papillomavirus type 16 E6 variants in relation to

RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";

RL J. Gen. Virol. 81:317-325(2000).

DR EMBL; AJ388062; CAB45117.1; -

DR InterPro; IPR000148; Papvi_E7.

DR Pfam; PF00527; E7; 1.

FT NON_TER 98

SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 100.0%; Score 56; DB 2; Length 98;

Best Local Similarity 100.0%; Pred. No. 0.11; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9

|||||

Db 58 CCKCDSTLR 66

Search completed: June 29, 2005, 01:34:41

Job time : 56.2473 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:32:21 ; Search time 11.2747 Seconds
(without alignments)
76.805 Million cell updates/sec

Title: US-08-170-344-61

Perfect score: 56

Sequence: 1 CCKCDSTLR 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:**

1: PIR1:**

2: PIR2:**

3: PIR3:**

4: PIR4:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	98	1 W7WLS	E7 protein - human
2	49	87.5	99	1 W7WLS35	E7 protein - human
3	46	82.1	92	1 S15622	E7 protein - human
4	45	80.4	98	1 W7WLS31	E7 protein - human
5	45	80.4	1188	2 I56985	Kallinin B1 - mouse
6	44	78.6	109	2 W7WLS39	E7 protein - human
7	42	75.0	93	2 S36474	E7 protein - human
8	42	75.0	352	2 T22384	hypothetical prote
9	42	75.0	1170	2 A53612	laminin Blk chain
10	41	73.2	92	1 S15615	E7 protein - human
11	41	73.2	98	1 W7WLS11	E7 protein - human
12	41	73.2	98	1 W7WLS6	E7 protein - human
13	41	73.2	823	2 T34472	hypothetical prote
14	39	69.6	99	2 S36574	E7 protein - human
15	39	69.6	106	2 S36562	E7 protein - human
16	39	69.6	348	2 S64041	probable membrane
17	38	67.9	110	1 W7WLSR	E7 protein - human
18	38	67.9	168	2 T45305	hypothetical prote
19	38	67.9	194	2 S70663	lectin heavy chain
20	38	67.9	194	2 S70664	lectin heavy chain
21	38	67.9	1292	2 T09229	galactose binding
22	37	66.1	115	2 S69297	probable membrane
23	37	66.1	333	2 AG2214	hypothetical prote
24	36	64.3	92	2 S36498	E7 protein - human
25	36	64.3	105	1 W7WLS18	E7 protein - human
26	36	64.3	105	2 S36528	E7 protein - human
27	36	64.3	248	2 T26584	hypothetical prote
28	36	64.3	298	2 E97032	probable permealase
29	36	64.3	312	2 T27255	hypothetical prote

protein F17F8.27 [probable ABC-type
hypothetical prote
E7 protein - human
hypothetical prote
hypothetical prote
E7 protein - human
probable membrane
neutrophil activat
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
G protein-coupled
probable membrane
hypothetical prote

30 36 64.3 739 2 E86434
31 36 64.3 1011 2 T07712
32 35 62.5 66 2 F84337
33 35 62.5 95 2 S36480
34 35 62.5 95 2 A84648
35 35 62.5 101 1 W7WLS1
36 35 62.5 160 2 S45981
37 35 62.5 189 2 A70186
38 35 62.5 250 2 T16342
39 35 62.5 301 2 T29384
40 35 62.5 311 2 T21845
41 35 62.5 342 2 H86336
42 381 2 A35300
43 35 62.5 428 2 T39773
44 35 62.5 450 2 AF0207
45 35 62.5 1302 2 T00038

ALIGNMENTS

RESULT 1

W7WLS

E7 protein - human papillomavirus type 16

C:Species: human papillomavirus type 16

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03688; S12367; T10428

R:Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virology 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03688

A:Molecule type: DNA

A:Residues: 1-98 <SEE>

A:Cross-references: UNIPROT:P03129; GB:K02718; NID:G333031; PIDN:AAA46940.1; PID:G333033

R:Barbosa, M.S.; Edmonds, C.; Fisher, C.; Schiller, J.T.; Lowy, D.R.; Vousden, K.H.

EMBO J. 9, 153-160, 1990

A:Title: The region of the HPV E7 oncoprotein homologous to adenovirus E1a and SV40 large

A:Reference number: S12367; MUID:90107938; PMID:2153075

A:Accession: S12367

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-98 <BAR>

R:Kennedy, I.M.; Haddock, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level

A:Reference number: Z17014; MUID:91162763; PMID:1848319

A:Accession: T10428

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-98 <KEN>

A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46940.1; PID:G333033

C:Genetics:

C:Gene: E7

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation; zinc finger

F:58-94/region: zinc finger CCCC motif

Query Match

Best Local Similarity 100.0%; Score 56; DB 1; Length 98;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 CCKCDSTLR 9

|||||

58 CCKCDSTLR 66

RESULT 2

W7WLS

E7 protein - human papillomavirus type 35

C:Species: human papillomavirus type 35

A:Note: host Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C;Accession: F40824; S36522
R;Marich, J.E.; Fonteler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776, 1992
A;Title: The phylogenetic relationship and complete nucleotide sequence of human papillomavirus type 31
A;Reference number: A40824; MUID:92124753; PMID:1310198
A;Accession: F40824
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-99 <MAR>
A;Cross-references: UNIPROT:P27230; GB:M74117; NID:G333050; PIDN:AAA46967.1; PID:G333052
R;Dellius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36522
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99
A;Cross-references: EMBL:X74477; NID:G396997; PIDN:CAA52562.1; PID:G396999
A;Experimental source: strain 35H
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F;59-95/Region: zinc finger CCCC motif

Query Match 87.5%; Score 49; DB 1; Length 99;
Best Local Similarity 77.8%; Pred. No. 0.89;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
DB 59 CCKCEATLR 67
|||||

RESULT 3
S15622
E7 protein - human papillomavirus type 57
C;Species: human papillomavirus type 57
A;Note: host Homo sapiens (man)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: S15622
R;Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.
Virus Res 18, 81-98, 1990
A;Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and 2b
A;Reference number: S15614; MUID:91186699; PMID:1964523
A;Accession: S15622
A;Molecule type: DNA
A;Residues: 1-92 <HIR>
A;Cross-references: UNIPROT:P22160; EMBL:X55965; NID:G60882; PIDN:CAA39431.1; PID:G60884
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F;55-91/Region: zinc finger CCCC motif

Query Match 82.1%; Score 46; DB 1; Length 92;
Best Local Similarity 77.8%; Pred. No. 2.4;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
DB 55 CCKCHSTVR 63
|||||

RESULT 4
W7WL31
E7 protein - human papillomavirus type 31
C;Species: human papillomavirus type 31
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: B32444
R;Goldsbrough, M.D.; Disilvestre, D.; Temple, G.F.; Lorincz, A.T.
Virology 171, 306-311, 1989
A;Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associated virus
A;Reference number: A94398; MUID:99299478; PMID:2545036
A;Accession: B32444

A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-98 <GOL>
A;Cross-references: UNIPROT:P17387; GB:J04353; NID:G333048; PIDN:AAA46951.1; PID:G459917
C;Comment: This protein may be involved in the oncogenic potential of this virus.
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F;58-94/Region: zinc finger CCCC motif

Query Match 80.4%; Score 45; DB 1; Length 98;
Best Local Similarity 77.8%; Pred. No. 3.5;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
DB 58 CCKCKSTLR 66
|||||

RESULT 5
I56985
kalinin B1 - mouse
C;Species: Mus sp. (mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 15-Mar-2004
C;Accession: I56985
R;Utani, A.; Kopp, J.B.; Kozak, C.A.; Matsuki, Y.; Amizuka, N.; Sugiyama, S.; Yamada, Y.
Lab. Invest. 72, 300-310, 1995
A;Title: Mouse kalinin B1 (laminin beta 3 chain): cloning and tissue distribution.
A;Reference number: I56985; MUID:95205823; PMID:7898049
A;Accession: I56985
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1168 <RES>
A;Cross-references: GB:S75486; NID:G912768; PID:G912769
F;376-425/Domain: laminin-type EGF-like homology <LEG>
F;428-475/Domain: laminin-type EGF-like homology <EG1>
F;478-528/Domain: laminin-type EGF-like homology <LEG1>
F;531-575/Domain: laminin-type EGF-like homology <LEG8>

Query Match 80.4%; Score 45; DB 2; Length 1168;
Best Local Similarity 87.5%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 8
DB 66 CCKCDSRL 73
|||||

RESULT 6
W7WL39
E7 protein - human papillomavirus type 39
C;Species: human papillomavirus type 39
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: B38502
R;Volpers, C.; Streeck, R.E.
Virology 181, 419-423, 1991
A;Title: Genome organization and nucleotide sequence of human papillomavirus type 39.
A;Reference number: A38502; MUID:91135017; PMID:1847266
A;Accession: B38502
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-109 <VOL>
A;Cross-references: UNIPROT:P24837; GB:M62849; EMBL:M38185; NID:G333245; PIDN:AAA47051.1; PID:G333245
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation

Query Match 78.6%; Score 44; DB 1; Length 109;
Best Local Similarity 66.7%; Pred. No. 5.3;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
DB 68 CCKCNNTLQ 76
|||||

RESULT 7
S36474
E7 protein - human papillomavirus type 15
C/Species: human papillomavirus type 15
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C/Accession: S36474
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A/Description: Primer-directed sequencing of human papillomavirus types.
A/Reference number: S36469
A/Accession: S36474
A/Molecule type: DNA
A/Residues: 1-93
A/Cross-references: UNIPROT:P36820; EMBL:X74468; NID:G36924; PIDN:CAA52507.1; PID:G3969
C/Suprafamily: papillomavirus E7 protein
C/Keywords: DNA binding, early protein; transcription regulation

Query Match 75.0%; Score 42; DB 2; Length 93;
Best Local Similarity 77.8%; Pred. No. 9.5;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
Db 50 CCFCDSKLR 58
||| ||| |||

RESULT 8
T22384
hypothetical protein F48F5.4 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T22384
R;Lloyd, C.
submitted to the EMBL Data Library, November 1996
A/Reference number: Z19558
A/Accession: T22384
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-352 <WIL>
A/Cross-references: UNIPROT:Q9KV08; EMBL:Z81541; PIDN:CA804413.1; GSPDB:GN00023; CESP:F4
A/Experimental source: clone F48F5
C/Genetics:
A/Gene: CESP:F48F5.4
A/Map position: 5
A/Introns: 17/1; 91/2; 123/3; 170/3; 263/3; 290/1

Query Match 75.0%; Score 42; DB 2; Length 352;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCKCDST 7
Db 8 CCNCDST 14
||| ||| |||

RESULT 9
A53612
laminin B1 chain precursor - human
N/Alternate names: kalinin B1 chain; nicein B1 chain
C/Species: Homo sapiens (man)
C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C/Accession: A53612
R;Gerecke, D.R.; Wagman, D.W.; Champlaud, M.F.; Burgeson, R.E.
J. Biol. Chem. 269, 11073-11080, 1994
A/Title: The complete primary structure for a novel laminin chain, the laminin B1 chain
A/Reference number: A53612; MUID:94209274; PMID:7512558
A/Accession: A53612
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1170 <GER>
A/Cross-references: UNIPROT:Q13751; GB:L25541; NID:G510702; PIDN:AAA61834.1; PID:G510703

A/Note: authors translated the codon CGA for residue 124 as Gln, GAG for residue 439 as /
C/Keywords: glycoprotein
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-1170/Product: laminin B1 chain #status predicted <WAT>
F;250-312/Domain: laminin-type EGF-like homology <LEG1>
F;378-427/Domain: laminin-type EGF-like homology <LEG>
F;430-476/Domain: laminin-type EGF-like homology <EG11>
F;532-576/Domain: laminin-type EGF-like homology <LEG2>

Query Match 75.0%; Score 42; DB 2; Length 1170;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDS 6
Db 66 CCKCDS 71
|||||

RESULT 10
S15615
E7 protein - human papillomavirus type 2a
C/Species: human papillomavirus type 2a
A/Note: host Homo sapiens (man)
C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C/Accession: S15615
R;Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.
Virus Res. 18, 81-98, 1990
A/Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and 1
A/Reference number: S15614; MUID:91188699; PMID:1964523
A/Accession: S15615
A/Molecule type: DNA
A/Residues: 1-92 <HR>
A/Cross-references: UNIPROT:P25485; EMBL:X55964
C/Suprafamily: papillomavirus E7 protein
C/Keywords: DNA binding; early protein; transcription regulation; zinc finger
F;55-91/Region: zinc finger CCCC motif

Query Match 73.2%; Score 41; DB 1; Length 92;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
Db 55 CCKCGRTVR 63
|||||

RESULT 11
W7WL11
E7 protein - human papillomavirus type 11
C/Species: human papillomavirus type 11
C/Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 09-Jul-2004
C/Accession: A03690
R;Bartmann, K.; Schwarz, E.; Gissmann, L.; zur Hausen, H.
Virology 151, 124-130, 1986
A/Title: The nucleotide sequence and genome organization of human papilloma virus type 11
A/Reference number: A94338; MUID:86181601; PMID:3008427
A/Accession: A03690
A/Molecule type: DNA
A/Residues: 1-98 <DAR>
A/Cross-references: UNIPROT:P04020; GB:M14119; NID:G333026; PIDN:AAA46928.1; PID:G496194
C/Suprafamily: papillomavirus E7 protein
C/Keywords: DNA binding; early protein; transcription regulation; zinc finger
F;58-94/Region: zinc finger CCCC motif

Query Match 73.2%; Score 41; DB 1; Length 98;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
Db 58 CCKCDSNR 66
|||||

S36574
E7 protein - human papillomavirus type 52
C/Species: human papillomavirus type 52
C/Date: 08-May-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C/Accession: S36574
R/Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A/Description: Primer-directed sequencing of human papillomavirus types.
A/Reference number: S36469
A/Accession: S36574
A/Molecule type: DNA
A/Residues: 1-99
A/Cross-references: UNIPROT:P36831; EMBL:X74481; NID:g397038; PIDN:CAA52586.1; PID:g397070
C/Superfamily: papillomavirus E7 protein.
C/Keywords: DNA binding; early protein; transcription regulation

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 05:18:25 ; Search time 53.8517 Seconds
(without alignments)
64.268 Million cell updates/sec

Title: US-08-170-344-61

Perfect score: 56

Sequence: 1 CCKCDSTLR 9

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	9	9 US-09-891-823-16	Sequence 16, Appl
2	56	100.0	9	14 US-10-365-908-16	Sequence 16, Appl
3	56	100.0	9	16 US-10-871-138-16	Sequence 16, Appl
4	56	100.0	10	9 US-09-891-823-30	Sequence 30, Appl
5	56	100.0	10	14 US-10-365-908-30	Sequence 30, Appl
6	56	100.0	10	16 US-10-871-138-30	Sequence 30, Appl
7	56	100.0	10	15 US-10-306-541-96	Sequence 96, Appl
8	56	100.0	15	16 US-10-432-465-49	Sequence 49, Appl
9	56	100.0	20	16 US-10-890-526-74	Sequence 74, Appl
10	56	100.0	98	9 US-09-728-466-1	Sequence 1, Appl
11	56	100.0	98	9 US-09-820-765-4	Sequence 4, Appl

12	56	100.0	98	9 US-09-824-017-4	Sequence 4, Appl
13	56	100.0	98	10 US-09-986-118A-4	Sequence 4, Appl
14	56	100.0	98	14 US-10-267-311-8	Sequence 8, Appl
15	56	100.0	98	14 US-10-177-390-8	Sequence 8, Appl
16	56	100.0	98	14 US-10-201-764-19	Sequence 19, Appl
17	56	100.0	98	15 US-10-392-113-29	Sequence 29, Appl
18	56	100.0	98	15 US-10-654-129-4	Sequence 4, Appl
19	56	100.0	98	15 US-10-681-410-19	Sequence 19, Appl
20	56	100.0	98	16 US-10-772-988-3	Sequence 3, Appl
21	56	100.0	98	16 US-10-479-541-5	Sequence 5, Appl
22	56	100.0	98	17 US-10-042-526A-4	Sequence 4, Appl
23	56	100.0	98	17 US-10-657-399-1	Sequence 1, Appl
24	56	100.0	98	17 US-10-858-384-12	Sequence 12, Appl
25	56	100.0	98	17 US-10-484-063-26	Sequence 26, Appl
26	56	100.0	98	17 US-10-343-448-5	Sequence 5, Appl
27	56	100.0	98	17 US-10-679-956-8	Sequence 8, Appl
28	56	100.0	98	17 US-10-367-057-17	Sequence 17, Appl
29	56	100.0	99	15 US-10-115-440-7	Sequence 7, Appl
30	56	100.0	111	16 US-10-472-724-4	Sequence 4, Appl
31	56	100.0	121	14 US-10-267-311-12	Sequence 12, Appl
32	56	100.0	121	17 US-10-679-956-12	Sequence 12, Appl
33	56	100.0	198	14 US-10-267-311-35	Sequence 35, Appl
34	56	100.0	198	17 US-10-679-956-35	Sequence 35, Appl
35	56	100.0	220	13 US-10-000-903-1	Sequence 1, Appl
36	56	100.0	220	13 US-10-000-903-8	Sequence 8, Appl
37	56	100.0	220	17 US-10-899-771-1	Sequence 1, Appl
38	56	100.0	220	17 US-10-899-771-8	Sequence 8, Appl
39	56	100.0	239	13 US-10-000-903-12	Sequence 12, Appl
40	56	100.0	239	17 US-10-899-771-12	Sequence 12, Appl
41	56	100.0	266	9 US-09-367-309A-1	Sequence 1, Appl
42	56	100.0	289	15 US-10-115-440-5	Sequence 5, Appl
43	56	100.0	295	14 US-10-267-311-33	Sequence 33, Appl
44	56	100.0	295	17 US-10-679-956-33	Sequence 33, Appl
45	56	100.0	324	14 US-10-267-311-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1

US-09-891-823-16
; Sequence 16, Application US/09891823
; Publication No. US20020110566A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/09/891,823
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-09-891-823-16

Query Match 100.0%; Score 56; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9

DB 1 CCKCDSTLR 9

RESULT 2

```

US-10-365-908-16
; Sequence 16, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-16

Query Match      100.0%; Score 56; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCKCDSTLR 9
Db 1 CCKCDSTLR 9

RESULT 3
US-10-871-138-16
; Sequence 16, Application US/10871138
; Publication No. US20040235741A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/871,138
; CURRENT FILING DATE: 2004-06-18
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-871-138-16

Query Match      100.0%; Score 56; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCKCDSTLR 9
Db 1 CCKCDSTLR 9

RESULT 4
US-09-891-823-30
; Sequence 30, Application US/09891823
; Publication No. US20020110566A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-09-891-823-30

Query Match      100.0%; Score 56; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.088;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCKCDSTLR 9
Db 1 CCKCDSTLR 9

RESULT 5
US-10-365-908-30
; Sequence 30, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-30

Query Match      100.0%; Score 56; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.088;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCKCDSTLR 9
Db 1 CCKCDSTLR 9

RESULT 6
US-10-871-138-30
; Sequence 30, Application US/10871138
; Publication No. US20040235741A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/871,138
; CURRENT FILING DATE: 2004-06-18
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-871-138-30

Query Match      100.0%; Score 56; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCKCDSTLR 9
Db 1 CCKCDSTLR 9

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; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/871.138
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-871-138-30

Query Match 100.0%; Score 56; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.088;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
| | | | |
Db 1 CCKCDSTLR 9

RESULT 7

US-10-306-541-96
; Sequence 96, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 96
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-96

Query Match 100.0%; Score 56; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
| | | | |
Db 5 CCKCDSTLR 13

RESULT 8

US-10-432-465-49
; Sequence 49, Application US/10432465
; Publication No. US20040091479A1
; GENERAL INFORMATION:
; APPLICANT: Kaufmann, John
; APPLICANT: Kather, Angela
; APPLICANT: Schinz, Manuela
; TITLE OF INVENTION: T-Cell Epitopes of the Papillomavirus L1
; TITLE OF INVENTION: Protein and E7 Protein and Their Use in Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/077001
; CURRENT APPLICATION NUMBER: US/10/432,465
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/14037
; PRIOR FILING DATE: 2001-11-30

; PRIOR APPLICATION NUMBER: DE 10059631.2
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-432-465-49

Query Match 100.0%; Score 56; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
| | | | |
Db 3 CCKCDSTLR 11

RESULT 9

US-10-890-526-74
; Sequence 74, Application US/10890526
; Publication No. US20040258708A1
; GENERAL INFORMATION:
; APPLICANT: Jochmus, Ingrid
; APPLICANT: Nieland, John
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
; TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/036001
; CURRENT APPLICATION NUMBER: US/10/890,526
; CURRENT FILING DATE: 2004-07-13
; PRIOR APPLICATION NUMBER: US/09/980,177
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: PCT/EP00/05006
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: DE 19925199.1
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 74
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-890-526-74

Query Match 100.0%; Score 56; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
| | | | |
Db 3 CCKCDSTLR 11

RESULT 10

US-09-728-466-1
; Sequence 1, Application US/09728466
; Patent No. US20010029022A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Christopher
; APPLICANT: He, Wanxia
; TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
; FILE REFERENCE: 28341/6216
; CURRENT APPLICATION NUMBER: US/09/728,466
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/382,616
; PRIOR FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 98
; TYPE: PRT

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; ORGANISM: Papillomavirus sylvilagi
US-09-728-466-1

Query Match      100.0%; Score 56; DB 9; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCKCDSTLR 9
DB      58 CCKCDSTLR 66

RESULT 11
US-09-820-765-4
; Sequence 4, Application US/09820765
; Publication No. US20020039584A1
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; HALLER, Michael
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/820,765
; FILING DATE: 30-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,896
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-824-017-4

Query Match      100.0%; Score 56; DB 9; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCKCDSTLR 9
DB      58 CCKCDSTLR 66

RESULT 12
US-09-824-017-4
; Sequence 4, Application US/09824017
; Publication No. US20020197669A1
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; HALLER, Michael
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/824,017
; FILING DATE: 03-Apr-2001
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/026,896
; FILING DATE: 1998-02-20
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-820-765-4

Query Match      100.0%; Score 56; DB 9; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCKCDSTLR 9
DB      58 CCKCDSTLR 66

RESULT 13
US-09-986-118A-4
; Sequence 4, Application US/09986118A
; Publication No. US20030021806A1
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; HALLER, Michael
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/986,118A
; FILING DATE: 07-No. US20030021806A1-2001
; CLASSIFICATION: <Unknown>
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,896
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-986-118A-4

Query Match      100.0%; Score 56; DB 10; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCKCDSTLR 9
Db      58 CCKCDSTLR 66

RESULT 14
US-10-267-311-8
; Sequence 8, Application US/10267311
; Publication No. US20030050469A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-8

Query Match      100.0%; Score 56; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCKCDSTLR 9
Db      58 CCKCDSTLR 66

RESULT 15
US-10-177-390-8
; Sequence 8, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerp Innovatiecentrum
; TITLE OF INVENTION: Improved transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
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; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: fragment of
; OTHER INFORMATION: human papilloma virus type 16 E7 gene
US-10-177-390-8

Query Match      100.0%; Score 56; DB 14; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCKCDSTLR 9
Db      58 CCKCDSTLR 66

Search completed: June 29, 2005, 05:48:11
Job time : 54.8517 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 23:37:59 ; Search time 16.8626 Seconds
(without alignments)
39.842 Million call updates/sec

Title: US-08-170-344-61
Perfect score: 56
Sequence: 1 CCKCDSTLR 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
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2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	9	4	US-10-365-908-16
2	56	100.0	10	4	US-10-365-908-30
3	56	100.0	19	3	US-08-075-541D-38
4	56	100.0	20	2	US-08-934-915-48
5	56	100.0	20	4	US-09-980-177A-74
6	56	100.0	25	3	US-08-075-541D-47
7	56	100.0	30	2	US-08-934-915-52
8	56	100.0	30	2	US-08-934-915-53
9	56	100.0	30	4	US-09-486-394-3
10	56	100.0	38	4	US-09-501-097A-6
11	56	100.0	98	1	US-08-406-248-6
12	56	100.0	98	3	US-08-075-541D-42
13	56	100.0	98	3	US-09-382-616A-1
14	56	100.0	98	3	US-08-944-368A-4
15	56	100.0	98	3	US-09-920-764-4
16	56	100.0	98	4	US-09-613-303-8
17	56	100.0	98	4	US-09-566-420-19
18	56	100.0	98	4	US-09-986-118A-4
19	56	100.0	98	4	US-09-728-466-1
20	56	100.0	98	4	US-09-824-017-4
21	56	100.0	98	4	US-10-267-311-8
22	56	100.0	98	4	US-10-201-764-19
23	56	100.0	98	4	US-09-637-746-3
24	56	100.0	98	4	US-09-501-097A-7
25	56	100.0	98	4	US-09-980-523A-12
26	56	100.0	121	4	US-09-613-303-12
27	56	100.0	121	4	US-10-267-311-12

28	56	100.0	172	3	US-08-860-165-12	Sequence 12, Appl
29	56	100.0	172	3	US-08-860-165-14	Sequence 14, Appl
30	56	100.0	172	3	US-09-359-382-12	Sequence 12, Appl
31	56	100.0	172	3	US-09-359-382-14	Sequence 14, Appl
32	56	100.0	198	4	US-09-613-303-35	Sequence 35, Appl
33	56	100.0	198	4	US-10-267-311-35	Sequence 35, Appl
34	56	100.0	220	3	US-09-485-885-1	Sequence 1, Appl
35	56	100.0	220	3	US-09-485-885-8	Sequence 8, Appl
36	56	100.0	239	3	US-09-485-885-12	Sequence 12, Appl
37	56	100.0	253	2	US-08-459-818-20	Sequence 20, Appl
38	56	100.0	253	2	US-08-889-666-20	Sequence 20, Appl
39	56	100.0	253	2	US-08-465-078-20	Sequence 20, Appl
40	56	100.0	253	2	US-08-725-776-20	Sequence 20, Appl
41	56	100.0	253	2	US-08-488-062-20	Sequence 20, Appl
42	56	100.0	263	1	US-08-117-083-9	Sequence 9, Appl
43	56	100.0	266	3	US-08-860-165-10	Sequence 10, Appl
44	56	100.0	266	3	US-09-359-382-10	Sequence 10, Appl
45	56	100.0	266	4	US-09-367-309A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-10-365-908-16
; Sequence 16, Application US/10365908
; Patent No. 6797491
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-16

Query Match 100.0%; Score 56; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
|||
Db 1 CCKCDSTLR 9

RESULT 2
US-10-365-908-30
; Sequence 30, Application US/10365908
; Patent No. 6797491
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823

;; PRIOR FILING DATE: 2001-10-19
;; PRIOR APPLICATION NUMBER: US 60/214,202
;; PRIOR FILING DATE: 2000-06-26
;; NUMBER OF SEQ ID NOS: 140
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 30
;; LENGTH: 10
;; TYPE: PRT
;; ORGANISM: Human papilloma virus
US-10-365-908-30

Query Match 100.0%; Score 56; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
Db 1 CCKCDSTLR 9

RESULT 3
US-08-075-541D-38
; Sequence 38, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P. C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLASSIFICATION: 424

PRIOR APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991

ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
TELEFAX: 215-567-2991

INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-075-541D-38

Query Match 100.0%; Score 56; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
Db 5 CCKCDSTLR 13

RESULT 4
US-08-934-915-48
; Sequence 48, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEI-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MASON & ASSOCIATES, P. A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820

TELEX:
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-934-915-48

Query Match 100.0%; Score 56; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
Db 12 CCKCDSTLR 20

RESULT 5
US-09-980-177A-74
; Sequence 74, Application US/09980177A
; Patent No. 6838084
; GENERAL INFORMATION:
; APPLICANT: Jochmus, Ingrid
; APPLICANT: Nieland, John
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
; TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/036001

;; CURRENT APPLICATION NUMBER: US/09/980,177A
;; CURRENT FILING DATE: 2001-11-29
;; PRIOR APPLICATION NUMBER: PCT/EP00/05006
;; PRIOR FILING DATE: 2000-05-31
;; PRIOR APPLICATION NUMBER: DE 19925199.1
;; PRIOR FILING DATE: 1999-06-01
;; NUMBER OF SEQ ID NOS: 77
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 74
;; LENGTH: 20
;; TYPE: PRT
;; ORGANISM: Human papillomavirus type 16
US-09-980-177A-74

Query Match 100.0%; Score 56; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCKCDSTLR 9
Db 3 CCKCDSTLR 11
|||||

RESULT 6
US-08-075-541D-47
; Sequence 47, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-47

Query Match 100.0%; Score 56; DB 3; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCKCDSTLR 9
Db 9 CCKCDSTLR 17
|||||

RESULT 7
US-08-934-915-52
; Sequence 52, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-52

Query Match 100.0%; Score 56; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCKCDSTLR 9
Db 15 CCKCDSTLR 23
|||||

RESULT 8
US-08-934-915-53
; Sequence 53, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING

```
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-934-915-53
Query Match 100.0%; Score 56; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
Db 1 CCKCDSTLR 9

RESULT 9
US-09-486-394-3
; Sequence 3, Application US/09486394
; Patent No. 6478749
; GENERAL INFORMATION:
; APPLICANT: Hopfl, Reinhard
; TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method
; FILE REFERENCE: 032929-001
; CURRENT APPLICATION NUMBER: US/09/486,394
; CURRENT FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/04773
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: DE 197 37 409.3
; PRIOR FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(30)
; OTHER INFORMATION: E7 peptide.

US-09-486-394-3
Query Match 100.0%; Score 56; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
Db 18 CCKCDSTLR 26

RESULT 10
US-09-501-097A-6
; Sequence 6, Application US/09501097A
; Patent No. 6734173
; GENERAL INFORMATION:
; APPLICANT: Tzyy-Choo Wu
; APPLICANT: Chien-Fu Hung
; TITLE OF INVENTION: IMPROVED HSP DNA VACCINES
; FILE REFERENCE: 2240-169349
; CURRENT APPLICATION NUMBER: US/09/501,097A
; CURRENT FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 38
; TYPE: PRT
; ORGANISM: human papillomavirus
;
US-09-501-097A-6
Query Match 100.0%; Score 56; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
Db 29 CCKCDSTLR 37

RESULT 11
US-08-406-248-6
; Sequence 6, Application US/08406248
; Patent No. 5736318
; GENERAL INFORMATION:
; APPLICANT: Munger, Karl
; APPLICANT: Jones, D. Leanne
; TITLE OF INVENTION: METHOD AND KIT FOR EVALUATING
; TITLE OF INVENTION: TRANSFORMED CELLS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ann-Louise Kerner, Ph.D., Lappin & Kusmer
; STREET: 200 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,248
; FILING DATE:
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: McDaniel, Patricia A.
; REGISTRATION NUMBER: 33,194
; REFERENCE/DOCKET NUMBER: HAZ-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-330-1300
; TELEFAX: 617-330-1311
; INFORMATION FOR SEQ ID NO: 6:
```


; SEQUENCE CHARACTERISTICS:

; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-406-248-6

Query Match 100.0%; Score 56; DB 1; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
Db 58 CCKCDSTLR 66

RESULT 12

US-08-075-541D-42
; Sequence 42, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398

COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-42

Query Match 100.0%; Score 56; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
Db 58 CCKCDSTLR 66

RESULT 13

US-09-382-616A-1
; Sequence 1, Application US/09382616A
; Patent No. 6200746
; GENERAL INFORMATION:
; APPLICANT: Fisher, Christopher
; APPLICANT: He, Wanxia
; TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
; FILE REFERENCE: 28341/6216
; CURRENT APPLICATION NUMBER: US/09/382,616A
; CURRENT FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/382,616
; PRIOR FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Papillomavirus sylvilagi
US-09-382-616A-1

Query Match 100.0%; Score 56; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
Db 58 CCKCDSTLR 66

RESULT 14

US-08-944-368A-4
; Sequence 4, Application US/08944368A
; Patent No. 6228368
; GENERAL INFORMATION:
; APPLICANT: Gissman, et al.
; TITLE OF INVENTION: Papilloma Virus Capsomere Vaccine
; TITLE OF INVENTION: Formulations and Methods of Use
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSER: Borun
; STREET: 233 South Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,368A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27013/34028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-944-368A-4

Query Match 100.0%; Score 56; DB 3; Length 98;

Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
Db 58 CCKCDSTLR 66

RESULT 15

US-09-820-764-4
; Sequence 4, Application US/09820764
; Patent No. 6352696
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/820,764
; FILING DATE: 30-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,896
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercok, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-820-764-4

Query Match 100.0%; Score 56; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCKCDSTLR 9
Db 58 CCKCDSTLR 66

Search completed: June 29, 2005, 01:44:20
Job time : 16.9126 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:24:19 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-60
Perfect score: 55
Sequence: 1 YNIVTFCK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	65	2 Q8B563	Q8B563 human papil.
2	55	100.0	77	2 Q8B5P5	Q8B5P5 human papil
3	55	100.0	93	2 Q9QDH2	Q9QDH2 human papil
4	55	100.0	93	2 Q9QDH4	Q9QDH4 human papil
5	55	100.0	93	2 Q9QDH6	Q9QDH6 human papil
6	55	100.0	93	2 Q9QDH8	Q9QDH8 human papil
7	55	100.0	94	2 Q8B5P6	Q8B5P6 human papil
8	55	100.0	98	1 VE7_HPV16	P03129 human papil
9	55	100.0	98	2 O11650	O11650 human papil
10	55	100.0	98	2 O12337	O12337 human papil
11	55	100.0	98	2 O12338	O12338 human papil
12	55	100.0	98	2 Q8QRD2	Q8QRD2 human papil
13	55	100.0	98	2 Q8QRD3	Q8QRD3 human papil
14	55	100.0	98	2 Q8QRD4	Q8QRD4 human papil
15	55	100.0	98	2 Q8V1J0	Q8V1J0 human papil
16	55	100.0	98	2 Q778H3	Q778H3 human papil
17	55	100.0	98	2 Q778H5	Q778H5 human papil
18	51	92.7	98	1 VE7_HPV31	P17387 human papil
19	51	92.7	98	2 Q6T377	Q6T377 human papil
20	47	85.5	99	1 VE7_HPV35	P27230 human papil
21	47	85.5	99	2 Q76WP2	Q76WP2 human papil
22	44	80.0	259	2 Q38410	Q38410 bacterioph
23	44	80.0	284	2 Q711TC6	Q711TC6 bacterioph
24	43	78.2	286	2 Q6QGM1	Q6QGM1 sus scrofa
25	43	78.2	292	2 Q6XGY1	Q6XGY1 homo sapien
26	43	78.2	377	2 Q6QGW2	Q6QGW2 sus scrofa
27	43	78.2	379	1 GRR2_CERA	Q95mh6 cercopithe
28	43	78.2	379	1 GRR2_HUMAN	Q96P88 homo sapien
29	43	78.2	380	1 GRR2_CALJA	Q95mg6 callithrix
30	43	78.2	1061	2 Q7S8B5	Q7S8B5 neurospora
31	42	76.4	230	2 Q6F419	Q6F419 oreochromis

32	42	76.4	269	2 Q90VX6	Q90VX6 rana catesb
33	42	76.4	421	2 Q6U104	Q6U104 oreochromis
34	42	76.4	424	2 Q7ZZP0	Q7ZZP0 rana ridibu
35	42	76.4	424	2 Q800V9	Q800V9 rana dybows
36	42	76.4	424	2 Q9DE63	Q9DE63 rana catesb
37	41	74.5	124	2 Q8R155	Q8R155 mus musculu
38	41	74.5	345	2 Q8DYH3	Q8DYH3 streptococc
39	40	72.7	92	1 VE7_HPV27	P36825 human papil
40	40	72.7	92	1 VE7_HPV2A	P25485 human papil
41	40	72.7	92	1 VE7_HPV57	P22160 human papil
42	39	70.9	505	2 Q81HW9	Q81HW9 plasmodium
43	39	70.9	775	2 Q7QTC1	Q7QTC1 giardia lam
44	38	69.1	47	2 Q7S3B5	Q7S3B5 neurospora
45	38	69.1	111	1 LY6G_MOUSE	P35461 mus musculu

ALIGNMENTS

RESULT 1
Q8B563 PRELIMINARY; PRT; 65 AA.
AC Q8B563;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DE E7 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF548023; AAO16240.1; -.
DR InterPro: IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON_TER 65
SQ SEQUENCE 65 AA; 7373 MW; E9D74D7923700195 CRC64;

Query Match 100.0%; Score 55; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNIVTFCK 9
Db 52 YNIVTFCK 60

RESULT 2
Q8B5P5 PRELIMINARY; PRT; 77 AA.
AC Q8B5P5;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF46198; AAO15694.1; -.
DR InterPro: IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON_TER 77
SQ SEQUENCE 77 AA; 8782 MW; CSDE3A7E546AC31B CRC64;
Query Match 100.0%; Score 55; DB 2; Length 77;

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Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNIVTFCK 9
Db 52 YNIVTFCK 60

RESULT 3
Q9QDH2
ID Q9QDH2 PRELIMINARY; PRT; 93 AA.
AC Q9QDH2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE E7 protein (Fragment)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187869; AAF13399.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 55; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNIVTFCK 9
Db 52 YNIVTFCK 60

RESULT 4
Q9QDH4
ID Q9QDH4 PRELIMINARY; PRT; 93 AA.
AC Q9QDH4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE E7 protein (Fragment)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187868; AAF13397.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 55; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNIVTFCK 9
Db 52 YNIVTFCK 60

RESULT 5
Q9QDH6
ID Q9QDH6 PRELIMINARY; PRT; 93 AA.
AC Q9QDH6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE E7 protein (Fragment)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187867; AAF13395.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10513 MW; 92C7054341326A1F CRC64;

Query Match 100.0%; Score 55; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNIVTFCK 9
Db 52 YNIVTFCK 60

RESULT 6
Q9QDH8
ID Q9QDH8 PRELIMINARY; PRT; 93 AA.
AC Q9QDH8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE E7 protein (Fragment)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187866; AAF13393.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 55; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNIVTFCK 9
Db 52 YNIVTFCK 60

RESULT 7
Q8B5P6
ID Q8B5P6 PRELIMINARY; PRT; 94 AA.
AC Q8B5P6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE E7 oncoprotein (Fragment)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.

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RA Ponglikitmongkol M., Vaeteewoottacharn K.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF469197; AA015692.1; -;
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 FT NON TER 94
 SQ SEQUENCE 94 AA; 10555 MW; 7CC3281B2AE2C8A CRC64;

Query Match 100.0%; Score 55; DB 2; Length 94;
 Best Local Similarity 100.0%; Pred. No. 0.055;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNIVTFCK 9
 |||||
 Db 52 YNIVTFCK 60

RESULT 8
 ID_VET_HPV16 STANDARD; PRT; 98 AA.
 AC P03129;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE E7 protein.
 GN Name=E7;
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85246220; PubMed=2990099;
 RA Seedorf K., Kramer G., Durst M., Suhai S., Rowekamp W.G.;
 RT "Human papillomavirus type 16 DNA sequence.";
 RL Virology 145:181-195(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90218027; PubMed=2157796;
 RA Schneider-Maunoury S., Pehau-Arnaut G., Breitburd P., Orth G.;
 RT "Expression of the human papillomavirus type 16 genome in SK-v cells,
 a line derived from a vulvar intraepithelial neoplasia.";
 RL J. Gen. Virol. 71:809-817(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Lee H.P.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
 RA Beth-Giraldo E., Giraldo G.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP FUNCTION.
 RX MEDLINE=88223347; PubMed=2836062;
 RA Phelps W.C., Yee C.L., Munger K., Howley P.M.;
 RT "The human papillomavirus type 16 E7 gene encodes transactivation and
 transformation functions similar to those of adenovirus E1A.";
 RL Cell 53:539-547(1988).
 CC -1- FUNCTION: E7 protein has both transforming and trans-activating
 CC activities.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; K02718; AAA46940.1; -;
 DR EMBL; D00735; BAA00633.1; -;
 DR EMBL; U76411; AAB18962.1; -;

DR EMBL; U76412; AAB18963.1; -;
 DR EMBL; U76413; AAB18964.1; -;
 DR EMBL; AF003020; AAB70737.1; -;
 DR EMBL; AF003023; AAB70740.1; -;
 DR EMBL; AF003024; AAB70741.1; -;
 DR EMBL; AF003025; AAB70742.1; -;
 DR EMBL; AF003026; AAB70743.1; -;
 DR PIR; A03688; W7WLHS.
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 KW DNA-binding; Early protein; Oncogene; Trans-acting factor;
 KW Transcription regulation.
 FT SITE 58 61 C-XX-C motif-1.
 FT SITE 91 94 C-XX-C motif-2.
 SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9B8 CRC64;

Query Match 100.0%; Score 55; DB 1; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.057;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNIVTFCK 9
 |||||
 Db 52 YNIVTFCK 60

RESULT 9
 ID_O11650 PRELIMINARY; PRT; 98 AA.
 AC O11650;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Putative transforming protein E7.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97407827; PubMed=9264576; DOI=10.1006/gyno.1997.4756;
 RA Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Chang W.H.,
 RA Lee H.P.;
 RT "Major sequence variants in E7 gene of human papillomavirus type 16
 from cervical cancerous and noncancerous lesions of Korean women.";
 RL Gynecol. Oncol. 66:275-281(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Song Y.-S., Kee S.-H., Kim J.-W., Park N.-H., Kang S.-B., Chang W.-H.,
 RA Lee H.-P.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Terai M., Ma Z., Burk R.D.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22182962; PubMed=12195358;
 RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
 RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
 RT "Human papillomavirus type 16 intratypic variant infection and risk
 for cervical neoplasia in southern China.";
 RL J. Infect. Dis. 186:696-700(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Terai M., Fu L., Ma Z., Burk R.D.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U76404; AAC58243.1; -;
 DR EMBL; AF472509; AAO15706.1; -;
 DR EMBL; AF486326; AAL96631.1; -;
 DR EMBL; AF486327; AAL96632.1; -;
 DR EMBL; AF486330; AAL96635.1; -;
 DR EMBL; AF486331; AAL96636.1; -;
 DR EMBL; AF486332; AAL96637.1; -;

DR EMBL; AF486333; AAL96638.1; -;
 DR EMBL; AF486334; AAL96639.1; -;
 DR EMBL; AF486336; AAL96641.1; -;
 DR EMBL; AF486338; AAL96643.1; -;
 DR EMBL; AF486346; AAL96651.1; -;
 DR EMBL; AF486350; AAL96655.1; -;
 DR EMBL; AF486351; AAL96656.1; -;
 DR EMBL; AF534061; AAL0404.1; -;
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 100.0%; Score 55; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.057;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNIVTFCK 9
 |||||
 Db 52 YNIVTFCK 60

RESULT 10

Q8QRD3
 ID O12337 PRELIMINARY; PRT; 98 AA.

DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE E7 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97437474; PubMed=9292007;
 RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
 RA Beth-Giraldo E., Giraldo G.;
 RT "Sequence variations and viral genomic state of human papillomavirus
 type 16 in penile carcinomas from Ugandan patients.";
 RL J. Gen. Virol. 78:2199-2208(1997).
 DR EMBL; AF003021; AAB70738.1; -;
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 SQ SEQUENCE 98 AA; 11056 MW; 19DEB8F14CD2C705 CRC64;

Query Match 100.0%; Score 55; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.057;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNIVTFCK 9
 |||||
 Db 52 YNIVTFCK 60

RESULT 11

Q12338
 ID O12338 PRELIMINARY; PRT; 98 AA.

AC O12338;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE E7 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97437474; PubMed=9292007;
 RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
 RA Beth-Giraldo E., Giraldo G.;
 RT "Sequence variations and viral genomic state of human papillomavirus

RT type 16 in penile carcinomas from Ugandan patients.";
 RL J. Gen. Virol. 78:2199-2208(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Jinhu X., Xinling W., Yun T.;
 RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF003022; AAB70739.1; -;
 DR EMBL; AF477385; AAM03025.1; -;
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 SQ SEQUENCE 98 AA; 10969 MW; 9BD612534CCEA59B CRC64;

Query Match 100.0%; Score 55; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.057;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNIVTFCK 9
 |||||
 Db 52 YNIVTFCK 60

RESULT 12

Q8QRD2
 ID Q8QRD2 PRELIMINARY; PRT; 98 AA.

AC Q8QRD2;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE E7 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22182962; PubMed=12195358;
 RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
 RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
 RT "Human papillomavirus type 16 intratypic variant infection and risk
 for cervical neoplasia in southern China.";
 RL J. Infect. Dis. 186:696-700(2002).
 DR EMBL; AF486345; AAL96650.1; -;
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 SQ SEQUENCE 98 AA; 11045 MW; 9C4F8C534CD76C4B CRC64;

Query Match 100.0%; Score 55; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.057;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNIVTFCK 9
 |||||
 Db 52 YNIVTFCK 60

RESULT 13

Q8QRD3
 ID Q8QRD3 PRELIMINARY; PRT; 98 AA.

AC Q8QRD3;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE E7 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22182962; PubMed=12195358;
 RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
 RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
 RT "Human papillomavirus type 16 intratypic variant infection and risk

RT for cervical neoplasia in southern China.";

RL J. Infect. Dis. 186:696-700(2002).

DR EMBL; AF486344; AAL96649.1; -

DR InterPro; IPR000148; Papvi_E7.

DR Pfam; PF00527; E7; 1.

SQ SEQUENCE 98 AA; 11021 MW; 9BD6125946D2C3E1 CRC64;

Query Match 100.0%; Score 55; DB 2; Length 98;

Best Local Similarity 100.0%; Pred. No. 0.057;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNIVTFCK 9

Db |||||

52 YNIVTFCK 60

RESULT 14

Q8QRD4

ID Q8QRD4 PRELIMINARY; PRT; 98 AA.

AC Q8QRD4;

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE E7 protein.

OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI_TaxID=10581;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22182962; PubMed=12195358;

RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,

Cheung J.L.K., Xu L.Y., Cheng A.F.;

RT "Human papillomavirus type 16 intratypic variant infection and risk

for cervical neoplasia in southern China.";

RL J. Infect. Dis. 186:696-700(2002).

DR EMBL; AF486329; AAL96634.1; -

DR InterPro; IPR000148; Papvi_E7.

DR Pfam; PF00527; E7; 1.

SQ SEQUENCE 98 AA; 11025 MW; 86E24B234CC3281B CRC64;

Query Match

Best Local Similarity 100.0%; Score 55; DB 2; Length 98;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YNIVTFCK 9

Db |||||

52 YNIVTFCK 60

RESULT 15

Q8VLJ0

ID Q8VLJ0 PRELIMINARY; PRT; 98 AA.

AC Q8VLJ0;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE E7 protein.

OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI_TaxID=10581;

RN [1]

RP SEQUENCE FROM N.A.

RA Jinhu X., Xinxiang W., Yun T.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF461264; AAL66736.1; -

DR Pfam; PF00527; E7; 1.

SQ SEQUENCE 98 AA; 10997 MW; 9BD610834CCEA59B CRC64;

Query Match

Best Local Similarity 100.0%; Score 55; DB 2; Length 98;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: June 29, 2005, 04:19:44 ; Search time 116.15 Seconds
(without alignments)
29.797 Million cell updates/sec

Title: US-08-170-344-60

Perfect score: 55

Sequence: 1 YNIVTFCK 9

Scoring table: BLASTSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA.*

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2: /cgn2_6/ptodata/1/pubpaa/ECT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	55	100.0	15	16	US-10-306-541-62
5	55	100.0	15	16	US-10-306-541-63
6	55	100.0	15	16	US-10-306-541-64
7	55	100.0	17	17	US-10-858-384-16
8	55	100.0	19	16	US-10-654-200-56
9	55	100.0	19	17	US-10-484-063-14
10	55	100.0	20	15	US-10-432-465-48
11	55	100.0	20	16	US-10-654-200-57

12	55	100.0	20	16	US-10-890-526-73	Sequence 73, Appl
13	55	100.0	21	16	US-10-306-541-107	Sequence 107, Appl
14	55	100.0	98	9	US-09-728-466-1	Sequence 1, Appl
15	55	100.0	98	9	US-09-820-765-4	Sequence 4, Appl
16	55	100.0	98	9	US-09-824-017-4	Sequence 4, Appl
17	55	100.0	98	10	US-09-986-118A-4	Sequence 4, Appl
18	55	100.0	98	14	US-10-267-311-8	Sequence 8, Appl
19	55	100.0	98	14	US-10-177-390-8	Sequence 8, Appl
20	55	100.0	98	14	US-10-201-764-19	Sequence 19, Appl
21	55	100.0	98	15	US-10-392-113-29	Sequence 29, Appl
22	55	100.0	98	15	US-10-654-129-4	Sequence 4, Appl
23	55	100.0	98	15	US-10-681-410-19	Sequence 19, Appl
24	55	100.0	98	16	US-10-772-988-3	Sequence 3, Appl
25	55	100.0	98	16	US-10-479-541-5	Sequence 5, Appl
26	55	100.0	98	17	US-10-042-526A-4	Sequence 4, Appl
27	55	100.0	98	17	US-10-657-399-1	Sequence 1, Appl
28	55	100.0	98	17	US-10-858-384-12	Sequence 12, Appl
29	55	100.0	98	17	US-10-484-063-26	Sequence 26, Appl
30	55	100.0	98	17	US-10-343-448-5	Sequence 5, Appl
31	55	100.0	98	17	US-10-679-956-8	Sequence 8, Appl
32	55	100.0	98	17	US-10-367-057-17	Sequence 17, Appl
33	55	100.0	99	15	US-10-115-440-7	Sequence 7, Appl
34	55	100.0	111	16	US-10-472-724-4	Sequence 4, Appl
35	55	100.0	121	14	US-10-267-311-12	Sequence 12, Appl
36	55	100.0	121	17	US-10-679-956-12	Sequence 12, Appl
37	55	100.0	198	14	US-10-267-311-35	Sequence 35, Appl
38	55	100.0	198	17	US-10-679-956-35	Sequence 35, Appl
39	55	100.0	220	13	US-10-000-903-1	Sequence 1, Appl
40	55	100.0	220	13	US-10-000-903-8	Sequence 8, Appl
41	55	100.0	220	17	US-10-899-771-1	Sequence 1, Appl
42	55	100.0	220	17	US-10-899-771-8	Sequence 8, Appl
43	55	100.0	239	13	US-10-000-903-12	Sequence 12, Appl
44	55	100.0	239	17	US-10-899-771-12	Sequence 12, Appl
45	55	100.0	266	9	US-09-367-309A-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-10-306-541-54
; Sequence 54, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 54
; LENGTH: 9
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-54

Query Match 100.0%; Score 55; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YNIVTFCK 9
Db 1 YNIVTFCK 9

RESULT 2
US-10-306-541-108
; Sequence 108, Application US/10306541
; Publication No. US20040171081A1

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; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 108
; LENGTH: 10
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-108

Query Match      100.0%; Score 55; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YNIVTFCK 9
Db      1 YNIVTFCK 9

RESULT 3
US-10-306-541-61
; Sequence 61, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 61
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-61

Query Match      100.0%; Score 55; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YNIVTFCK 9
Db      4 YNIVTFCK 12

RESULT 4
US-10-306-541-62
; Sequence 62, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 62
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-62

Query Match      100.0%; Score 55; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YNIVTFCK 9
Db      7 YNIVTFCK 15

RESULT 5
US-10-306-541-63
; Sequence 63, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 63
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-63

Query Match      100.0%; Score 55; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YNIVTFCK 9
Db      5 YNIVTFCK 13

RESULT 6
US-10-306-541-64
; Sequence 64, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 64
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-64

Query Match      100.0%; Score 55; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 YNIVTFCK 9
Db      7 YNIVTFCK 15
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RESULT 7
US-10-858-384-16
; Sequence 16, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 16
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
; OTHER INFORMATION: for E7 of HPV
US-10-858-384-16

Query Match      100.0%; Score 55; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YNIVTFCK 9
Db      9 YNIVTFCK 17

RESULT 8
US-10-654-200-56
; Sequence 56, Application US/10654200
; Publication No. US20040170606A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology Corporation
; TITLE OF INVENTION: PRODUCTION OF PEPTIDES IN PLANTS AS VIRAL COAT PROTEIN FUSIONS
; FILE REFERENCE: N9739
; CURRENT APPLICATION NUMBER: US/10/654,200
; CURRENT FILING DATE: 2003-09-03
; PRIOR APPLICATION NUMBER: 60/407,795
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: 60/386,921
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 10/457,082
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Human Papilloma Virus
US-10-654-200-56

Query Match      100.0%; Score 55; DB 16; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YNIVTFCK 9
Db      9 YNIVTFCK 17

RESULT 9
US-10-484-063-14
; Sequence 14, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-14

Query Match      100.0%; Score 55; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YNIVTFCK 9
Db      9 YNIVTFCK 17

RESULT 10
US-10-432-465-48
; Sequence 48, Application US/10432465
; Publication No. US20040091479A1
; GENERAL INFORMATION:
; APPLICANT: Kaufmann, John
; APPLICANT: Kaufmann, Andreas
; APPLICANT: Schinz, Manuela
; TITLE OF INVENTION: T-Cell Epitopes of the Papillomavirus L1
; TITLE OF INVENTION: Protein and E7 Protein and Their Use in Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/077001
; CURRENT APPLICATION NUMBER: US/10/432,465
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: PCT/EP01/14037
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: DE 10059631.2
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-432-465-48

Query Match      100.0%; Score 55; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YNIVTFCK 9
Db      8 YNIVTFCK 16

RESULT 11
US-10-654-200-57
; Sequence 57, Application US/10654200
; Publication No. US20040170606A1
; GENERAL INFORMATION:
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; APPLICANT: Large Scale Biology Corporation
; TITLE OF INVENTION: PRODUCTION OF PEPTIDES IN PLANTS AS VIRAL COAT PROTEIN FUSIONS
; FILE REFERENCE: N9739
; CURRENT APPLICATION NUMBER: US/10/654,200
; PRIOR FILING DATE: 2003-09-03
; CURRENT FILING DATE: 2003-09-03
; PRIOR APPLICATION NUMBER: 60/407,795
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: 60/386,921
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 10/457,082
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human Papilloma Virus
US-10-654-200-57

Query Match      100.0%; Score 55; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YNIVTFCK 9
Db      10 YNIVTFCK 18

RESULT 12
US-10-890-526-73
; Sequence 73, Application US/10890526
; Publication No. US20040258708A1
; GENERAL INFORMATION:
; APPLICANT: Jochmus, Ingrid
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
; TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 50125/036001
; CURRENT APPLICATION NUMBER: US/10/890,526
; CURRENT FILING DATE: 2004-07-13
; PRIOR APPLICATION NUMBER: US/09/980,177
; PRIOR FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: PCT/EP00/05006
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: DE 19925199.1
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-890-526-73

Query Match      100.0%; Score 55; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YNIVTFCK 9
Db      8 YNIVTFCK 16

RESULT 13
US-10-306-541-107
; Sequence 107, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
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; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 107
; LENGTH: 21
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-107

Query Match      100.0%; Score 55; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YNIVTFCK 9
Db      8 YNIVTFCK 16

RESULT 14
US-09-728-466-1
; Sequence 1, Application US/09728466
; Patent No. US20010029022A1
; GENERAL INFORMATION:
; APPLICANT: Fisher, Christopher
; APPLICANT: He, Wanxia
; TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
; FILE REFERENCE: 28341/6216
; CURRENT APPLICATION NUMBER: US/09/728,466
; CURRENT FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: 09/382,616
; PRIOR FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Papillomavirus sylvilagi
US-09-728-466-1

Query Match      100.0%; Score 55; DB 9; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YNIVTFCK 9
Db      52 YNIVTFCK 60

RESULT 15
US-09-820-765-4
; Sequence 4, Application US/09820765
; Publication No. US20020039584A1
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; APPLICANT: HALLEK, Michael
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/820,765
; FILING DATE: 30-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,896
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-820-765-4

Query Match 100.0%; Score 55; DB 9; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNIVTFCK 9
Db 52 YNIVTFCK 60

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Job time : 116.15 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:33:36 ; Search time 17.05 Seconds
(without alignments)
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Title: US-08-170-344-60

Perfect score: 55

Sequence: 1 YNIVFCK 9

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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7	55	100.0	18	3	US-08-075-541D-30
8	55	100.0	19	3	US-08-075-541D-3
9	55	100.0	20	2	US-08-934-915-48
10	55	100.0	20	2	US-08-934-915-155
11	55	100.0	20	3	US-08-075-541D-10
12	55	100.0	20	4	US-09-980-177A-73
13	55	100.0	25	3	US-08-075-541D-47
14	55	100.0	26	3	US-08-075-541D-20
15	55	100.0	30	2	US-08-934-915-52
16	55	100.0	30	4	US-09-486-394-3
17	55	100.0	32	3	US-08-075-541D-7
18	55	100.0	32	4	US-08-075-541D-8
19	55	100.0	38	4	US-09-501-097A-6
20	55	100.0	98	1	US-08-406-248-6
21	55	100.0	98	3	US-08-075-541D-42
22	55	100.0	98	3	US-09-382-616A-1
23	55	100.0	98	3	US-08-944-368A-4
24	55	100.0	98	3	US-09-820-764-4
25	55	100.0	98	4	US-09-613-303-8
26	55	100.0	98	4	US-09-566-420-19
27	55	100.0	98	4	US-09-986-118A-4

28 55 100.0 98 4 US-09-728-466-1 Sequence 1, Appli
29 55 100.0 98 4 US-09-824-017-4 Sequence 4, Appli
30 55 100.0 98 4 US-10-267-311-8 Sequence 8, Appli
31 55 100.0 98 4 US-10-201-764-19 Sequence 19, Appli
32 55 100.0 98 4 US-09-637-746-3 Sequence 3, Appli
33 55 100.0 98 4 US-09-501-097A-7 Sequence 7, Appli
34 55 100.0 98 4 US-09-980-523A-12 Sequence 12, Appli
35 55 100.0 121 4 US-09-613-303-12 Sequence 12, Appli
36 55 100.0 121 4 US-10-267-311-12 Sequence 12, Appli
37 55 100.0 172 3 US-08-860-165-12 Sequence 12, Appli
38 55 100.0 172 3 US-08-860-165-14 Sequence 14, Appli
39 55 100.0 172 3 US-09-359-382-12 Sequence 12, Appli
40 55 100.0 172 3 US-09-359-382-14 Sequence 14, Appli
41 55 100.0 198 4 US-09-613-303-35 Sequence 35, Appli
42 55 100.0 198 4 US-10-267-311-35 Sequence 35, Appli
43 55 100.0 220 3 US-09-485-885-1 Sequence 1, Appli
44 55 100.0 220 3 US-09-485-885-8 Sequence 8, Appli
45 55 100.0 239 3 US-09-485-885-12 Sequence 12, Appli

ALIGNMENTS

RESULT 1

US-08-075-541D-27
; Sequence 27, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU Pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-27

Query Match

100.0%; Score 55; DB 3; Length 12;


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;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/075,541D
;/ FILING DATE: 10-JUN-1993
;/ CLASSIFICATION: 424
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: AU pk 3876
;/ FILING DATE: 12-DEC-1990
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: pct/au91/00575
;/ FILING DATE: 12-DEC-1991
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: NADEL, ALAN S
;/ REGISTRATION NUMBER: 27,363
;/ REFERENCE/DOCKET NUMBER: 8795-4
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 215-567-2020
;/ TELEFAX: 215-567-2991
;/ INFORMATION FOR SEQ ID NO: 18:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 15 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ US-08-075-541D-18

Query Match 100.0%; Score 55; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNIVTFCK 9
Db 5 YNIVTFCK 13

RESULT 5
US-08-075-541D-25
; Sequence 25, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
```

```
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 215-567-2020
;/ TELEFAX: 215-567-2991
;/ INFORMATION FOR SEQ ID NO: 25:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 17 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ US-08-075-541D-25

Query Match 100.0%; Score 55; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNIVTFCK 9
Db 9 YNIVTFCK 17

RESULT 6
US-09-980-523A-16
; Sequence 16, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO/01/00100
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Human Papillomavirus
; US-09-980-523A-16

Query Match 100.0%; Score 55; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNIVTFCK 9
Db 9 YNIVTFCK 17

RESULT 7
US-08-075-541D-30
; Sequence 30, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
```

STATE: PENNSYLVANIA
COUNTRY: USA
ZIP: 19103-2398
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-075-541D-30

Query Match 100.0%; Score 55; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNIVTFCK 9
Db 8 YNIVTFCK 16

RESULT 8
US-08-075-541D-3
Sequence 3, Application US/08075541D
Patent No. 6183745
GENERAL INFORMATION:
APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERMAIN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
CITY: PHILADELPHIA
STATE: PENNSYLVANIA
COUNTRY: USA
ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-075-541D-3

Query Match 100.0%; Score 55; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNIVTFCK 9
Db 9 YNIVTFCK 17

RESULT 9
US-08-934-915-48
Sequence 48, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: CHENG, HWEI-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-08-934-915-48

Query Match 100.0%; Score 55; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNIVTFCK 9
Db 6 YNIVTFCK 14

RESULT 10

US-08-934-915-155
Sequence 155, Application US/08934915
Patent No. 5932412

GENERAL INFORMATION:

APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
STATE: FLORIDA
COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: LOUISE A. FOUTCH
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
TELEX:

INFORMATION FOR SEQ ID NO: 155:

SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-934-915-155

Query Match 100.0%; Score 55; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNIVTFCK 9
Db 6 YNIVTFCK 14

RESULT 11

US-08-075-541D-10
Sequence 10, Application US/08075541D
Patent No. 6183745

GENERAL INFORMATION:

APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERMAIN
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
CITY: PHILADELPHIA
STATE: PENNSYLVANIA
COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/au91/00575
FILING DATE: 12-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
TELEFAX: 215-567-2991

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-075-541D-10

Query Match 100.0%; Score 55; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNIVTFCK 9
Db 10 YNIVTFCK 18

RESULT 12

US-09-980-177A-73
Sequence 73, Application US/09980177A
Patent No. 6838084

GENERAL INFORMATION:

APPLICANT: Jochmus, Ingrid
APPLICANT: Nieland, John
TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and
TITLE OF INVENTION: Therapy
FILE REFERENCE: 50125/036001
CURRENT APPLICATION NUMBER: US/09/980,177A
CURRENT FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: PCT/EP00/05006
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: DE 19925199.1
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 77
SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 73
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-980-177A-73

Query Match 100.0%; Score 55; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.018; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNIVTFCK 9
| | | | | | | | | |
DB 8 YNIVTFCK 16

RESULT 13
US-08-075-541D-47
; Sequence 47, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-47

Query Match 100.0%; Score 55; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.022; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNIVTFCK 9
| | | | | | | | | |
DB 3 YNIVTFCK 11

RESULT 14
US-08-075-541D-20
; Sequence 20, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-20

Query Match 100.0%; Score 55; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.022; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YNIVTFCK 9
| | | | | | | | | |
DB 16 YNIVTFCK 24

RESULT 15
US-08-934-915-52
; Sequence 52, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
US-08-934-915-52

```

; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-934-915-52

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Query Match      100.0%; Score 55; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.025; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

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QY      1 YNIVTFCK 9
      |||||
Db      9 YNIVTFCK 17

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Search completed: June 28, 2005, 23:37:55
Job time : 18.05 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 17:44:26 ; Search time 55.3 Seconds
(without alignments)
83.340 Million cell updates/sec

Title: US-08-170-344-6
Perfect score: 45
Sequence: 1 LQTTIHDI 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	26	Q81956	Q81956 human papil
2	45	100.0	138	Q919D2	Q919D2 human papil
3	45	100.0	143	Q919B6	Q919B6 human papil
4	45	100.0	143	Q919C4	Q919C4 human papil
5	45	100.0	151	Q12335	Q12335 human papil
6	45	100.0	151	Q12336	Q12336 human papil
7	45	100.0	151	Q76TS0	Q76TS0 human papil
8	45	100.0	151	Q778I6	Q778I6 human papil
9	45	100.0	151	Q778I6	Q778I6 human papil
10	45	100.0	151	Q773C7	Q773C7 human papil
11	45	100.0	151	Q772J5	Q772J5 human papil
12	45	100.0	151	Q80963	Q80963 human papil
13	45	100.0	151	Q80966	Q80966 human papil
14	45	100.0	151	Q89648	Q89648 human papil
15	45	100.0	151	Q89708	Q89708 human papil
16	45	100.0	151	Q89755	Q89755 human papil
17	45	100.0	151	Q89852	Q89852 human papil
18	45	100.0	151	Q89887	Q89887 human papil
19	45	100.0	151	Q88B20	Q88B20 human papil
20	45	100.0	151	Q9W8C3	Q9W8C3 human papil
21	45	100.0	151	Q9W931	Q9W931 human papil
22	45	100.0	151	Q9WNP2	Q9WNP2 human papil
23	45	100.0	151	Q9WNP4	Q9WNP4 human papil
24	45	100.0	158	1 VE6 HPV16	P03126 human papil
25	45	100.0	158	Q8JMU8	Q8JMU8 human papil
26	45	100.0	158	Q8QMU0	Q8QMU0 human papil
27	45	100.0	158	Q8QHP5	Q8QHP5 human papil
28	45	100.0	158	Q8QRD5	Q8QRD5 human papil
29	45	100.0	158	Q8QRD6	Q8QRD6 human papil
30	45	100.0	158	Q8QRD7	Q8QRD7 human papil
31	45	100.0	158	Q8QRD8	Q8QRD8 human papil

32 45 100.0 158 2 Q71B17 Q71B17 human papil
33 45 100.0 158 2 Q9WH13 Q9WH13 human papil
34 45 100.0 161 2 Q919C6 Q919C6 human papil
35 43 95.6 151 2 Q9WNP5 Q9WNP5 human papil
36 41 91.1 151 2 Q89640 Q89640 human papil
37 41 91.1 151 2 Q8BB21 Q8BB21 human papil
38 41 91.1 151 2 Q9WNP3 Q9WNP3 human papil
39 41 91.1 158 2 Q8QHT0 Q8QHT0 human papil
40 41 91.1 158 2 Q8QRD9 Q8QRD9 human papil
41 41 91.1 158 2 Q8QRE0 Q8QRE0 human papil
42 41 91.1 158 2 Q8QRE1 Q8QRE1 human papil
43 41 91.1 158 2 Q9QDH3 Q9QDH3 human papil
44 41 91.1 158 2 Q9QDH9 Q9QDH9 human papil
45 41 91.1 161 2 Q919A9 Q919A9 human papil

ALIGNMENTS

RESULT 1
Q81956 PRELIMINARY; PRT; 26 AA.
AC Q81956;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DE E6E7 (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SIHA;
RA Shippy R., Siwkowski A., Hampel A.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U59900; AAB03505.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 26 AA; 3208 MW; F06EBBE995EB67D5 CRC64;

Query Match 100.0%; Score 45; DB 2; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.059; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 LQTTIHDI 9
Db |||||
2 LQTTIHDI 10

RESULT 2
Q919D2 PRELIMINARY; PRT; 138 AA.
ID Q919D2;
AC Q919D2;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404694; AAL01345.1; -.

DR GO: 0042025; C:host cell nucleus; IEA.
 DR GO: 0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON_TER 1
 SQ SEQUENCE 138 AA; 16696 MW; 48185A9A90895FC2 CRC64;
 Query Match 100.0%; Score 45; DB 2; Length 138;
 Best Local Similarity 100.0%; Pred. No. 0.35; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;
 QY 1 LQTTIHDII 9
 Db 6 LQTTIHDII 14
 RESULT 3
 Q919B6 PRELIMINARY; PRT; 143 AA.
 AC Q919B6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404702; AAL01361.1; --
 DR GO: 0042025; C:host cell nucleus; IEA.
 DR GO: 0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON_TER 1
 SQ SEQUENCE 143 AA; 17272 MW; 071F14BE3EG6BE2AC CRC64;
 Query Match 100.0%; Score 45; DB 2; Length 143;
 Best Local Similarity 100.0%; Pred. No. 0.36; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;
 QY 1 LQTTIHDII 9
 Db 11 LQTTIHDII 19
 RESULT 4
 Q919C4 PRELIMINARY; PRT; 143 AA.
 AC Q919C4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404698; AAL01353.1; --
 DR GO: 0042025; C:host cell nucleus; IEA.
 DR GO: 0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.

FT NON_TER 1
 SQ SEQUENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;
 Query Match 100.0%; Score 45; DB 2; Length 143;
 Best Local Similarity 100.0%; Pred. No. 0.36; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;
 QY 1 LQTTIHDII 9
 Db 11 LQTTIHDII 19
 RESULT 5
 O12335 PRELIMINARY; PRT; 151 AA.
 AC O12335;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97437474; PubMed=9292007;
 RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
 RA Beth-Giraldo E., Giraldo G.;
 RT "Sequence variations and viral genomic state of human papillomavirus type 16 in penile carcinomas from Ugandan patients.";
 RL J. Gen. Virol. 78:2199-2208(1997).
 DR EMBL; AF003015; AAB70732.1; --
 DR GO: 0042025; C:host cell nucleus; IEA.
 DR GO: 0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18238 MW; BEF32A8B016CC88B CRC64;
 Query Match 100.0%; Score 45; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.38; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;
 QY 1 LQTTIHDII 9
 Db 19 LQTTIHDII 27
 RESULT 6
 O12336 PRELIMINARY; PRT; 151 AA.
 AC O12336;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE E6 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97437474; PubMed=9292007;
 RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
 RA Beth-Giraldo E., Giraldo G.;
 RT "Sequence variations and viral genomic state of human papillomavirus type 16 in penile carcinomas from Ugandan patients.";
 RL J. Gen. Virol. 78:2199-2208(1997).
 DR EMBL; AF003016; AAB70733.1; --
 DR GO: 0042025; C:host cell nucleus; IEA.
 DR GO: 0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR Pfam; PF00518; E6; 1.


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SQ SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;
Query Match 100.0%; Score 45; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDII 9
Db 19 LQTTIHDII 27

RESULT 7
Q76TS0 PRELIMINARY; PRT; 151 AA.
AC Q76TS0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RA Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34114; AAA91661.1; -
DR EMBL; U34125; AAA91672.1; -
DR EMBL; U34130; AAA91677.1; -
DR EMBL; U34131; AAA91678.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;

Query Match 100.0%; Score 45; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDII 9
Db 19 LQTTIHDII 27

RESULT 8
Q77816 PRELIMINARY; PRT; 151 AA.
AC Q77816;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT J. Gen. Virol. 81:317-325(2000).
DR EMBL; AF469197; AAO15691.1; -
DR EMBL; AJ388063; CAB45118.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;

Query Match 100.0%; Score 45; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDII 9
Db 19 LQTTIHDII 27

RESULT 9
Q77E16 PRELIMINARY; PRT; 151 AA.
AC Q77E16;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 oncoprotein (E6 protein).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewootacharn K.;
RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT J. Gen. Virol. 81:317-325(2000).
DR EMBL; AF469197; AAO15691.1; -
DR EMBL; AJ388063; CAB45118.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CF1F CRC64;

Query Match 100.0%; Score 45; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDII 9
Db 19 LQTTIHDII 27

RESULT 10
Q77JC7 PRELIMINARY; PRT; 151 AA.
AC Q77JC7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6 variant (Transforming protein E6).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
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RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388056; CAB45104.1; -
DR EMBL; AJ388061; CAB45114.1; -
DR EMBL; AJ388066; CAB45124.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18334 MW; FF8F2A2FCBBA6C02 CRC64;

Query Match 100.0%; Score 45; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDII 9
Db 19 LQTTIHDII 27

RESULT 9
Q77E16 PRELIMINARY; PRT; 151 AA.
AC Q77E16;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 oncoprotein (E6 protein).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewootacharn K.;
RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT J. Gen. Virol. 81:317-325(2000).
DR EMBL; AF469197; AAO15691.1; -
DR EMBL; AJ388063; CAB45118.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CF1F CRC64;

Query Match 100.0%; Score 45; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDII 9
Db 19 LQTTIHDII 27

RESULT 10
Q77JC7 PRELIMINARY; PRT; 151 AA.
AC Q77JC7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6 variant (Transforming protein E6).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
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RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Xinjiang; Ma J., Lin R., Ming W., Zhong Z., Zhang Q., Zhang F.;
RA  Ma Z., Qian D., Ma J., Lin R., Ming W., Zhong Z., Zhang Q., Zhang F.;
RT  "Cloning and Sequencing of HPV16 E6 gene from Cervical Carcinoma
RL  Biopsies in Xinjiang.";
RN  Sheng Wu Hua Xue Yu Sheng Wu Li Jin Zhan 0:0-0(2001).
RP  [2]
RX  SEQUENCE FROM N.A.
RA  MEDLINE=20112892; PubMed=10644829;
RT  van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RN  Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT  "Analysis of human papillomavirus type 16 E6 variants in relation to
RN  p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL  J. Gen. Virol. 81:317-325(2000).
RP  [3]
RX  SEQUENCE FROM N.A.
RA  MEDLINE=2224222; PubMed=12355268; DOI=10.1007/s00239-002-2344-Y;
RN  DeFilippis V.R., Ayala F.J., Villarreal L.P.;
RT  "Evidence of diversifying selection in human papillomavirus type 16 E6
RN  but not E7 oncogenes.";
RL  J. Mol. Evol. 55:491-499(2002).
RP  [4]
RX  SEQUENCE FROM N.A.
RA  Cruz Mr., Cerqueira D.M., Camata G.N.L., Silva E.O., Carvalho L.G.S.,
RN  Martins C.R.F.;
RT  Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN  [5]
RX  SEQUENCE FROM N.A.
RA  Cruz M.R., Martins C.R.F.;
RN  Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RL  EMBL; AJ327851; AAG45940.1; -
DR  EMBL; AJ388057; CAB45106.1; -
DR  EMBL; AJ388069; CAB45130.1; -
DR  EMBL; AY089951; AAM11875.1; -
DR  EMBL; AY089954; AAM11881.1; -
DR  EMBL; AY112663; AAM51854.1; -
DR  GO; GO:0043025; C:host cell nucleus; IEA.
DR  InterPro; IPR001334; E6.
DR  Pfam; PF00518; E6; 1.
SQ  SEQUENCE 151 AA; 18320 MW; 617D2A2FDB4F8C17 CRC64;

Query Match 100.0%; Score 45; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDI 9
Db 19 LQTTIHDI 27

RESULT 11
Q77ZJ5 PRELIMINARY; PRT; 151 AA.
AC Q77ZJ5 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RN Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RL type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003019; AAB70736.1; -
```

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DR EMBL; AF003018; AAB70735.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18221 MW; 60CD2A34DAF48CB7 CRC64;

Query Match 100.0%; Score 45; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDI 9
Db 19 LQTTIHDI 27

RESULT 12
Q80963 PRELIMINARY; PRT; 151 AA.
AC Q80963 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBLrel. 01, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RN Jensen S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34122; AAA91669.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18291 MW; 97C7028D5169382D CRC64;

Query Match 100.0%; Score 45; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDI 9
Db 19 LQTTIHDI 27

RESULT 13
Q80966 PRELIMINARY; PRT; 151 AA.
AC Q80966 (TREMBLrel. 01, Created)
AC Q80964; Q80965;
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBLrel. 01, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
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RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
 RA "Sequence variations and viral genomic state of human papillomavirus
 RT type 16 in penile carcinomas from Ugandan patients.",
 RL J. Gen. Virol. 78:2199-2208(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Terai M., Ma Z., Burk R.D.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20112892; PubMed=10644829;
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
 RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
 RT "Analysis of human papillomavirus type 16 E6 variants in relation to
 RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.",
 RL J. Gen. Virol. 81:317-325(2000).
 DR EMBL; AF003014; AAB70731.1; -
 DR EMBL; AF003017; AAB70734.1; -
 DR EMBL; AF472508; AAO15697.1; -
 DR EMBL; AJ388068; CAB45128.1; -
 DR EMBL; AF003013; AAB70730.1; -
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR PFAM; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;
 Query Match 100.0%; Score 45; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LQTTIHDII 9
 Db 19 LQTTIHDII 27
 RESULT 14
 Q89648 PRELIMINARY; PRT; 151 AA.
 ID Q89648; O12653; O12654; O12928; O12929;
 AC Q89648; O12653; O12654; O12928; O12929;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Early transforming protein E6.
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OC NCBI_TaxID=10566;
 OX [1]
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96079021; PubMed=7494284;
 RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
 RA Jenison S.A.;
 RT "Human papillomavirus type 16 variant lineages in United States
 RT populations characterized by nucleotide sequence analysis of the E6,
 RT L2, and L1 coding segments.",
 RL J. Virol. 69:7743-7753(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Farmer A.D.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U341128; AAA91675.1; -
 DR EMBL; U34117; AAA91664.1; -
 DR EMBL; U34118; AAA91665.1; -
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR PFAM; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18304 MW; 0F312A8BDA6CF1F CRC64;
 Query Match 100.0%; Score 45; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LQTTIHDII 9
 Db 19 LQTTIHDII 27
 RESULT 15
 Q89708 PRELIMINARY; PRT; 151 AA.
 ID Q89708; O12928; O12929; O12930; O12931;
 AC Q89708; O12928; O12929; O12930; O12931;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Early transforming protein E6.
 OS Human papillomavirus.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OC NCBI_TaxID=10566;
 OX [1]
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96079021; PubMed=7494284;
 RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
 RA Jenison S.A.;
 RT "Human papillomavirus type 16 variant lineages in United States
 RT populations characterized by nucleotide sequence analysis of the E6,
 RT L2, and L1 coding segments.",
 RL J. Virol. 69:7743-7753(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Farmer A.D.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U341128; AAA91675.1; -
 DR EMBL; U34117; AAA91664.1; -
 DR EMBL; U34118; AAA91665.1; -
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR InterPro; IPR001334; E6.
 DR PFAM; PF00518; E6; 1.
 SQ SEQUENCE 151 AA; 18304 MW; 0F312A8BDA6CF1F CRC64;
 Query Match 100.0%; Score 45; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LQTTIHDII 9
 Db 19 LQTTIHDII 27
 Search completed: June 28, 2005, 19:19:21
 Job time : 55.3 secs

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GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: June 28, 2005, 18:23:48 ; Search time 11.2 Seconds
(without alignments)
77.317 Million cell updates/sec

Title: US-08-170-344-6
Perfect score: 45
Sequence: 1 LQTTIHDI 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	158	1 W6WLS	protein E6 - human
2	37	82.2	248	1 LNDGPS	pulmonary surfactant
3	36	80.0	377	2 T12042	cysteine proteinase
4	36	80.0	601	2 A55921	serine/threonine k
5	35	77.8	132	2 G84274	hypothetical prote
6	35	77.8	470	2 T49278	hypothetical prote
7	34	75.6	212	2 B47698	hemagglutinin hag2
8	34	75.6	233	2 D69614	purine nucleoside
9	33	73.3	32	2 S19906	E6-II protein - hu
10	33	73.3	35	2 S19909	E6-III protein - h
11	33	73.3	47	2 S23825	E6-I protein - hum
12	33	73.3	67	2 AE0792	probable membrane
13	33	73.3	149	1 W6WL33	E6 protein - human
14	33	73.3	158	1 W6WLP	E6 protein - human
15	33	73.3	340	1 RNLVA	DNA-directed RNA p
16	33	73.3	376	1 NMEBST	exo-alpha-sialidas
17	33	73.3	431	2 T23809	hypothetical prote
18	33	73.3	433	2 AG1858	hypothetical prote
19	33	73.3	501	2 S44258	sucrose-6-phosphat
20	33	73.3	1215	2 S60904	hypothetical prote
21	33	73.3	1417	2 T18418	hypothetical prote
22	32	71.1	62	2 S18571	otc2 protein - Str
23	32	71.1	171	2 T48286	hypothetical prote
24	32	71.1	485	2 G71527	probable pyruvate
25	32	71.1	495	2 T36043	probable integrase
26	32	71.1	513	2 A95154	sodium/solute symp
27	32	71.1	553	2 G71543	probable fructose-
28	32	71.1	617	2 T15104	hypothetical prote
29	32	71.1	642	2 I39839	beta-hexosaminidas

30 32 71.1 776 2 S67053
31 32 71.1 1015 2 C84918
32 32 71.1 1258 2 T40737
33 31 68.9 86 2 T06391
34 31 68.9 241 2 G90190
35 31 68.9 335 2 T34296
36 31 68.9 359 2 G70860
37 31 68.9 383 2 D89975
38 31 68.9 419 2 T07371
39 31 68.9 420 2 S71199
40 31 68.9 420 2 T49127
41 31 68.9 423 2 T09338
42 31 68.9 429 2 T41560
43 31 68.9 449 2 T31546
44 31 68.9 563 2 D84717
45 31 68.9 589 2 D84044

probable membrane
probable ATP-depen
probable calcium-t
isoprenylated prot
conserved hypotet
hypothetical prote
probable fecB - My
conserved hypotet
dnaJ protein homol
dnaJ protein homol
dnaJ protein homol
DnaJ-like protein
phenylalanyl-trna
hypothetical prote
probable cysteinyl
two-component sens

ALIGNMENTS

RESULT 1

W6WLS

protein E6 - human papillomavirus type 16

C;Species: human papillomavirus type 16

C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C;Accession: A03682; T10427

R;Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virology 145, 181-185, 1985

A;Title: Human papillomavirus type 16 DNA sequence.

A;Reference number: A23255; MUID:85246220; PMID:2990099

A;Accession: A03682

A;Molecule type: DNA

A;Residues: 1-158 <SEE>

A;Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

J.Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

R. Virol. 65, 2093-2097, 1991

A;Title: A negative element in the human poapillomavirus type 16 genome acts at the level

A;Reference number: Z17014; MUID:91162763; PMID:1848319

A;Accession: T10427

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-158 <KEN>

A;Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

C;Genetics:

C;Gene: E6

C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; zinc finger

F;37-73/Region: zinc finger CCCC motif

F;110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 45; DB 1; Length 158;
Best Local Similarity 100.0%; Pred.No. 0.093;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LQTTIHDI 9

DB 26 LQTTIHDI 34

RESULT 2

LNDGPS

pulmonary surfactant protein A precursor - dog

N;Alternate names: pulmonary surfactant 32K apoprotein; pulmonary surfactant-associated i

C;Species: Canis lupus familiaris (dog)

C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999

C;Accession: A25296; A61227; A60142

R;Benson, B.; Hawgood, S.; Schilling, J.; Clements, J.; Damm, D.; Cordell, B.; White, R.J

Proc. Natl. Acad. Sci. U.S.A. 82, 6379-6383, 1985

A;Title: Structure of canine pulmonary surfactant apoprotein: cDNA and complete amino aci

A;Reference number: A25296; MUID:86016705; PMID:3863100

A;Accession: A25296

A;Molecule type: mRNA

A;Residues: 1-248 <BEN>
A;Note: the authors translated the codon TTC for residue 60 as Pro
R;Liau, D.F.; Ryan, S.F.
Chem. Phys. Lipids 59, 29-38, 1991
A;Title: Purification of surfactant protein A from dog lung by reconstitution with surfactant
A;Reference number: A61227; MUID:92163993; PMID:1790579
A;Accession: A61227
A;Molecule type: protein
A;Residues: 18-32 <LIA>
R;Ross, G.F.; Muth, J.; Ohning, B.; Kim, Y.; Whitsett, J.A.
Biochem. Biophys. Acta 870, 267-278, 1986
A;Title: Purification of canine surfactant-associated glycoproteins A. Identification of
A;Reference number: A60142; MUID:86159848; PMID:3006781
A;Accession: A60142
A;Molecule type: protein
A;Residues: 24-34;95-101,'X',103-108 <ROS>
R;Patthy, L.
Nature 325, 490, 1987
A;Reference number: A93388; MUID:87115834; PMID:3808053
A;Contents: annotation; animal lectin domain homology
C;Comment: Pulmonary surfactant is a complex of phospholipids and proteins that lowers the surface tension of the lung. This protein is a sialoglycoprotein synthesized by alveolar type II cells. It is dependent on the presence of calcium ions.
C;Superfamily: mannose-binding lectin; C-type lectin homology
C;Keywords: alveolar proteinosis; calcium; disulfide bond; gaseous exchange; hydroxyproline
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-248/Product: pulmonary surfactant protein A #status experimental <MPT>
F;28-102/Region: collagen-like
F;127-246/Domain: C-type lectin homology <LCH>
F;20,207/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;30/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 82.2%; Score 37; DB 1; Length 248;
Best Local Similarity 75.0%; Pred. No. 6.4;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDI 8
|||||:
DB 107 LQTTLHDL 114

RESULT 3
T12042
cysteine proteinase (EC 3.4.22.-) 4 precursor - kidney bean
C;Species: Phaseolus vulgaris (kidney bean)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12042
R;Senyuk, V.; Becker, C.; Muentz, K.
submitted to the EMBL Data Library, October 1997
A;Description: Isolation of cDNA clone encoding cysteine proteinase (CP4) from a cotyledon of Phaseolus vulgaris
A;Reference number: Z17388
C;Genetics:
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-377 <SEN>
A;Cross-references: UNIPROT:O24324; EMBL:Z99955
A;Experimental source: cultivar Moldavian; cotyledon; clone cp4
C;Superfamily: papain
C;Keywords: cysteine proteinase; hydrolase
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-137/Domain: propeptide #status predicted <PRO>
F;138-377/Product: cysteine proteinase 4 #status predicted <MAT>
F;162,305,332/Active site: Cys, His, Asn #status predicted

Query Match 80.0%; Score 36; DB 2; Length 377;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QTTIHDI 8
|||||:
DB 29 QTTVHDI 35

RESULT 4
A55921
serine/threonine kinase Atr-1 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
A;Accession: A55921
R;Wrana, J.L.; Tran, H.; Attisano, L.; Arora, K.; Childs, S.R.; Massague, J.; O'Connor, R.
Mol. Cell. Biol. 14, 944-950, 1994
A;Title: Two distinct transmembrane serine/threonine kinases from Drosophila melanogaster
A;Reference number: A55921; MUID:94119112; PMID:8289834
A;Accession: A55921
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-601 <WRA>
A;Cross-references: UNIPROT:Q23975; GB:U04692; NID:G436960; PIDN:AAA18959.1; PID:G436961
C;Genetics:
A;Gene: FlyBase:babo
A;Cross-references: FlyBase:FBgn0011300
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C;Keywords: ATP
F;301-597/Domain: protein kinase homology <KIN>
F;309-317/Region: protein kinase ATP-binding motif

Query Match 80.0%; Score 36; DB 2; Length 601;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 TTIHDI 9
|||||:
DB 273 TTIHDI 279

RESULT 5
G84274
hypothetical protein Vngl189h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: G84274
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Laaky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: G84274
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-132 <STO>
A;Cross-references: UNIPROT:Q9HQF2; GB:AE004437; NID:g10580723; PIDN:AAG19563.1; GSPDB:G
C;Genetics:
A;Gene: VNG1189H

Query Match 77.8%; Score 35; DB 2; Length 132;
Best Local Similarity 66.7%; Pred. No. 8;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQTTIHDI 9
|||||:
DB 93 VQTTIHDI 101

RESULT 6
T49278
hypothetical protein T21J18.90 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T49278
R;Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Rudd, S.,
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z25021
A;Accession: T49278

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-470 <RI>
A:Cross-references: UNIPROT:Q9M301; EMBL:AL132963; GSPDB:GNO00061; ATSP:T21J18.90
A:Experimental source: cultivar Columbia; BAC clone T21J18
C:Genetics:
A:Gene: ATSP-T21J18.90
A:Map position: 3
A:Introns: 35/2; 71/3; 123/3; 157/2; 174/2; 238/3; 269/1; 290/3; 342/2; 369/3; 406/2

Query Match 77.8%; Score 35; DB 2; Length 470;
Best Local Similarity 66.7%; Pred. No. 33;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQTTIHDII 9
::|||||:
Db 277 VKTTHDIM 285

RESULT 7
B47698 hemagglutinin hag2 - Eikenella corrodens
C:Species: Eikenella corrodens
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: B47698; S23848
F:Rao, V.K.; Whitlock, J.A.; Prokuske-Fox, A.
J. Gen. Microbiol. 139, 639-650, 1993
A:Title: Cloning, characterization and sequencing of two haemagglutinin genes from Eikenella corrodens
A:Reference number: A47698; MUID:93232781; PMID:8473870
A:Accession: B47698
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-212 <RAO>
A:Cross-references: UNIPROT:P35648; EMBL:Z13610; NID:g41653; PIDN:CAA78254.1; PID:g41655
A:Experimental source: ATCC 23834
A>Note: sequence extracted from NCBI backbone (NCBIN:129988, NCBIP:129990)
C:Superfamily: Eikenella corrodens hemagglutinin hag2

Query Match 75.6%; Score 34; DB 2; Length 212;
Best Local Similarity 66.7%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LQTTIHDII 9
::|||||:
Db 161 LQSTIHDA 169

RESULT 8
D69614 purine nucleoside phosphorylase deoD - Bacillus subtilis
C:Species: Bacillus subtilis
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: D69614
F:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azavedo, V.; Bertero, C.; Bron, S.; Brouillet, S.; Bruschii, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chai, A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.; Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Hulio, M.F.; Koether, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadiaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Tosato, V.; Uchiyama, A.; Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: D69614
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-233 <KUN>

R.;Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, P.M.C.; Me submitted to the EMBL Data Library, January 1992
A:Description: HPV type 33 in a tonsillar carcinoma generates its putative E7 mRNA via d
A:Reference number: S19906
A:Accession: S23825
A:Molecule type: mRNA
A:Residues: 1-47 <SNI>
A:Cross-references: UNIPROT:Q81883; UNIPROT:Q81884; EMBL:X64084; NID:g60273; PIDN:CAA454
A:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger

Query Match 73.3%; Score 33; DB 2; Length 47;
Best Local Similarity 75.0%; Pred. No. 6.5;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDII 8
|:|||||:
Db 7 LETTIHNI 14

RESULT 12
AE0792
probable membrane protein STY2516 [imported] - Salmonella enterica subsp. enterica serov
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
A:Accession: AE0792
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AE0792
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-67 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD07519.1; PID:g16503512; GSPDB:GN00176
C:Genetics:
A:Gene: STY2516

Query Match 73.3%; Score 33; DB 2; Length 67;
Best Local Similarity 77.8%; Pred. No. 9.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQTTIHDII 9
|:|||||:
Db 22 LQIIHDII 30

RESULT 13
W6WL33
E6 protein - human papillomavirus type 33
C:Species: human papillomavirus type 33
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
A:Accession: A03683
R:Cole, S.T.; Strecek, R.E.
J. Virol. 58, 991-995, 1986
A:Title: Genome organization and nucleotide sequence of human papillomavirus type 33, wh
A:Reference number: A93020; MUID:86200464; PMID:3009902
A:Accession: A03683
A:Molecule type: DNA
A:Residues: 1-149 <COL>
A:Cross-references: UNIPROT:P06427; GB:M12732; NID:g333049; PIDN:AAA46958.1; PID:g463177
A:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match 73.3%; Score 33; DB 1; Length 149;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDII 8
|:|||||:
Db 19 LETTIHNI 26

RESULT 14

W6WLPR

E6 protein - human papillomavirus type ME180 (provirus)

C:Species: human papillomavirus type ME180

A:Note: host Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C:Accession: C40509

R:Reuter, S.; Delius, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.

J. Virol. 65, 5564-5568, 1991

A:Title: Characterization of a novel human papillomavirus DNA in the cervical carcinoma

A:Reference number: A40509; MUID:91374616; PMID:1716694

A:Accession: C40509

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-158 <REU>

A:Cross-references: UNIPROT:P27962; GB:M73258

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:32-68/Region: zinc finger CCCC motif

F:105-141/Region: zinc finger CCCC motif

Query Match 73.3%; Score 33; DB 1; Length 158;
Best Local Similarity 62.5%; Pred. No. 25;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQTTIHDII 8
|:|||||:
Db 21 LDTTLHDV 28

RESULT 15

RNLVA

DNA-directed RNA polymerase (EC 2.7.7.6) alpha chain - liverwort (Marchantia polymorpha)

C:Species: chloroplast Marchantia polymorpha

C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004

C:Accession: A00687; S01565

R:Ohyama, K.

submitted to the EMBL Data Library, October 1986

A:Reference number: A00150

A:Accession: A00687

A:Molecule type: DNA

A:Residues: 1-340 <OHV>

A:Cross-references: UNIPROT:P06270

R:Ohyama, K.; Fukuzawa, H.; Kohchi, T.; Shirai, H.; Sano, T.; Sano, S.; Umesono, K.; Shi

Nature 322, 572-574, 1986

A:Title: Chloroplast gene organization deduced from complete sequence of liverwort March

A:Reference number: A38014

A:Contents: annotation; gene organization, sites, features

R:Fukuzawa, H.; Kohchi, T.; Sano, T.; Shirai, H.; Umesono, K.; Inokuchi, H.; Ozeki, H.; C

J. Mol. Biol. 203, 333-351, 1988

A:Title: Structure and organization of Marchantia polymorpha chloroplast genome. III. Ge

A:Reference number: S01529; MUID:89068687; PMID:3199436

A:Accession: S01565

A:Molecule type: DNA

A:Residues: 1-340 <FKU>

A:Cross-references: EMBL:X04465; NID:g11640; PIDN:CAA28117.1; PID:g11706

C:Genetics:

A:Gene: rpoA

A:Genome: chloroplast

C:Superfamily: DNA-directed RNA polymerase alpha chain

C:Keywords: chloroplast; nucleotidyltransferase; transcription

Query Match 73.3%; Score 33; DB 1; Length 340;
Best Local Similarity 66.7%; Pred. No. 58;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQTTIHDII 9

Db ||:||||:
 80 LQSIHDIL 88

Search completed: June 28, 2005, 19:23:19
Job time : 12.2 secs

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OM protein - protein search, using sw model

Run on: June 29, 2005, 01:35:30 ; Search time 57.55 Seconds
(without alignments)
60.138 Million cell updates/sec

Title: US-08-170-344-6
Perfect score: 45
Sequence: 1 LQTTIHDI 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
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- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	9	9	US-09-909-460-102
2	45	100.0	9	11	US-09-872-836-102
3	45	100.0	9	14	US-10-133-210-279
4	45	100.0	9	17	US-10-758-970-102
5	45	100.0	9	17	US-10-751-845-56
6	45	100.0	10	17	US-10-484-063-2
7	45	100.0	15	16	US-10-476-570-21
8	45	100.0	15	16	US-10-476-570-22
9	45	100.0	21	16	US-10-476-570-8
10	45	100.0	30	16	US-10-476-570-53
11	45	100.0	30	17	US-10-858-384-4
					Sequence 102, App
					Sequence 102, App
					Sequence 279, App
					Sequence 102, App
					Sequence 56, Appl
					Sequence 2, Appli
					Sequence 21, Appl
					Sequence 22, Appl
					Sequence 8, Appli
					Sequence 53, Appl
					Sequence 4, Appli

12	45	100.0	32	16	US-10-476-570-9	Sequence 9, Appli
13	45	100.0	33	16	US-10-476-570-19	Sequence 19, Appl
14	45	100.0	151	14	US-10-177-390-6	Sequence 6, Appli
15	45	100.0	151	17	US-10-484-063-20	Sequence 20, Appl
16	45	100.0	151	17	US-10-484-063-27	Sequence 27, Appl
17	45	100.0	158	17	US-10-858-384-2	Sequence 2, Appli
18	45	100.0	158	17	US-10-367-057-16	Sequence 16, Appl
19	45	100.0	171	16	US-10-472-724-2	Sequence 2, Appli
20	45	100.0	266	9	US-09-367-309A-1	Sequence 1, Appli
21	45	100.0	273	13	US-10-000-903-4	Sequence 4, Appli
22	45	100.0	273	17	US-10-899-771-4	Sequence 4, Appli
23	45	100.0	292	13	US-10-000-903-10	Sequence 10, Appl
24	45	100.0	292	17	US-10-899-771-10	Sequence 10, Appl
25	45	100.0	371	13	US-10-000-903-6	Sequence 6, Appli
26	45	100.0	371	17	US-10-899-771-6	Sequence 6, Appli
27	45	100.0	390	13	US-10-000-903-14	Sequence 14, Appl
28	45	100.0	390	17	US-10-899-771-14	Sequence 14, Appl
29	45	100.0	536	15	US-10-367-095-10	Sequence 10, Appl
30	45	100.0	536	15	US-10-368-046-10	Sequence 10, Appl
31	45	100.0	536	16	US-10-367-367-10	Sequence 10, Appl
32	45	100.0	536	17	US-10-918-337-10	Sequence 10, Appl
33	36	80.0	15	16	US-10-476-570-23	Sequence 23, Appl
34	36	80.0	151	16	US-10-425-115-237192	Sequence 237192,
35	36	80.0	1082	15	US-10-282-122A-49664	Sequence 49664, A
36	36	80.0	1198	15	US-10-452-024-95	Sequence 95, Appl
37	35	77.8	97	16	US-10-767-701-50864	Sequence 50864, A
38	35	77.8	156	16	US-10-425-115-263392	Sequence 263392,
39	35	77.8	165	15	US-10-425-114-55470	Sequence 55470, A
40	35	77.8	316	15	US-10-424-599-168462	Sequence 168462,
41	35	77.8	336	15	US-10-424-599-230648	Sequence 230648,
42	35	77.8	403	16	US-10-437-963-117225	Sequence 117225,
43	35	77.8	448	16	US-10-425-115-263390	Sequence 263390,
44	35	77.8	463	15	US-10-425-114-49312	Sequence 49312, A
45	35	77.8	537	15	US-10-424-599-230650	Sequence 230650,

ALIGNMENTS

RESULT 1
US-09-909-460-102
; Sequence 102, Application US/09909460
; Publication No. US20020182258A1
; GENERAL INFORMATION:
; APPLICANT: Lunsford, Lynn B.
; APPLICANT: Putnam, David
; APPLICANT: Hedley, Mary Lynn
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF NUCLEIC ACID
; FILE REFERENCE: 08191/014001
; CURRENT APPLICATION NUMBER: US/09/909,460
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/321,346
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 102
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-909-460-102

Query Match	100.0%	Score 45;	DB 9;	Length 9;
Best Local Similarity	100.0%	Pred. No. 1.6e+06;		
Matches	9;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;

Qv	1	LQTTIHDI 9
Db	1	LQTTIHDI 9

RESULT 2
US-09-872-836-102

; Sequence 102, Application US/09872836
; Publication No. US20040142475A1
; GENERAL INFORMATION:
; APPLICANT: Barman, Shikha P.
; APPLICANT: McKeever, Una
; APPLICANT: Hedley, Mary Lynne
; TITLE OF INVENTION: DELIVERY SYSTEMS FOR BIOACTIVE AGENTS
; FILE REFERENCE: 08191-018001
; CURRENT APPLICATION NUMBER: US/09/872,836
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/208,830
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-872-836-102

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Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDII 9
Db 1 LQTTIHDII 9

RESULT 3

US-10-133-210-279
; Sequence 279, Application US/10133210
; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: Delisi, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakar
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Ziping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; TITLE OF INVENTION: COMPOSITIONS THEREOF
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 279
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-279

Query Match 100.0%; Score 45; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDII 9
Db 1 LQTTIHDII 9

RESULT 4

US-10-758-970-102
; Sequence 102, Application US/10758970
; Publication No. US20050037086A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Hsu, Yung-Yueh
; APPLICANT: Iyo, Michael
; TITLE OF INVENTION: CONTINUOUS-FLOW METHOD FOR PREPARING MICROPARTICLES

; FILE REFERENCE: 08191-012001
; CURRENT APPLICATION NUMBER: US/10/758,970
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US/09/715,708A
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/166,516
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 102
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-758-970-102

Query Match 100.0%; Score 45; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDII 9
Db 1 LQTTIHDII 9

RESULT 5

US-10-751-845-56
; Sequence 56, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiccz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-56

Query Match 100.0%; Score 45; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDII 9
Db 1 LQTTIHDII 9

RESULT 6

US-10-484-063-2
; Sequence 2, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198

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; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-2

Query Match          100.0%; Score 45; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.053; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDII 9
Db 2 LQTTIHDII 10

RESULT 7
US-10-476-570-21
; Sequence 21, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 20-34
US-10-476-570-21

Query Match          100.0%; Score 45; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.083; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDII 9
Db 7 LQTTIHDII 15

RESULT 8
US-10-476-570-22
; Sequence 22, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-34
US-10-476-570-22

Query Match          100.0%; Score 45; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.12; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDII 9
Db 13 LQTTIHDII 21

RESULT 10
US-10-476-570-53
; Sequence 53, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 21
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-34
US-10-476-570-8

Query Match          100.0%; Score 45; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.083; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDII 9
Db 3 LQTTIHDII 11

RESULT 9
US-10-476-570-8
; Sequence 8, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 21
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-34
US-10-476-570-8

Query Match          100.0%; Score 45; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.12; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDII 9
Db 13 LQTTIHDII 21

RESULT 10
US-10-476-570-53
; Sequence 53, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
```

```

; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 30
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 15-44
US-10-476-570-53

Query Match      100.0%; Score 45; DB 16; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LOTTIHDII 9
Db      12 LOTTIHDII 20

RESULT 11
US-10-858-384-4
; Sequence 4, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
; OTHER INFORMATION: for E6 of HPV
US-10-858-384-4

Query Match      100.0%; Score 45; DB 17; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LOTTIHDII 9
Db      12 LOTTIHDII 20

RESULT 12
US-10-476-570-9
; Sequence 9, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:

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; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 32
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-45
US-10-476-570-9

Query Match      100.0%; Score 45; DB 16; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LOTTIHDII 9
Db      13 LOTTIHDII 21

RESULT 13
US-10-476-570-19
; Sequence 19, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 33
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 14-46
US-10-476-570-19

Query Match      100.0%; Score 45; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 LOTTIHDII 9
Db      13 LOTTIHDII 21

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RESULT 14
US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerps Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wG/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6

Query Match      100.0%; Score 45; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQTTIHDI 9
DB      19 LQTTIHDI 27

RESULT 15
US-10-484-063-20
; Sequence 20, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; TITLE OF INVENTION: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-20

Query Match      100.0%; Score 45; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQTTIHDI 9
DB      19 LQTTIHDI 27

Search completed: June 29, 2005, 03:24:06
Job time : 57.55 secs
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OM protein - protein search, using sw model

Run on: June 28, 2005, 18:27:48 ; Search time 17.15 Seconds
(without alignments)
39.174 Million cell updates/sec

Title: US-08-170-344-6
Perfect score: 45
Sequence: 1 LQTTIHDI 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
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3: /cgn2_6/prodata/1/iaa/6A COMB.pep: *
4: /cgn2_6/prodata/1/iaa/6B COMB.pep: *
5: /cgn2_6/prodata/1/iaa/6C COMB.pep: *
6: /cgn2_6/prodata/1/iaa/6D COMB.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	100.0	9	1	US-08-787-547-102
2	45	100.0	9	3	US-08-159-339A-248
3	45	100.0	14	1	US-07-909-122-3
4	45	100.0	30	1	US-08-363-586-4
5	45	100.0	30	4	US-09-980-523A-4
6	45	100.0	158	4	US-09-980-523A-2
7	45	100.0	162	1	US-08-316-239B-3
8	45	100.0	162	1	US-08-316-239B-4
9	45	100.0	172	3	US-08-860-165-14
10	45	100.0	172	3	US-09-359-382-14
11	45	100.0	182	1	US-08-117-083-10
12	45	100.0	266	3	US-08-860-165-10
13	45	100.0	266	3	US-09-359-382-10
14	45	100.0	266	4	US-09-367-309A-1
15	45	100.0	273	3	US-09-485-885-4
16	45	100.0	292	3	US-09-485-885-10
17	45	100.0	371	3	US-09-485-885-6
18	45	100.0	390	3	US-09-485-885-14
19	40	88.9	20	2	US-08-934-915-159
20	40	88.9	317	3	US-08-913-159-14
21	33	73.3	166	4	US-09-270-767-33046
22	33	73.3	166	4	US-09-270-767-48263
23	33	73.3	297	3	US-08-706-281A-8
24	33	73.3	297	3	US-09-097-231-8
25	33	73.3	297	4	US-09-353-099-8
26	33	73.3	500	4	US-09-354-123-6
27	32	71.1	168	4	US-09-270-767-32894

28	71.1	467	4	US-09-489-039A-14156	Sequence 14156, A
29	71.1	532	4	US-09-252-991A-30492	Sequence 30492, A
30	71.1	572	4	US-09-543-681A-6825	Sequence 6825, Ap
31	71.1	781	4	US-09-248-796A-19137	Sequence 19137, A
32	68.9	10	4	US-08-197-484-72	Sequence 72, Appl
33	68.9	10	4	US-09-601-729-273	Sequence 273, Appl
34	68.9	10	5	PCT-US95-02121-72	Sequence 72, Appl
35	68.9	56	3	US-08-936-165A-297	Sequence 297, Appl
36	68.9	59	1	US-08-118-270-256	Sequence 256, App
37	68.9	59	3	US-09-390-027-6	Sequence 6, Appli
38	68.9	59	5	PCT-US93-08528-256	Sequence 256, App
39	68.9	86	2	US-08-785-795-1	Sequence 1, Appli
40	68.9	277	4	US-09-248-796A-21807	Sequence 21807, A
41	68.9	326	4	US-09-252-991A-27158	Sequence 27158, A
42	68.9	383	4	US-09-603-208A-62	Sequence 62, Appl
43	68.9	695	4	US-09-248-796A-20895	Sequence 20895, A
44	68.9	1016	4	US-09-949-016-11304	Sequence 11304, A
45	68.9	1193	3	US-09-227-725A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-787-547-102
; Sequence 102, Application US/08787547
; Patent No. 5783567
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Curley, Joanne M.
; APPLICANT: Langer, Robert S.
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY
; TITLE OF INVENTION: OF NUCLEIC ACID
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: Fast-Seq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,547
; FILING DATE: 22-JAN-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 08191/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 102:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-787-547-102

Query Match 100.0%; Score 45; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 LQTTIHDII 9
      |||||
Db      1 LQTTIHDII 9

RESULT 2
US-08-159-339A-248
; Sequence 248, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 248:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-248

Query Match      100.0%; Score 45; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQTTIHDII 9
      |||||
Db      1 LQTTIHDII 9

RESULT 3
US-07-909-122-3
; Sequence 3, Application US/07909122
; Patent No. 5415995
; GENERAL INFORMATION:
; APPLICANT: SCHOOLNIK, GARY K.
; APPLICANT: PALEFSKY, JOEL M.

```

```

; TITLE OF INVENTION: DIAGNOSTIC PEPTIDES OF HUMAN PAPILLOMA
; TITLE OF INVENTION: VIRUS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSER: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/909,122
; FILING DATE: 19920706
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: BENZ, WILLIAM H.
; REGISTRATION NUMBER: 25,952
; REFERENCE/DOCKET NUMBER: 28600-20105.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-909-122-3

Query Match      100.0%; Score 45; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LQTTIHDII 9
      |||||
Db      3 LQTTIHDII 11

RESULT 4
US-08-363-586-4
; Sequence 4, Application US/08363586
; Patent No. 5629161
; GENERAL INFORMATION:
; APPLICANT: Mueller, Martin
; APPLICANT: Gissmann, Lutz
; TITLE OF INVENTION: Use of HPV-16 E6 and E7-Gene Derived
; TITLE OF INVENTION: Peptides for the Diagnostic Purpose
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSER: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,586
; FILING DATE: 23-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/909,296

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/ FILING DATE: 09-JUL-1992
/ APPLICATION NUMBER: EP 9111720.8
/ FILING DATE: 13-JUL-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Wadler, Linda A.
/ REGISTRATION NUMBER: 33,218
/ REFERENCE/DOCKET NUMBER: 02481-1195-00000
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-408-4000
/ TELEFAX: 202-408-4400
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 30 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-363-586-4

Query Match 100.0%; Score 45; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOTTIHDII 9
DB 19 LOTTIHDII 27

RESULT 5

US-09-980-523A-4
/ Sequence 4, Application US/09980523A
/ Patent No. 6783763
/ GENERAL INFORMATION:

/ APPLICANT: CHOPPIN, JEANNINE
/ APPLICANT: BOURGAULT VILLADA, ISABELLE
/ APPLICANT: GUILLET, JEAN-GERARD
/ APPLICANT: CONNAN, FRANCINE
/ APPLICANT: FERRIES, ESTELLE
/ TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
/ TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
/ TITLE OF INVENTION: PARTICULARLY IN VACCINATION
/ FILE REFERENCE: WOBI AO INS

/ CURRENT APPLICATION NUMBER: US/09/980,523A
/ CURRENT FILING DATE: 2002-04-29
/ PRIOR APPLICATION NUMBER: PCT/FR00/01513
/ PRIOR FILING DATE: 2000-05-31
/ PRIOR APPLICATION NUMBER: FR 99/07012
/ PRIOR FILING DATE: 1999-06-03
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 30
/ TYPE: PRT
/ ORGANISM: Human Papillomavirus
US-09-980-523A-4

Query Match 100.0%; Score 45; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOTTIHDII 9
DB 12 LOTTIHDII 20

RESULT 6

US-09-980-523A-2
/ Sequence 2, Application US/09980523A
/ Patent No. 6783763
/ GENERAL INFORMATION:

/ APPLICANT: CHOPPIN, JEANNINE
/ APPLICANT: BOURGAULT VILLADA, ISABELLE
/ APPLICANT: GUILLET, JEAN-GERARD
/ APPLICANT: CONNAN, FRANCINE

/ APPLICANT: FERRIES, ESTELLE
/ TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
/ TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
/ TITLE OF INVENTION: PARTICULARLY IN VACCINATION
/ FILE REFERENCE: WOBI AO INS
/ CURRENT APPLICATION NUMBER: US/09/980,523A
/ CURRENT FILING DATE: 2002-04-29
/ PRIOR APPLICATION NUMBER: PCT/FR00/01513
/ PRIOR FILING DATE: 2000-05-31
/ PRIOR APPLICATION NUMBER: FR 99/07012
/ PRIOR FILING DATE: 1999-06-03
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 158
/ TYPE: PRT
/ ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 45; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOTTIHDII 9
DB 26 LOTTIHDII 34

RESULT 7

US-08-316-239B-3
/ Sequence 3, Application US/08316239B
/ Patent No. 5679509
/ GENERAL INFORMATION:

/ APPLICANT: Wheeler, Cosette M.
/ APPLICANT: Parmenter, Cheryl A.
/ TITLE OF INVENTION: Methods and a Diagnostic Aid for
/ TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
/ TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
/ TITLE OF INVENTION: Cervical Cancer
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Jagtiani & Associates
/ STREET: 6126 Rocky Way Court
/ CITY: Centreville
/ STATE: VA
/ COUNTRY: USA
/ ZIP: 20120-3400

/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/316,239B
/ FILING DATE: 30-SEP-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Jagtiani, Ajay A.
/ REGISTRATION NUMBER: 35,205
/ REFERENCE/DOCKET NUMBER: UNME-0001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (703) 817-9453
/ TELEFAX: (703) 803-9387
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 162 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: not relevant
/ MOLECULE TYPE: protein
/ HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 100.0%; Score 45; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.42; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDII 9
Db 26 LQTTIHDII 34

RESULT 8
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 100.0%; Score 45; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.42; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDII 9
Db 26 LQTTIHDII 34

RESULT 9
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14

Query Match 100.0%; Score 45; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.44; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDII 9
Db 95 LQTTIHDII 103

RESULT 10
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match 100.0%; Score 45; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.44; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDII 9
Db 95 LQTTIHDII 103

RESULT 11
US-08-117-083-10
; Sequence 10, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Bourns, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Walter H. Dreger
;; STREET: 4 Embarcadero Center, Suite 3400
;; CITY: San Francisco
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94111
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/117,083
;; FILING DATE: 10-SEP-1993
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Dreger, Walter H.
;; REGISTRATION NUMBER: 24,190
;; REFERENCE/DOCKET NUMBER: A-58783
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-781-1989
;; TELEFAX: 415-398-3249
;; TELEX: 910 277299
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 182 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FEATURE:
;; NAME/KEY: Protein
;; LOCATION: 1..182
;; OTHER INFORMATION: /note= "Xaa refers to stop codon in
;; OTHER INFORMATION: the open reading frame."
US-08-117-083-10

Query Match 100.0%; Score 45; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.47; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDII 9
|||
Db 27 LQTTIHDII 35

RESULT 12
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; PRIOR FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 45; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.7; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQTTIHDII 9
|||
Db 26 LQTTIHDII 34

RESULT 13
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 45; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.7; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDII 9
|||
Db 26 LQTTIHDII 34

RESULT 14
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 45; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.7; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDII 9
| | | | | | | |
Db 26 LQTTIHDII 34

RESULT 15
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match 100.0%; Score 45; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.72;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQTTIHDII 9
| | | | | | | |
Db 132 LQTTIHDII 140

Search completed: June 28, 2005, 19:29:10
Job time : 25.15 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:24:19 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-59
Perfect score: 58
Sequence: 1 HYNIVTFCC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	65	2 Q8B563	Q8B563 human papil
2	58	100.0	77	2 Q8B5P5	Q8B5P5 human papil
3	58	100.0	93	2 Q9QDH2	Q9QDH2 human papil
4	58	100.0	93	2 Q9QDH4	Q9QDH4 human papil
5	58	100.0	93	2 Q9QDH6	Q9QDH6 human papil
6	58	100.0	93	2 Q9QDH8	Q9QDH8 human papil
7	58	100.0	94	2 Q8B5P6	Q8B5P6 human papil
8	58	100.0	98	1 VE7 HPV16	P03129 human papil
9	58	100.0	98	2 O11650	O11650 human papil
10	58	100.0	98	2 O12337	O12337 human papil
11	58	100.0	98	2 O12338	O12338 human papil
12	58	100.0	98	2 Q8QRD2	Q8QRD2 human papil
13	58	100.0	98	2 Q8QRD3	Q8QRD3 human papil
14	58	100.0	98	2 Q8QRD4	Q8QRD4 human papil
15	58	100.0	98	2 Q8VJ0	Q8VJ0 human papil
16	58	100.0	98	2 Q778H3	Q778H3 human papil
17	58	100.0	98	2 Q778H5	Q778H5 human papil
18	51	87.9	98	1 VE7 HPV31	P17387 human papil
19	51	87.9	98	2 Q6T377	Q6T377 human papil
20	44	75.9	98	2 Q9QLP4	Q9QLP4 human papil
21	44	75.9	98	2 Q38410	Q38410 bacterioph
22	44	75.9	264	2 Q71TC6	Q71TC6 bacterioph
23	43	74.1	99	1 VE7 HPV35	P27230 human papil
24	43	74.1	99	2 Q76WP2	Q76WP2 human papil
25	43	74.1	286	2 Q6QGW1	Q6QGW1 sus scrofa
26	43	74.1	292	2 Q6XGY1	Q6XGY1 homo sapien
27	43	74.1	377	2 Q6QGW2	Q6QGW2 sus scrofa
28	43	74.1	379	1 GRR2_CERAE	Q95mh6 cercopithec
29	43	74.1	379	1 GRR2_HUMAN	Q96P88 homo sapien
30	43	74.1	380	1 GRR2_CALJA	Q95mg6 callithrix
31	43	74.1	1061	2 Q7S8B5	Q7S8B5 neurospora

RESULT 1

Q8B563 ID Q8B563 PRELIMINARY; PRT; 65 AA.
AC Q8B563;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP Ponglikitmongkol M., Vaeteewoottacharn K.;
RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF548023; RAO16240.1;
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 65
SQ SEQUENCE 65 AA; 7373 MW; E9D74D7923700195 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 65;
Best Local Similarity 100.0%; Pred. No. 0.0087;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
DB 51 HYNIVTFCC 59

RESULT 2

Q8B5P5 ID Q8B5P5 PRELIMINARY; PRT; 77 AA.
AC Q8B5P5;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP Ponglikitmongkol M., Vaeteewoottacharn K.;
RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF469198; RAO15694.1;
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 77
SQ SEQUENCE 77 AA; 8782 MW; C5DE3A7E546AC31B CRC64;

Query Match 100.0%; Score 58; DB 2; Length 77;

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Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Gaps 0;
Matches 9; Conservative 0; Indels 0;

QY 1 HYNIVTFCC 9
Db 51 HYNIVTFCC 59

RESULT 3
Q9QDH2
ID Q9QDH2 PRELIMINARY; PRT; 93 AA.
AC Q9QDH2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF187869; AAF13399.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 58; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
Db 51 HYNIVTFCC 59

RESULT 4
Q9QDH4
ID Q9QDH4 PRELIMINARY; PRT; 93 AA.
AC Q9QDH4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF187868; AAF13397.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 58; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
Db 51 HYNIVTFCC 59

RESULT 5
Q9QDH6
ID Q9QDH6 PRELIMINARY; PRT; 93 AA.

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AC Q9QDH6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF187867; AAF13395.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10513 MW; 92C7054341326A1F CRC64;

Query Match 100.0%; Score 58; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
Db 51 HYNIVTFCC 59

RESULT 6
Q9QDH8
ID Q9QDH8 PRELIMINARY; PRT; 93 AA.
AC Q9QDH8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE E7 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF187866; AAF13393.1; -.
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
FT NON TER 93
SQ SEQUENCE 93 AA; 10452 MW; 83281BB2AE2C8A1F CRC64;

Query Match 100.0%; Score 58; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
Db 51 HYNIVTFCC 59

RESULT 7
Q8B5P6
ID Q8B5P6 PRELIMINARY; PRT; 94 AA.
AC Q8B5P6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE E7 oncoprotein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.

```


RA Ponglikitmongkol M., Vaeteewattacharn K.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF469197; AAC015692.1; -;
 DR InterPro; IPR000148; Papvi_E7.

DR Pfam; PF00527; E7; 1.
 FT NON TER 94 94
 SQ SEQUENCE 94 AA; 10555 MW; 7CC3281BB2AE2CBA CRC64;

Query Match 100.0%; Score 58; DB 2; Length 94;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
 Db 51 HYNIVTFCC 59

RESULT 8

VE7_HPV16 STANDARD; PRT; 98 AA.

AC P03129;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE E7 protein.

GN Name=E7;

OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI_TaxID=10581;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=85246220; PubMed=2990099;

RA Seedorf K., Krammer G., Dürst M., Suhai S., Rowekamp W.G.;

RT "Human papillomavirus type 16 DNA sequence.";

RL Virology 145:181-185(1985).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=90218027; PubMed=2157796;

RA Schneider-Maunoury S., Pehau-Arnaut G., Breitburd F., Orth G.;

RT "Expression of the human papillomavirus type 16 genome in SK-v cells,

RT a line derived from a vulvar intraepithelial neoplasia.";

RL J. Gen. Virol. 71:809-817(1990).

RN [3]

RP SEQUENCE FROM N.A.

RA Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Lee H.P.;

RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,

RA Beth-Giraldo E., Giraldo G.;

RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

RN [5]

RP FUNCTION.

RX MEDLINE=88223347; PubMed=2836062;

RA Phelps W.C., Yee C.L., Munger K., Howley P.M.;

RT "The human papillomavirus type 16 E7 gene encodes transactivation and

RT transformation functions similar to those of adenovirus E1A.";

RL Cell 53:539-547(1988).

CC -!

CC FUNCTION: E7 protein has both transforming and trans-activating

CC activities.

CC -----

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CC -----

CC EMBL; K02718; AAA46940.1; -;
 DR EMBL; D00735; BAA00633.1; -;
 DR EMBL; U76411; AAB18962.1; -;

DR EMBL; U76412; AAB18963.1; -;

DR EMBL; U76413; AAB18964.1; -;

DR EMBL; AF003020; AAB70737.1; -;

DR EMBL; AF003023; AAB70740.1; -;

DR EMBL; AF003024; AAB70741.1; -;

DR EMBL; AF003025; AAB70742.1; -;

DR EMBL; AF003026; AAB70743.1; -;

DR FIR; A03688; W7WLHS.

DR InterPro; IPR000148; Papvi_E7.

DR Pfam; PF00527; E7; 1.

KW DNA-binding; Early protein; Oncogene; Trans-acting factor;

FT Transcription regulation.

FT SITE 58 61 C-XX-C motif-1.

FT SITE 91 94 C-XX-C motif-2.

SQ SEQUENCE 98 AA; 11022 MW; 9BD612534CD2C9EB CRC64;

Query Match 100.0%; Score 58; DB 1; Length 98;

Best Local Similarity 100.0%; Pred. No. 0.013; 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9

Db 51 HYNIVTFCC 59

RESULT 9

O11650

ID O11650 PRELIMINARY; PRT; 98 AA.

AC O11650;

DT 01-JUL-1997 (TREMBLrel. 04, Created)

DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE Putative transforming protein E7.

OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI_TaxID=10581;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97407827; PubMed=9264576; DOI=10.1006/gyno.1997.4756;

RA Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang S.B., Chang W.H.,

RA Lee H.P.;

RT "Major sequence variants in E7 gene of human papillomavirus type 16

RT from cervical cancerous and noncancerous lesions of Korean women.";

RL Gynecol. Oncol. 66:275-281(1997).

RN [2]

RP SEQUENCE FROM N.A.

RA Song Y.-S., Kee S.-H., Kim J.-W., Park N.-H., Kang S.-B., Chang W.-H.,

RA Lee H.-P.;

RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Terai M., Ma Z., Burk R.D.;

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=22182962; PubMed=12195358;

RA Chan P.K.S., Lam C.W., Cheng T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,

RA Cheung J.L.K., Xu L.Y., Cheng A.F.;

RT "Human papillomavirus type 16 intratypic variant infection and risk

RT for cervical neoplasia in southern China.";

RL J. Infect. Dis. 186:696-700(2002).

RN [5]

RP SEQUENCE FROM N.A.

RA Terai M., Fu L., Ma Z., Burk R.D.;

RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; U76404; AAC58243.1; -;

DR EMBL; AF472509; AAO15706.1; -;

DR EMBL; AF486326; AAL96631.1; -;

DR EMBL; AF486327; AAL96632.1; -;

DR EMBL; AF486330; AAL96635.1; -;

DR EMBL; AF486331; AAL96636.1; -;

DR EMBL; AF486332; AAL96637.1; -;

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DR EMBL; AF486333; AAL96638.1; -
DR EMBL; AF486334; AAL96639.1; -
DR EMBL; AF486336; AAL96641.1; -
DR EMBL; AF486338; AAL96643.1; -
DR EMBL; AF486346; AAL96651.1; -
DR EMBL; AF486350; AAL96655.1; -
DR EMBL; AF486351; AAL96656.1; -
DR EMBL; AF534061; AAL96656.1; -
DR EMBL; AF534061; AAL96656.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
SQ SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CRC64;

Query Match 100.0%; Score 58; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
Db 51 HYNIVTFCC 59

RESULT 10
O12337
ID O12337 PRELIMINARY; PRT; 98 AA.
AC O12337;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003021; AAB70738.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR SEQUENCE 98 AA; 11056 MW; 19DEB8F14CD2C705 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
Db 51 HYNIVTFCC 59

RESULT 11
O12338
ID O12338 PRELIMINARY; PRT; 98 AA.
AC O12338;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003021; AAB70738.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR SEQUENCE 98 AA; 11045 MW; 9C4F8C534CD76C4B CRC64;

Query Match 100.0%; Score 58; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
Db 51 HYNIVTFCC 59

RESULT 12
O8QRD2
ID O8QRD2 PRELIMINARY; PRT; 98 AA.
AC O8QRD2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486345; AAL96650.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR SEQUENCE 98 AA; 11045 MW; 9C4F8C534CD76C4B CRC64;

Query Match 100.0%; Score 58; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
Db 51 HYNIVTFCC 59

RESULT 13
O8QRD3
ID O8QRD3 PRELIMINARY; PRT; 98 AA.
AC O8QRD3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE E7 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22182962; PubMed=12195358;
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
RA Cheung J.L.K., Xu L.Y., Cheng A.F.;
RT "Human papillomavirus type 16 intratypic variant infection and risk
RT for cervical neoplasia in southern China.";
RL J. Infect. Dis. 186:696-700(2002).
DR EMBL; AF486345; AAL96650.1; -
DR InterPro; IPR000148; Papvi_E7.
DR Pfam; PF00527; E7; 1.
DR SEQUENCE 98 AA; 11045 MW; 9C4F8C534CD76C4B CRC64;

Query Match 100.0%; Score 58; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
Db 51 HYNIVTFCC 59
```

RT for cervical neoplasia in southern China.";
 RL J. Infect. Dis. 186:696-700(2002).
 DR EMBL; AF486344; AAL96649.1; -;
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 SQ SEQUENCE 98 AA; 11021 MW; 9BD6125946D2C3E1 CRC64;

Query Match 100.0%; Score 58; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
 DB 51 HYNIVTFCC 59

RESULT 14

Q8QRD4 Q8QRD4 PRELIMINARY; PRT; 98 AA.
 AC Q8QRD4;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE E7 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22182962; PubMed=12195358;
 RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
 RA Cheung J.L.K., Xu L.Y., Cheng A.P.;
 RT "Human papillomavirus type 16 intratypic variant infection and risk
 RT for cervical neoplasia in southern China.";
 RL J. Infect. Dis. 186:696-700(2002).
 DR EMBL; AF486329; AAL96634.1; -;
 DR InterPro; IPR000148; Papvi_E7.
 DR Pfam; PF00527; E7; 1.
 SQ SEQUENCE 98 AA; 11025 MW; 86E24B234CC3281B CRC64;

Query Match 100.0%; Score 58; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
 DB 51 HYNIVTFCC 59

RESULT 15

Q8VLJ0 Q8VLJ0 PRELIMINARY; PRT; 98 AA.
 AC Q8VLJ0;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE E7 protein.
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jinhu X., Xinxiang W., Yun T.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF461264; AAL66736.1; -;
 DR Pfam; PF00527; E7; 1.
 SQ SEQUENCE 98 AA; 10997 MW; 9BD610834CCEA59B CRC64;

Query Match 100.0%; Score 58; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
 DB 51 HYNIVTFCC 59

Search completed: June 28, 2005, 23:28:15
 Job time : 57.1 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:28:02 ; Search time 11.05 Seconds
(without alignments)
78.367 Million cell updates/sec

Title: US-08-170-344-59
Perfect score: 58
Sequence: 1 HYNIVTFCC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	98	1 W7WLHS	E7 protein - human
2	51	87.9	98	1 W7WL31	E7 protein - human
3	44	75.9	259	2 B4C337	sim region ORF2 pr
4	43	74.1	99	1 W7WL35	E7 protein - human
5	41	70.7	98	1 W7WL11	E7 protein - human
6	41	70.7	322	2 F8B987	protein C5OH11.16
7	40	69.0	98	1 W7WL6	E7 protein - human
8	40	69.0	1101	2 T26919	hypothetical prote
9	39	67.2	337	2 T33793	hypothetical prote
10	39	67.2	405	2 G75027	hypothetical prote
11	38	65.5	184	2 A81561	alanyl-tRNA synthe
12	38	65.5	184	2 G72110	hypothetical prote
13	38	65.5	184	2 D86513	hypothetical prote
14	37	63.8	71	2 T09312	hypothetical prote
15	37	63.8	346	2 T21398	hypothetical prote
16	37	63.8	350	2 T25172	hypothetical prote
17	37	63.8	354	2 T22967	hypothetical prote
18	37	63.8	628	2 S44629	F22B7.10 protein -
19	37	63.8	679	2 T25895	hypothetical prote
20	37	63.8	737	2 F85092	MLH1 protein limpo
21	37	63.8	737	2 T51620	DNA mismatch repai
22	36	62.1	271	2 E89950	hema concentration
23	36	62.1	279	2 S57139	probable membrane
24	36	62.1	403	2 H64861	hypothetical prote
25	36	62.1	445	2 S65734	mitosis-specific c
26	36	62.1	1092	2 H96619	protein T30E16.17
27	35.5	61.2	98	1 W7WLC1	E7 protein - pygmy
28	35	60.3	92	1 S15615	E7 protein - human
29	35	60.3	92	1 S15622	E7 protein - human

ALIGNMENTS

RESULT 1

W7WLHS

E7 protein - human papillomavirus type 16

C:Species: human papillomavirus type 16

C:Date: 28-May-1986 #sequence revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03688; S12367; T10428

R:Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virology 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03688

A:Molecule type: DNA

A:Residues: 1-98 <SEE>

A:Cross-references: UNIPROT:P03129; GB:K02718; NID:g333031; PIDN:AAA46940.1; PID:g333033

R:Barbosa, M.S.; Edmonds, C.; Fisher, C.; Schaller, J.T.; Lowy, D.R.; Vousden, K.H.

EMBO J. 9, 153-160, 1990

A:Title: The region of the HPV E7 oncoprotein homologous to adenovirus E1a and SV40 large

A:Reference number: S12367; MUID:90107938; PMID:2153075

A:Accession: S12367

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-98 <BAR>

R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level

A:Reference number: Z17014; MUID:91162763; PMID:1848319

A:Accession: T10428

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-98 <KEN>

A:Cross-references: EMBL:K02718; NID:g333031; PIDN:AAA46940.1; PID:g333033

C:Genetics:

A:Gene: E7

C:Superfamily: papillomavirus E7 protein

C:Keywords: DNA binding; early protein; transcription regulation; zinc finger

F:58-94/Region: zinc finger CCCC motif

Query Match 100.0%; Score 58; DB 1; Length 98;

Best Local Similarity 100.0%; Pred. No. 0.0067;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9

DB 51 HYNIVTFCC 59

RESULT 2

W7WL31

E7 protein - human papillomavirus type 31

C:Species: human papillomavirus type 31

A:Note: host Homo sapiens (man)

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004

C:Accession: B32444
R:Goldsborough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.
Virology 171, 306-311, 1989
A:Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associated
A:Reference number: A94398; MUID:89299478; PMID:2545036
A:Accession: B32444
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-98 <GOL>
A:Cross-references: UNIPROT:P17387; GB:J04353; NID:G333048; PIDN:AAA46951.1; PID:G459917
C:Comment: This protein may be involved in the oncogenic potential of this virus.
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
F:58-94/Region: zinc finger CCCC motif

Query Match 87.9%; Score 51; DB 1; Length 98;
Best Local Similarity 88.9%; Pred. No. 0.1;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
DB 51 NYNIVTFCC 59

RESULT 3
B46337
slm region ORF2 protein - phase P1
C:Species: phase P1
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C:Accession: B46337
R:Mailou, J.; Dreiseikelmann, B.
Virology 175, 500-507, 1990
A:Title: The sim gene of Escherichia coli phase P1: nucleotide sequence and purification
A:Reference number: A46337; MUID:90223995; PMID:2327075
A:Accession: B46337
A:Molecule type: DNA
A:Status: preliminary
A:Residues: 1-259 <MAI>
A:Cross-references: UNIPROT:Q38410; GB:M34382; NID:G215661; PIDN:AAA32426.1; PID:G215663
C:Superfamily: phase P1 slm region ORF2 protein

Query Match 75.9%; Score 44; DB 2; Length 259;
Best Local Similarity 62.5%; Pred. No. 3.2;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 YNIVTFCC 9
DB 4 FNVITFCC 11

RESULT 4
W7WLJ3
E7 protein - human papillomavirus type 35
C:Species: human papillomavirus type 35
A:Note: host Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: F40824; S36522
R:Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776, 1992
A:Title: The phylogenetic relationship and complete nucleotide sequence of human papillomavirus type 35
A:Reference number: A40824; MUID:92124753; PMID:1310198
A:Accession: F40824
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-99 <MAR>
A:Cross-references: UNIPROT:P27230; GB:M74117; NID:G333050; PIDN:AAA46967.1; PID:G333052
R:Delius, H.; Hofmann, B.
Submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36522
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-99
A:Cross-references: EMBL:X74477; NID:G396997; PIDN:CAA52562.1; PID:G396999
A:Experimental source: strain 35H
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
F:59-95/Region: zinc finger CCCC motif

Query Match 74.1%; Score 43; DB 1; Length 99;
Best Local Similarity 77.8%; Pred. No. 2.3;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
DB 52 NYNIVTSCC 60

RESULT 5
W7WLJ1
E7 protein - human papillomavirus type 11
C:Species: human papillomavirus type 11
C:Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 09-Jul-2004
C:Accession: A03690
R:Dartmann, K.; Schwarz, E.; Gissmann, L.; zur Hausen, H.
Virology 151, 124-130, 1986
A:Title: The nucleotide sequence and genome organization of human papilloma virus type 11
A:Reference number: A94338; MUID:86181601; PMID:3008427
A:Accession: A03690
A:Molecule type: DNA
A:Residues: 1-98 <DAR>
A:Cross-references: UNIPROT:P04020; GB:M14119; NID:G333026; PIDN:AAA46928.1; PID:G496194
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
F:58-94/Region: zinc finger CCCC motif

Query Match 70.7%; Score 41; DB 1; Length 98;
Best Local Similarity 66.7%; Pred. No. 4.9;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
DB 51 HYQILTCCC 59

RESULT 6
F88987
protein C50H11.16 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C:Accession: F88987
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: F88987
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-322 <STO>
A:Cross-references: GB:chr_V; PIDN:AAB65980.1; PID:G2315479; GSPDB:GNO00023; CESP:C50H11.1
A:Gene: C50H11.16
A:Map position: 5
C:Superfamily: Caenorhabditis elegans hypothetical protein C4SH4.12

Query Match 70.7%; Score 41; DB 2; Length 322;
Best Local Similarity 55.6%; Pred. No. 12;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
DB 197 HYVITFCC 205

```

RESULT 7
W7WL6
E7 protein - human papillomavirus type 6b
C:Species: human papillomavirus type 6b
C>Date: 10-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: D20558
R:Schwarz, E.; Durst, M.; Demankowski, C.; Lattermann, O.; Zech, R.; Wolfesberger, E.; Su
EMBO J. 2, 2341-2348, 1983
A:Title: DNA sequence and genome organization of genital human papillomavirus type 6b.
A:Reference number: A90975; MUID:84131949; PMID:6321162
A:Accession: D20558
A:Molecule type: DNA
A:Residues: 1-98 <SCH>
A:Cross-references: UNIPROT:P06464; GB:X00203; NID:G60955; PIDN:CAA25019.1; PID:G60957
C:Superfamily: papillomavirus E7 protein
C:Keywords: DNA binding; early protein; transcription regulation; zinc finger
P:58-94/Region: zinc finger CCCC motif

Query Match 69.0%; Score 40; DB 1; Length 98;
Best Local Similarity 66.7%; Pred. No. 7.3;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
DB 51 HFQIVTCCC 59

RESULT 8
T26919
Hypothetical protein Y45F10B.10 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T26919
R:McMurray, A.
Submitted to the EMBL Data Library, January 1998
A:Reference number: Z20286
A:Accession: T26919
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1101 <WIL>
A:Cross-references: UNIPROT:O62471; EMBL:AL021487; PIDN:CAA16357.1; GSPDB:GN00022; CESP:
A:Experimental source: clone Y45F10B
C:Genetics:
A:Gene: CESP:Y45F10B.10
A:Map position: 4
A:Introns: 217/3; 292/1; 451/3; 556/2; 637/3; 755/3; 823/2; 946/1; 1078/3

Query Match 69.0%; Score 40; DB 2; Length 1101;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
DB 886 HENVVTCCC 894

RESULT 9
T33793
Hypothetical protein Y73C8C.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T33793
R:Bemis, G.; Courtney, L.; Wohldmann, P.
Submitted to the EMBL Data Library, October 1998
A:Description: The sequence of C. elegans cosmid Y73C8C.
A:Reference number: Z21412
A:Accession: T33793
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-337 <BEM>
A:Cross-references: UNIPROT:Q9TXW3; EMBL:AF101318; PIDN:AAC69346.1; GSPDB:GN00023; CESP:
A:Experimental source: strain Bristol N2; clone Y73C8C

```

```

C:Genetics:
A:Gene: CESP:Y73C8C.6
A:Map position: 5
A:Introns: 163/2; 313/1
C:Superfamily: Caenorhabditis elegans hypothetical protein C45H4.12

```

```

Query Match 67.2%; Score 39; DB 2; Length 337;
Best Local Similarity 55.6%; Pred. No. 28;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 HYNIVTFCC 9
DB 209 HYIIIIYCC 217

```

RESULT 10

```

G75027
alanyl-tRNA synthetase related protein PAB1190 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: G75027
R:anonymous, Genoscope
Submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
A:Reference number: A75001
A:Accession: G75027
A>Status: preliminary
A:Accession: G75027
A:Molecule type: DNA
A:Residues: 1-405 <KAW>
A:Cross-references: UNIPROT:Q9UXV2; GB:AJ248288; GB:AL096836; NID:G5458960; PIDN:CAB50661
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB1190

```

```

Query Match 67.2%; Score 39; DB 2; Length 405;
Best Local Similarity 85.7%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 HYNIVTF 7
DB 307 HYNVTF 313

```

RESULT 11

```

A81561
Hypothetical protein CP0588 [imported] - Chlamydia pneumoniae (strain AR39)
C:Species: Chlamydia pneumoniae; Chlamydia pneumoniae
C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
C:Accession: A81561
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, J.
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: A81561
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-184 <REA>
A:Cross-references: GB:AE002217; GB:AE002161; NID:G7189493; PIDN:AAF38406.1; PID:G7189501
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: CP0588

```

```

Query Match 65.5%; Score 38; DB 2; Length 184;
Best Local Similarity 62.5%; Pred. No. 26;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 HYNIVTF 8
DB 51 HYSVTFCC 58

```

RESULT 12

C72110
 hypothetical protein - Chlamydothila pneumoniae (strain CWL029)
 C:Species: Chlamydothila pneumoniae, Chlamydia pneumoniae
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C:Accession: C72110
 R:Kallman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.; Nature Genet. 21, 385-389, 1999
 A:Title: Comparative Genomes of Chlamydia pneumoniae and C. trachomatis.
 A:Reference number: A72000; MUID:99206606; PMID:10192388
 A:Accession: C72110
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-184 <ARN>
 A:Cross-references: UNIPROT:Q9Z904; GB:AE001604; GB:AE001363; NID:g4376438; PIDN:RAD1833
 A:Experimental source: strain CWL029
 C:Genetics:
 A:Gene: CPn0180

Query Match 65.5%; Score 38; DB 2; Length 184;
 Best Local Similarity 62.5%; Pred. No. 26;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYNIVTFC 8
 ||:|
 Db 51 HYSVTFPC 58

RESULT 13
 D86513
 hypothetical protein CPj0180 [imported] - Chlamydothila pneumoniae (strain J138)
 C:Species: Chlamydothila pneumoniae, Chlamydia pneumoniae
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: D86513
 R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is Nucleic Acids Res. 28, 2311-2314, 2000
 A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
 A:Reference number: A86491; MUID:20330349; PMID:10871362
 A:Accession: D86513
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-184 <STO>
 A:Cross-references: UNIPROT:Q9Z904; GB:BA000008; NID:g8978553; PIDN:BAA98390.1; GSPDB:GN
 A:Experimental source: strain J138
 C:Genetics:
 A:Gene: CPj0180

Query Match 65.5%; Score 38; DB 2; Length 184;
 Best Local Similarity 62.5%; Pred. No. 26;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYNIVTFC 8
 ||:|
 Db 51 HYSVTFPC 58

RESULT 14
 T09312
 immediate-early protein homolog - human herpesvirus 6 (strain UI102)
 C:Species: human herpesvirus 6
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C:Accession: T09312
 R:Nicholas, J.; Martin, M.
 J. Virol. 68, 597-610, 1994
 A:Title: Nucleotide sequence analysis of a 38.5-kilobase-pair region of the genome of hu
 A:Reference number: Z16644; MUID:94118404; PMID:8289364
 A:Accession: T09312
 A:Status: preliminary; translated from GB/EMBL/DBBJ
 A:Molecule type: DNA
 A:Residues: 1-71 <NIC>
 A:Cross-references: UNIPROT:Q69042; EMBL:L25528; NID:g451932; PIDN:AAA16725.1; PID:g4519
 C:Genetics:
 A:Gene: BTLF5

Query Match 63.8%; Score 37; DB 2; Length 71;
 Best Local Similarity 55.6%; Pred. No. 18;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 HYNIVTFC 9
 ||:|
 Db 6 HFQIYLFCC 14

RESULT 15
 T21398
 hypothetical protein F26D2.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T21398
 R:McMurray, A.
 submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19418
 A:Accession: T21398
 A:Status: preliminary; translated from GB/EMBL/DBBJ
 A:Molecule type: DNA
 A:Residues: 1-346 <WIL>
 A:Cross-references: UNIPROT:O17841; EMBL:Z81513; PIDN:CAB04174.1; GSPDB:GN000023; CESP:F2
 A:Experimental source: clone F26D2
 C:Genetics:
 A:Gene: CESP:F26D2.1
 A:Map position: 5
 A:Introns: 163/2; 313/1
 C:Superfamily: Caenorhabditis elegans hypothetical protein C4SH4.12

Query Match 63.8%; Score 37; DB 2; Length 346;
 Best Local Similarity 62.5%; Pred. No. 61;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYNIVTFC 8
 ||:|
 Db 209 HYSIIIFC 216

Search completed: June 28, 2005, 23:32:14
 Job time : 12.05 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 04:19:44 ; Search time 116.15 Seconds
(without alignments)
29.797 Million cell updates/sec

Title: US-08-170-344-59
Perfect score: 58
Sequence: 1 HYNIVTFCC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PTCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	9	9	US-09-891-823-9
2	58	100.0	9	14	US-10-365-908-9
3	58	100.0	9	16	US-10-871-138-9
4	58	100.0	15	16	US-10-306-541-61
5	58	100.0	15	16	US-10-306-541-62
6	58	100.0	15	16	US-10-306-541-63
7	58	100.0	15	16	US-10-306-541-64
8	58	100.0	15	16	US-10-306-541-74
9	58	100.0	17	17	US-10-858-384-16
10	58	100.0	19	16	US-10-654-200-56
11	58	100.0	19	17	US-10-484-063-14

12	58	100.0	20	15	US-10-432-455-48	Sequence 48, Appl
13	58	100.0	20	16	US-10-654-200-57	Sequence 57, Appl
14	58	100.0	20	16	US-10-890-526-73	Sequence 73, Appl
15	58	100.0	21	16	US-10-306-541-107	Sequence 107, Appl
16	58	100.0	98	9	US-09-728-466-1	Sequence 1, Appl
17	58	100.0	98	9	US-09-820-765-4	Sequence 4, Appl
18	58	100.0	98	9	US-09-824-017-4	Sequence 4, Appl
19	58	100.0	98	10	US-09-986-118A-4	Sequence 4, Appl
20	58	100.0	98	14	US-10-267-311-8	Sequence 8, Appl
21	58	100.0	98	14	US-10-177-390-8	Sequence 8, Appl
22	58	100.0	98	14	US-10-201-764-19	Sequence 19, Appl
23	58	100.0	98	15	US-10-392-113-29	Sequence 29, Appl
24	58	100.0	98	15	US-10-654-129-4	Sequence 4, Appl
25	58	100.0	98	15	US-10-681-410-19	Sequence 19, Appl
26	58	100.0	98	16	US-10-772-988-3	Sequence 3, Appl
27	58	100.0	98	16	US-10-479-541-5	Sequence 5, Appl
28	58	100.0	98	17	US-10-042-526A-4	Sequence 4, Appl
29	58	100.0	98	17	US-10-657-399-1	Sequence 1, Appl
30	58	100.0	98	17	US-10-858-384-12	Sequence 12, Appl
31	58	100.0	98	17	US-10-484-063-26	Sequence 26, Appl
32	58	100.0	98	17	US-10-343-448-5	Sequence 5, Appl
33	58	100.0	98	17	US-10-679-956-8	Sequence 8, Appl
34	58	100.0	98	17	US-10-367-057-17	Sequence 17, Appl
35	58	100.0	99	15	US-10-115-440-7	Sequence 7, Appl
36	58	100.0	111	16	US-10-472-724-4	Sequence 4, Appl
37	58	100.0	121	14	US-10-267-311-12	Sequence 12, Appl
38	58	100.0	121	17	US-10-679-956-12	Sequence 12, Appl
39	58	100.0	198	14	US-10-267-311-35	Sequence 35, Appl
40	58	100.0	198	17	US-10-679-956-35	Sequence 35, Appl
41	58	100.0	220	13	US-10-000-903-1	Sequence 1, Appl
42	58	100.0	220	13	US-10-000-903-8	Sequence 8, Appl
43	58	100.0	220	17	US-10-899-771-1	Sequence 1, Appl
44	58	100.0	220	17	US-10-899-771-8	Sequence 8, Appl
45	58	100.0	239	13	US-10-000-903-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-09-891-823-9
; Sequence 9, Application US/09891823
; Publication No. US20020110566A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/09/891,823
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-09-891-823-9

Query Match 100.0%; Score 58; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYNIVTFCC 9

Db 1 HYNIVTFCC 9

RESULT 2

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US-10-365-908-9
; Sequence 9, Application US/10365908
; Publication No. US20030170268A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-9

Query Match          100.0%; Score 58; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
Db 1 HYNIVTFCC 9

RESULT 3
US-10-871-138-9
; Sequence 9, Application US/10871138
; Publication No. US20040235741A1
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/871,138
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-871-138-9

Query Match          100.0%; Score 58; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
Db 1 HYNIVTFCC 9

US-10-306-541-61
; Sequence 61, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 61
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-61

Query Match          100.0%; Score 58; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
Db 3 HYNIVTFCC 11

RESULT 5
US-10-306-541-62
; Sequence 62, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 62
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-62

Query Match          100.0%; Score 58; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
Db 4 HYNIVTFCC 12

RESULT 6
US-10-306-541-63
; Sequence 63, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 63
; LENGTH: 15
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; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-63

Query Match      100.0%; Score 58; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
Db 1 HYNIVTFCC 9

RESULT 7
US-10-306-541-64
; Sequence 64, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 64
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-64

Query Match      100.0%; Score 58; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
Db 6 HYNIVTFCC 14

RESULT 8
US-10-306-541-74
; Sequence 74, Application US/10306541
; Publication No. US20040171081A1
; GENERAL INFORMATION:
; APPLICANT: Mittelman, Abraham
; APPLICANT: Kanduc, Darja
; TITLE OF INVENTION: Improved Antigens
; FILE REFERENCE: 12354/4
; CURRENT APPLICATION NUMBER: US/10/306,541
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 74
; LENGTH: 15
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-74

Query Match      100.0%; Score 58; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
Db 7 HYNIVTFCC 15

RESULT 9
US-10-858-384-16
; Sequence 16, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 16
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
; OTHER INFORMATION: for E7 of HPV
US-10-858-384-16

Query Match      100.0%; Score 58; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
Db 8 HYNIVTFCC 16

RESULT 10
US-10-654-200-56
; Sequence 56, Application US/10654200
; Publication No. US20040170606A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology Corporation
; TITLE OF INVENTION: PRODUCTION OF PEPTIDES IN PLANTS AS VIRAL COAT PROTEIN FUSIONS
; FILE REFERENCE: N9739
; CURRENT APPLICATION NUMBER: US/10/654,200
; CURRENT FILING DATE: 2003-09-03
; PRIOR APPLICATION NUMBER: 60/407,795
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: 60/386,921
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 10/457,082
; PRIOR FILING DATE: 2003-06-06
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Human Papilloma Virus
US-10-654-200-56

Query Match      100.0%; Score 58; DB 16; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
Db 8 HYNIVTFCC 16

RESULT 11
US-10-484-063-14
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; Sequence 14, Application US/10484063
 ; Publication No. US20050048467A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SASTRY, K. JAGANNADHA
 ; APPLICANT: TORTOLERO-LUNA, GUILLERMO
 ; APPLICANT: POLLEN, MICHELE
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
 ; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
 ; FILE REFERENCE: UTSC:560US
 ; CURRENT APPLICATION NUMBER: US/10/484,063
 ; CURRENT FILING DATE: 2004-01-16
 ; PRIOR APPLICATION NUMBER: PCT/US02/23198
 ; PRIOR FILING DATE: 2002-07-19
 ; PRIOR APPLICATION NUMBER: 60/306,809
 ; PRIOR FILING DATE: 2001-07-20
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 14
 ; LENGTH: 19
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus
 US-10-484-063-14

Query Match 100.0%; Score 58; DB 17; Length 19;
 Best Local Similarity 100.0%; Pred. No. 0.012; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;

QY 1 HYNIVTFCC 9
 Db 8 HYNIVTFCC 16
 |||||

RESULT 12
 US-10-432-465-48
 ; Sequence 48, Application US/10432465
 ; Publication No. US20040091479A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nieland, John
 ; APPLICANT: Kaufmann, Andreas
 ; APPLICANT: Kather, Angela
 ; APPLICANT: Schinz, Manuela
 ; TITLE OF INVENTION: T-Cell Epitopes of the Papillomavirus L1
 ; TITLE OF INVENTION: Protein and E7 Protein and Their Use in Diagnosis and
 ; TITLE OF INVENTION: Therapy
 ; FILE REFERENCE: 50125/077001
 ; CURRENT APPLICATION NUMBER: US/10/432,465
 ; CURRENT FILING DATE: 2003-12-10
 ; PRIOR APPLICATION NUMBER: PCT/EP01/14037
 ; PRIOR FILING DATE: 2001-11-30
 ; PRIOR APPLICATION NUMBER: DE 10059631.2
 ; PRIOR FILING DATE: 2000-12-01
 ; NUMBER OF SEQ ID NOS: 116
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 48
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus
 US-10-432-465-48

Query Match 100.0%; Score 58; DB 15; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.013; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;

QY 1 HYNIVTFCC 9
 Db 7 HYNIVTFCC 15
 |||||

RESULT 13
 US-10-654-200-57
 ; Sequence 57, Application US/10654200
 ; Publication No. US20040170606A1
 ; GENERAL INFORMATION:

; APPLICANT: Large Scale Biology Corporation
 ; TITLE OF INVENTION: PRODUCTION OF PEPTIDES IN PLANTS AS VIRAL COAT PROTEIN FUSIONS
 ; FILE REFERENCE: N9739
 ; CURRENT APPLICATION NUMBER: US/10/654,200
 ; CURRENT FILING DATE: 2003-09-03
 ; PRIOR APPLICATION NUMBER: 60/407,795
 ; PRIOR FILING DATE: 2002-09-03
 ; PRIOR APPLICATION NUMBER: 60/386,921
 ; PRIOR FILING DATE: 2002-06-07
 ; PRIOR APPLICATION NUMBER: 10/457,082
 ; PRIOR FILING DATE: 2003-06-06
 ; NUMBER OF SEQ ID NOS: 106
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 57
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Human Papilloma Virus
 US-10-654-200-57

Query Match 100.0%; Score 58; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.013; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;

QY 1 HYNIVTFCC 9
 Db 9 HYNIVTFCC 17
 |||||

RESULT 14
 US-10-890-526-73
 ; Sequence 73, Application US/10890526
 ; Publication No. US20040258708A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jochmus, Ingrid
 ; APPLICANT: Nieland, John
 ; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
 ; TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and
 ; TITLE OF INVENTION: Therapy
 ; FILE REFERENCE: 50125/036001
 ; CURRENT APPLICATION NUMBER: US/10/890,526
 ; CURRENT FILING DATE: 2004-07-13
 ; PRIOR APPLICATION NUMBER: US/09/980,177
 ; PRIOR FILING DATE: 2002-05-02
 ; PRIOR APPLICATION NUMBER: PCT/EP00/05006
 ; PRIOR FILING DATE: 2000-05-31
 ; PRIOR APPLICATION NUMBER: DE 19925199.1
 ; PRIOR FILING DATE: 1999-06-01
 ; NUMBER OF SEQ ID NOS: 77
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 73
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus type 16
 US-10-890-526-73

Query Match 100.0%; Score 58; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.013; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;

QY 1 HYNIVTFCC 9
 Db 7 HYNIVTFCC 15
 |||||

RESULT 15
 US-10-306-541-107
 ; Sequence 107, Application US/10306541
 ; Publication No. US20040171081A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mittelman, Abraham
 ; APPLICANT: Kanduc, Darja
 ; TITLE OF INVENTION: Improved Antigens
 ; FILE REFERENCE: 12354/4

```
; CURRENT APPLICATION NUMBER: US/10/306,541
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/333,249
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 107
; LENGTH: 21
; TYPE: PRT
; ORGANISM: human papillomavirus
US-10-306-541-107
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Query Match      100.0%; Score 58; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYNIVTFCC 9
        |||||
Db       7 HYNIVTFCC 15
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Search completed: June 29, 2005, 05:18:17
Job time : 117.15 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:33:36 ; Search time 17.05 Seconds
(without alignments)
39.404 Million cell updates/sec

Title: US-08-170-344-59
Perfect score: 58
Sequence: 1 HYNIVTFCC 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/iaa/5B COMB.pep.*
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6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	9	US-10-365-908-9	Sequence 9, Appli
2	58	100.0	12	US-08-075-541D-27	Sequence 27, Appli
3	58	100.0	13	US-08-075-541D-28	Sequence 28, Appli
4	58	100.0	14	US-08-075-541D-29	Sequence 29, Appli
5	58	100.0	15	US-08-075-541D-18	Sequence 18, Appli
6	58	100.0	17	US-08-075-541D-25	Sequence 25, Appli
7	58	100.0	17	US-09-980-523A-16	Sequence 16, Appli
8	58	100.0	18	US-08-075-541D-30	Sequence 30, Appli
9	58	100.0	19	US-08-075-541D-3	Sequence 3, Appli
10	58	100.0	20	US-08-934-915-48	Sequence 48, Appli
11	58	100.0	20	US-08-934-915-155	Sequence 155, App
12	58	100.0	20	US-08-075-541D-10	Sequence 10, Appli
13	58	100.0	20	US-09-980-177A-73	Sequence 73, Appli
14	58	100.0	25	US-08-075-541D-47	Sequence 47, Appli
15	58	100.0	26	US-08-075-541D-20	Sequence 20, Appli
16	58	100.0	30	US-08-934-915-52	Sequence 52, Appli
17	58	100.0	30	US-09-486-394-3	Sequence 3, Appli
18	58	100.0	32	US-08-075-541D-7	Sequence 7, Appli
19	58	100.0	32	US-08-075-541D-8	Sequence 8, Appli
20	58	100.0	38	US-09-501-097A-6	Sequence 6, Appli
21	58	100.0	98	US-08-406-248-6	Sequence 6, Appli
22	58	100.0	98	US-08-075-541D-42	Sequence 42, Appli
23	58	100.0	98	US-09-382-616A-1	Sequence 1, Appli
24	58	100.0	98	US-08-944-368A-4	Sequence 4, Appli
25	58	100.0	98	US-09-820-764-4	Sequence 4, Appli
26	58	100.0	98	US-09-613-303-8	Sequence 8, Appli
27	58	100.0	98	US-09-566-420-19	Sequence 19, Appli

28	58	100.0	98	4	US-09-986-118A-4	Sequence 4, Appli
29	58	100.0	98	4	US-09-728-466-1	Sequence 1, Appli
30	58	100.0	98	4	US-09-824-017-4	Sequence 4, Appli
31	58	100.0	98	4	US-10-267-311-8	Sequence 8, Appli
32	58	100.0	98	4	US-10-201-764-19	Sequence 19, Appli
33	58	100.0	98	4	US-09-637-746-3	Sequence 3, Appli
34	58	100.0	98	4	US-09-501-097A-7	Sequence 7, Appli
35	58	100.0	98	4	US-09-980-523A-12	Sequence 12, Appli
36	58	100.0	121	4	US-09-613-303-12	Sequence 12, Appli
37	58	100.0	121	4	US-10-267-311-12	Sequence 12, Appli
38	58	100.0	172	3	US-08-860-165-12	Sequence 12, Appli
39	58	100.0	172	3	US-08-860-165-14	Sequence 14, Appli
40	58	100.0	172	3	US-09-359-382-12	Sequence 12, Appli
41	58	100.0	172	3	US-09-359-382-14	Sequence 14, Appli
42	58	100.0	198	4	US-09-613-303-35	Sequence 35, Appli
43	58	100.0	198	4	US-10-267-311-35	Sequence 35, Appli
44	58	100.0	220	3	US-09-485-885-1	Sequence 1, Appli
45	58	100.0	220	3	US-09-485-885-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-10-365-908-9
; Sequence 9, Application US/10365908
; Patent No. 6797491
; GENERAL INFORMATION:
; APPLICANT: Neefe, John R.
; APPLICANT: Boux, Leslie J.
; APPLICANT: Winnett, Mark T.
; APPLICANT: Goldstone, Stephen E.
; APPLICANT: Siegel, Marvin
; TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS TREATMENT
; FILE REFERENCE: 12071-003001
; CURRENT APPLICATION NUMBER: US/10/365,908
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/891,823
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/214,202
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human papilloma virus
US-10-365-908-9

Query Match 100.0%; Score 58; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HYNIVTFCC 9
Db 1 HYNIVTFCC 9
|||||||

RESULT 2
US-08-075-541D-27
; Sequence 27, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA

```
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-075-541D-27

Query Match 100.0%; Score 58; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
Db 1 HYNIVTFCC 9

RESULT 3
US-08-075-541D-28
; Sequence 28, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; FILING DATE: 12-DEC-1990
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-075-541D-28

Query Match 100.0%; Score 58; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
Db 2 HYNIVTFCC 10

RESULT 4
US-08-075-541D-29
; Sequence 29, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
```


; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-29

Query Match 100.0%; Score 58; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0036;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
Db 3 HYNIVTFCC 11

RESULT 5

US-08-075-541D-18
; Sequence 18, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-075-541D-18

Query Match 100.0%; Score 58; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
Db 4 HYNIVTFCC 12

RESULT 6

US-08-075-541D-25

; Sequence 25, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-075-541D-25

Query Match 100.0%; Score 58; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
Db 8 HYNIVTFCC 16

RESULT 7

US-09-980-523A-16
; Sequence 16, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE B6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WOBI AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513

1 PRIOR FILING DATE: 2000-05-31
2 PRIOR APPLICATION NUMBER: FR 99/07012
3 PRIOR FILING DATE: 1999-06-03
4 NUMBER OF SEQ ID NOS: 24
5 SOFTWARE: PatentIn Ver. 2.1
6 SEQ ID NO 16
7 LENGTH: 17
8 TYPE: PRT
9 ORGANISM: Human Papillomavirus
10 US-09-980-523A-16

Query Match 100.0%; Score 58; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
Db 8 HYNIVTFCC 16

RESULT 8

US-08-075-541D-30
1 Sequence 30, Application US/08075541D
2 Patent No. 6183745
3 GENERAL INFORMATION:
4 APPLICANT: TINDLE, ROBERT
5 APPLICANT: FERNANDO, GERMAIN
6 APPLICANT: FRAZER, IAN
7 TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
8 TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
9 NUMBER OF SEQUENCES: 56
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
12 STREET: 1601 MARKET STREET, 36TH FLOOR
13 CITY: PHILADELPHIA
14 STATE: PENNSYLVANIA
15 COUNTRY: USA
16 ZIP: 19103-2398

COMPUTER READABLE FORM:
1 MEDIUM TYPE: Floppy disk
2 COMPUTER: IBM PC compatible
3 OPERATING SYSTEM: PC-DOS/MS-DOS
4 SOFTWARE: PatentIn Release #1.0, Version #1.25
5 CURRENT APPLICATION DATA:
6 APPLICATION NUMBER: US/08/075,541D
7 FILING DATE: 10-JUN-1993
8 CLASSIFICATION: 424
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: AU pk 3876
11 FILING DATE: 12-DEC-1990

PRIOR APPLICATION DATA:
1 APPLICATION NUMBER: pct/au91/00575
2 FILING DATE: 12-DEC-1991
3 ATTORNEY/AGENT INFORMATION:
4 NAME: NADEL, ALAN S
5 REGISTRATION NUMBER: 27,363
6 REFERENCE/DOCKET NUMBER: 8795-4
7 TELECOMMUNICATION INFORMATION:
8 TELEPHONE: 215-567-2991
9 TELEFAX: 215-567-2991

INFORMATION FOR SEQ ID NO: 30:
1 SEQUENCE CHARACTERISTICS:
2 LENGTH: 18 amino acids
3 TYPE: amino acid
4 STRANDEDNESS: single
5 TOPOLOGY: linear
6 MOLECULE TYPE: peptide
7 US-08-075-541D-30

Query Match 100.0%; Score 58; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
Db 7 HYNIVTFCC 15

RESULT 9

US-08-075-541D-3
1 Sequence 3, Application US/08075541D
2 Patent No. 6183745
3 GENERAL INFORMATION:
4 APPLICANT: TINDLE, ROBERT
5 APPLICANT: FERNANDO, GERMAIN
6 APPLICANT: FRAZER, IAN
7 TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
8 TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
9 NUMBER OF SEQUENCES: 56
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
12 STREET: 1601 MARKET STREET, 36TH FLOOR
13 CITY: PHILADELPHIA
14 STATE: PENNSYLVANIA
15 COUNTRY: USA
16 ZIP: 19103-2398

COMPUTER READABLE FORM:
1 MEDIUM TYPE: Floppy disk
2 COMPUTER: IBM PC compatible
3 OPERATING SYSTEM: PC-DOS/MS-DOS
4 SOFTWARE: PatentIn Release #1.0, Version #1.25
5 CURRENT APPLICATION DATA:
6 APPLICATION NUMBER: US/08/075,541D
7 FILING DATE: 10-JUN-1993
8 CLASSIFICATION: 424
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: AU pk 3876
11 FILING DATE: 12-DEC-1990

PRIOR APPLICATION DATA:
1 APPLICATION NUMBER: pct/au91/00575
2 FILING DATE: 12-DEC-1991
3 ATTORNEY/AGENT INFORMATION:
4 NAME: NADEL, ALAN S
5 REGISTRATION NUMBER: 27,363
6 REFERENCE/DOCKET NUMBER: 8795-4
7 TELECOMMUNICATION INFORMATION:
8 TELEPHONE: 215-567-2020
9 TELEFAX: 215-567-2991

INFORMATION FOR SEQ ID NO: 3:
1 SEQUENCE CHARACTERISTICS:
2 LENGTH: 19 amino acids
3 TYPE: amino acid
4 STRANDEDNESS: single
5 TOPOLOGY: linear
6 MOLECULE TYPE: peptide
7 US-08-075-541D-3

Query Match 100.0%; Score 58; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.0047;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYNIVTFCC 9
Db 8 HYNIVTFCC 16

RESULT 10

US-08-934-915-48
1 Sequence 48, Application US/08934915
2 Patent No. 5932412
3 GENERAL INFORMATION:
4 APPLICANT: DILLNER, JOAKIM
5 APPLICANT: DILLNER, LENA
6 APPLICANT: CHENG, HWEE-MING
7 TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
8 TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,

;/ TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
;/ TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
;/ TITLE OF INVENTION: DIAGNOSTIC PURPOSES
;/ NUMBER OF SEQUENCES: 193
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: MASON & ASSOCIATES, P.A.
;/ STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
;/ CITY: CLEARWATER
;/ STATE: FLORIDA
;/ COUNTRY: U.S.A.
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: Windows 3.0
;/ SOFTWARE: Microsoft Word 6.0
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/934,915
;/ FILING DATE: 22-SEP-1997
;/ CLASSIFICATION: 435
;/ PRIOR APPLICATION NUMBER: 07/949,836
;/ FILING DATE:
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: LOUISE A. FOUTCH
;/ REGISTRATION NUMBER: 37,133
;/ REFERENCE/DOCKET NUMBER: 1946.6
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 813-538-3800
;/ TELEFAX: 813-538-3820
;/ TELEX:
;/ INFORMATION FOR SEQ ID NO: 48:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 20 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ US-08-934-915-48
;/
Query Match 100.0%; Score 58; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYNIVTFCC 9
Db 5 HYNIVTFCC 13
;/
RESULT 11
US-08-934-915-155
;/ Sequence 155, Application US/08934915
;/ Patent No. 5932412
;/ GENERAL INFORMATION:
;/ APPLICANT: DILLNER, JOAKIM
;/ APPLICANT: DILLNER, LENA
;/ APPLICANT: CHENG, HWEI-MING
;/ TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
;/ TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
;/ TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
;/ TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
;/ TITLE OF INVENTION: DIAGNOSTIC PURPOSES
;/ NUMBER OF SEQUENCES: 193
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: MASON & ASSOCIATES, P.A.
;/ STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
;/ CITY: CLEARWATER
;/ STATE: FLORIDA
;/ COUNTRY: U.S.A.
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: Windows 3.0
;/ SOFTWARE: Microsoft Word 6.0
;/ CURRENT APPLICATION DATA:

;/ APPLICATION NUMBER: US/08/934,915
;/ FILING DATE: 22-SEP-1997
;/ CLASSIFICATION: 435
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 07/949,836
;/ FILING DATE:
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: LOUISE A. FOUTCH
;/ REGISTRATION NUMBER: 37,133
;/ REFERENCE/DOCKET NUMBER: 1946.6
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 813-538-3800
;/ TELEFAX: 813-538-3820
;/ TELEX:
;/ INFORMATION FOR SEQ ID NO: 155:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 20 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ MOLECULE TYPE: peptide
;/ US-08-934-915-155
;/
Query Match 100.0%; Score 58; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HYNIVTFCC 9
Db 5 HYNIVTFCC 13
;/
RESULT 12
US-08-075-541D-10
;/ Sequence 10, Application US/08075541D
;/ Patent No. 6183745
;/ GENERAL INFORMATION:
;/ APPLICANT: TINDLE, ROBERT
;/ APPLICANT: FERNANDO, GERMAIN
;/ APPLICANT: FRAZER, IAN
;/ TITLE OF INVENTION: SURUNIT PAPILLOMA VIRUS VACCINE AND
;/ TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
;/ NUMBER OF SEQUENCES: 56
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
;/ STREET: 1601 MARKET STREET, 36TH FLOOR
;/ CITY: PHILADELPHIA
;/ STATE: PENNSYLVANIA
;/ COUNTRY: USA
;/ ZIP: 19103-2398
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/075,541D
;/ FILING DATE: 10-JUN-1993
;/ CLASSIFICATION: 424
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: AU pk 3876
;/ FILING DATE: 12-DEC-1990
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: pct/au91/00575
;/ FILING DATE: 12-DEC-1991
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: NADEL, ALAN S
;/ REGISTRATION NUMBER: 27,363
;/ REFERENCE/DOCKET NUMBER: 8795-4
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 215-567-2020
;/ TELEFAX: 215-567-2991
;/ INFORMATION FOR SEQ ID NO: 10:
;/ SEQUENCE CHARACTERISTICS:


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; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-20

Query Match      100.0%; Score 58; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0083;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HYNIVTFCC 9
        |||||
Db      15 HYNIVTFCC 23

Search completed: June 28, 2005, 23:37:54
Job time : 17.05 secs
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:24:19 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-58
Perfect score: 51
Sequence: 1 CCRSRTTR 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	51	100.0	103	2	Q919D6 human papill
2	51	100.0	130	2	Q919B4 human papill
3	51	100.0	130	2	Q919B8 human papill
4	51	100.0	130	2	Q919C0 human papill
5	51	100.0	130	2	Q919C2 human papill
6	51	100.0	130	2	Q919C8 human papill
7	51	100.0	130	2	Q919D0 human papill
8	51	100.0	138	2	Q919D2 human papill
9	51	100.0	143	2	Q919B6 human papill
10	51	100.0	143	2	Q919C4 human papill
11	51	100.0	151	2	O12335 human papill
12	51	100.0	151	2	O12336 human papill
13	51	100.0	151	2	Q76TS0 human papill
14	51	100.0	151	2	Q77816 human papill
15	51	100.0	151	2	Q77816 human papill
16	51	100.0	151	2	Q77J37 human papill
17	51	100.0	151	2	Q77J35 human papill
18	51	100.0	151	2	Q80963 human papill
19	51	100.0	151	2	Q80966 human papill
20	51	100.0	151	2	Q89640 human papill
21	51	100.0	151	2	Q89648 human papill
22	51	100.0	151	2	Q89708 human papill
23	51	100.0	151	2	Q89755 human papill
24	51	100.0	151	2	Q89852 human papill
25	51	100.0	151	2	Q89887 human papill
26	51	100.0	151	2	Q89887 human papill
27	51	100.0	151	2	Q8B564 human papill
28	51	100.0	151	2	Q8BB19 human papill
29	51	100.0	151	2	Q8BB20 human papill
30	51	100.0	151	2	Q8BB21 human papill
31	51	100.0	151	2	Q9W8C3 human papill
32	51	100.0	151	2	Q9W931 human papill

32 51 100.0 151 2 Q9WMP2 human papill
33 51 100.0 151 2 Q9WMP3 human papill
34 51 100.0 151 2 Q9WMP4 human papill
35 51 100.0 151 2 Q9WMP5 human papill
36 51 100.0 158 1 VE6 HPV16
37 51 100.0 158 2 Q8JMU8 human papill
38 51 100.0 158 2 Q8QHNO human papill
39 51 100.0 158 2 Q8QHP5 human papill
40 51 100.0 158 2 Q8QHT0 human papill
41 51 100.0 158 2 Q8QRTD5 human papill
42 51 100.0 158 2 Q8QRTD6 human papill
43 51 100.0 158 2 Q8QRTD7 human papill
44 51 100.0 158 2 Q8QRTD8 human papill
45 51 100.0 158 2 Q8QRTD9 human papill

ALIGNMENTS

RESULT 1

Q919D6 PRELIMINARY; PRT; 103 AA.
AC Q919D6;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404692; AAL01342.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 103 AA; 12422 MW; 6F90CBAF1F25449B CRC64;

Query Match 100.0%; Score 51; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.3; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 CCRSRTTR 9

Db 91 CCRSRTTR 99

RESULT 2

Q919B4 PRELIMINARY; PRT; 130 AA.
AC Q919B4;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).

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DR EMBL; AF404703; AAL01363.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227EEDDC CRC64;

Query Match 100.0%; Score 51; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSRTTR 9
Db 118 CCRSRTTR 126

RESULT 3
Q919B8
ID Q919B8 PRELIMINARY; PRT; 130 AA.
AC Q919B8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404701; AAL01359.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 15775 MW; 92D3C07BF96B092F CRC64;

Query Match 100.0%; Score 51; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSRTTR 9
Db 118 CCRSRTTR 126

RESULT 4
Q919C0
ID Q919C0 PRELIMINARY; PRT; 130 AA.
AC Q919C0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404700; AAL01357.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;

DR EMBL; AF404703; AAL01363.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSRTTR 9
Db 118 CCRSRTTR 126

RESULT 5
Q919C2
ID Q919C2 PRELIMINARY; PRT; 130 AA.
AC Q919C2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404699; AAL01355.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSRTTR 9
Db 118 CCRSRTTR 126

RESULT 6
Q919C8
ID Q919C8 PRELIMINARY; PRT; 130 AA.
AC Q919C8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404696; AAL01349.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;

```



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Query Match      100.0%; Score 51; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSRTTR 9
DB 118 CCRSRTTR 126

RESULT 7
Q919D0 PRELIMINARY; PRT; 130 AA.
AC Q919D0;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404695; AAL01347.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR Pfam; PF00518; E6; 1.
DR NON_TER 1
FT SEQUENCE 130 AA; 15735 MW; 9EPB30BEDCA21AF3 CRC64;
SQ

Query Match      100.0%; Score 51; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSRTTR 9
DB 118 CCRSRTTR 126

RESULT 8
Q919D2 PRELIMINARY; PRT; 138 AA.
AC Q919D2;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404694; AAL01345.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR Pfam; PF003677; F:DNA binding; IEA.
DR NON_TER 1
FT SEQUENCE 138 AA; 16696 MW; 481E5AEA90895FC2 CRC64;
SQ

Query Match      100.0%; Score 51; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.4;

QY 1 CCRSRTTR 9
DB 118 CCRSRTTR 126

RESULT 9
Q919B6 PRELIMINARY; PRT; 143 AA.
AC Q919B6;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404702; AAL01361.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR Pfam; PF003677; F:DNA binding; IEA.
DR NON_TER 1
FT SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;
SQ

Query Match      100.0%; Score 51; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSRTTR 9
DB 131 CCRSRTTR 139

RESULT 10
Q919C4 PRELIMINARY; PRT; 143 AA.
AC Q919C4;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404698; AAL01353.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR Pfam; PF00518; E6; 1.
DR NON_TER 1
FT SEQUENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;
SQ

Query Match      100.0%; Score 51; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSRTTR 9
```

Db 131 CCRSRTTR 139
|||||

RESULT 11

O12335 PRELIMINARY; PRT; 151 AA.
AC O12335
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003015; AAB70732.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18238 MW; BEF32A8B016CC88B CRC64;

Query Match 100.0%; Score 51; DB 2; Length 151;

Best Local Similarity 100.0%; Pred. No. 0.43; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSRTTR 9
|||||

RESULT 12

O12336 PRELIMINARY; PRT; 151 AA.
AC O12336
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003016; AAB70733.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;

Query Match 100.0%; Score 51; DB 2; Length 151;

Best Local Similarity 100.0%; Pred. No. 0.43; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSRTTR 9
|||||

Db 139 CCRSRTTR 147

RESULT 13

Q76TSO PRELIMINARY; PRT; 151 AA.
AC Q76TSO
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34114; AAA91661.1; -;
DR EMBL; U34125; AAA91672.1; -;
DR EMBL; U34130; AAA91677.1; -;
DR EMBL; U34131; AAA91678.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 151;

Best Local Similarity 100.0%; Pred. No. 0.43; Mismatches 9; Conservative 0; Indels 0; Gaps 0;

QY 1 CCRSRTTR 9
|||||

RESULT 14

Q7816 PRELIMINARY; PRT; 151 AA.
AC Q7816
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388056; CAB45104.1; -;
DR EMBL; AJ388061; CAB45114.1; -;
DR EMBL; AJ388066; CAB45124.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.

```

DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18334 MW; FF8F2A2FCBBA6C02 CRC64;

Query Match      100.0%; Score 51; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSSTRR 9
DB 139 CCRSSTRR 147

RESULT 15
Q77E16
ID Q77E16 PRELIMINARY; PRT; 151 AA.
AC Q77E16;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 oncoprotein (E6 protein).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus
OC NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AF469197; AAO15691.1; -.
DR EMBL; AJ388063; CAB45118.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18304 MW; 0F312A9BDBA6CF1F CRC64;

Query Match      100.0%; Score 51; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSSTRR 9
DB 139 CCRSSTRR 147

```

Search completed: June 28, 2005, 23:28:13
Job time : 55.1 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:28:02 ; Search time 11.05 Seconds
(without alignments)
78.367 Million cell updates/sec

Title: US-08-170-344-58
Perfect score: 51
Sequence: 1 CCRSRTTR 9
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	51	100.0	158	1	W6WLHS	protein E6 - human
2	38	74.5	98	2	I54366	dopamine D4 recept
3	37	72.5	212	2	T47947	hypothetical prote
4	37	72.5	389	2	T23167	hypothetical prote
5	37	72.5	849	1	T09349	S-receptor kinase
6	36	70.6	214	2	D84899	hypothetical prote
7	35	68.6	114	2	D72600	hypothetical prote
8	35	68.6	152	2	T34649	hypothetical prote
9	35	68.6	229	2	S60454	glucose starvation
10	35	68.6	303	2	AE3504	tryptophan synthas
11	35	68.6	371	2	G97530	probable zinc-bind
12	35	68.6	414	2	T45639	hypothetical prote
13	35	68.6	640	2	T08179	LRG5 protein - Chl
14	35	68.6	826	2	C96694	hypothetical prote
15	34	66.7	48	2	S29973	protamine 1 - guin
16	34	66.7	141	2	C70575	probable PPE prote
17	34	66.7	222	2	T26209	hypothetical prote
18	34	66.7	321	2	A58458	isopenicillin N sy
19	34	66.7	409	2	C97527	hypothetical prote
20	34	66.7	438	2	T14494	hypothetical prote
21	34	66.7	811	2	E97040	phage related prot
22	34	66.7	1548	2	S34583	serine proteinase
23	33.5	65.7	49	2	S00228	protamine - horse
24	33.5	65.7	49	2	S02007	protamine 1 - rabb
25	33.5	65.7	51	1	HSWS81	protamine - mouse
26	33.5	65.7	51	2	S03997	protamine 1 - rat
27	33.5	65.7	206	2	T01788	aminoglycoside 6'-
28	33.5	65.7	451	2	H84479	probable PttA-like
29	33	64.7	105	2	T27719	hypothetical prote

ALIGNMENTS

RESULT 1

W6WLHS
protein E6 - human papillomavirus type 16
C:Species: human papillomavirus type 16
C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C:Accession: A03682; T10427
R:Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Roweckamp, W.G.
Virology 145, 181-185, 1985
A:Title: Human papillomavirus type 16 DNA sequence.
A:Reference number: A22355; MUID:85246220; PMID:2990099
A:Accession: A03682
A:Molecule type: DNA
A:Residues: 1-158 <SEE>
A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level
A:Reference number: Z17014; MUID:91162763; PMID:1848319
A:Accession: T10427
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-158 <KEN>
A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
C:Genetics:
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:37-73/Region: zinc finger CCCC motif
F:110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 51; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCRSRTTR 9
Db 146 CCRSRTTR 154

RESULT 2

I54366
dopamine D4 receptor - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: I54366
R:Nothen, M.M.; Cichon, S.; Hemmer, S.; Hebebrand, J.; Remschmidt, H.; Lehmkuhl, G.; Pour
Hum. Mol. Genet. 3, 2207-2212, 1994
A:Title: Human dopamine D4 receptor gene: frequent occurrence of a null allele and obser
A:Reference number: I54366; MUID:95187162; PMID:7881421
A:Accession: I54366
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

hypothetical protein APE1268 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: D72600
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Maeda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; KDNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: D72600
A:Molecule type: DNA
A:Status: preliminary
A:Residues: 1-114 <KAW>
A:Cross-references: UNIPROT:Q9YCI9; DDBJ:AP000061; NID:95104821; PIDN:BAA80258.1; PID:dl
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE1268

Query Match 68.6%; Score 35; DB 2; Length 114;
Best Local Similarity 75.0%; Pred. No. 63;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCRSRR 8
||| :
DB 10 CCRSLR 17

RESULT 8
T34649
hypothetical protein SC1A11.02c - Streptomyces coelicolor (fragment)
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C:Accession: T34649
R:Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, January 1999
A:Reference number: Z11551
A:Accession: T34649
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-152 <SE>
A:Cross-references: EMBL:AL035205; PIDN:CAA22742.1; GSPDB:GN00070; SCOEDB:SC1A11.02c
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC1A11.02c

Query Match 68.6%; Score 35; DB 2; Length 152;
Best Local Similarity 85.7%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCRSRT 7
||| :
DB 19 CCRSRT 25

RESULT 9
S60454
glucose starvation-induced protein (clone pzSS3) - maize (fragment)
C:Species: Zea mays (maize)
C:Date: 27-Apr-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: S60454; S49585
R:Chevallier, C.; Bourgeois, E.; Pradet, A.; Raymond, P. Plant Mol. Biol. 28, 473-485, 1995
A:Title: Molecular cloning and characterization of six cDNAs expressed during glucose starvation
A:Reference number: S60453; MUID:95359405; PMID:7632917
A:Accession: S60454
A:Molecule type: mRNA
A:Residues: 1-229 <CHE>
A:Cross-references: UNIPROT:Q41855; EMBL:X82617; NID:9575425; PIDN:CAA57939.1; PID:95754

Query Match 68.6%; Score 35; DB 2; Length 229;
Best Local Similarity 55.6%; Pred. No. 96;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCRSRT 7
||| :
DB 19 CCRSRT 25

RESULT 10
A3504
tryptophan synthase (SC 4.2.1.20) [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002
C:Accession: AE3504
R:DelVecchio, V.G.; Kaputal, V.; Redkar, R.J.; Patra, G.; Muler, C.; Los, T.; Ivanova, P.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letessier, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AE3504
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-303 <KUR>
A:Cross-references: GB:AE008917; PIDN:AAL53200.1; PID:gl7984074; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI2019
A:Map position: 1
C:Superfamily: tryptophan synthase alpha chain; tryptophan synthase alpha chain homology
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 68.6%; Score 35; DB 2; Length 303;
Best Local Similarity 85.7%; Pred. No. 11e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCRSRT 7
||| :
DB 11 CCRSRT 17

RESULT 11
G97530
probable zinc-binding alcohol dehydrogenase [imported] - Agrobacterium tumefaciens (strain 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004)
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: G97530
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: G97530
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-371 <KUR>
A:Cross-references: UNIPROT:Q8UFI9; GB:AE007869; PIDN:AAK87200.1; PID:g15156478; GSPDB:G97530
C:Genetics:
A:Gene: AGR_C_2601
A:Map position: circular chromosome
C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

Query Match 68.6%; Score 35; DB 2; Length 371;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCRSRT 7
||| :
DB 3 CCRSRT 9

RESULT 12
T45639
hypothetical protein F13112.80 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T45639

R:Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa
submitted to the Protein Sequence Database, November 1999

A:Reference number: Z23010
A:Accession: T45639
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-414 <CHO>
A:Cross-references: UNIPROT:Q9SD70; EMBL:AL133292
A:Experimental source: cultivar Columbia; BAC clone F13112
C:Genetics:
A:Map position: 3
A:Note: F13112.80
C:Superfamily: Arabidopsis thaliana hypothetical protein At2g23160

Query Match 68.6%; Score 35; DB 2; Length 414;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSSRT 7
DB 149 CCKSKT 155

RESULT 13

T08179
LRG5 protein - Chlamydomonas reinhardtii
C:Species: Chlamydomonas reinhardtii
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
R:Gloeckner, G.; Beck, C.F.
C:Accession: T08179
submitted to the EMBL Data Library, October 1996
A:Description: Molecular characterization of a gene (LRG5) involved in blue light signal
A:Reference number: Z16399
A:Accession: T08179
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-640 <GLO>
A:Cross-references: UNIPROT:Q96397; EMBL:U73817; NID:G1644369; PID:G1644370
C:Genetics:
A:Gene: LRG5

Query Match 68.6%; Score 35; DB 2; Length 640;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCRSSRTR 9
DB 576 CCRGSRAPR 584

RESULT 14

C96694
hypothetical protein F1019.10 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: C96694
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: C96694

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-826 <STO>
A:Cross-references: UNIPROT:Q9FZH7; GB:AE005173; NID:G9755453; PIDN:AAF98214.1; GSPDB:GN
C:Genetics:

A:Gene: F1019.10
A:Map position: 1

Query Match 68.6%; Score 35; DB 2; Length 826;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCRSSRTR 9
DB 499 CCRETKEK 507

RESULT 15

S29973
protamine 1 - guinea pig
C:Species: Cavia porcellus (guinea pig)
C>Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004
C:Accession: S29973; S29972
R:Oliva, R.

submitted to the EMBL Data Library, December 1991

A:Reference number: S29972
A:Accession: S29973
A:Molecule type: DNA
A:Residues: 1-48 <OLI>
A:Cross-references: UNIPROT:P35304; EMBL:Z11545; NID:G49561; PIDN:CAA77644.1; PID:G49562
A:Accession: S29972
A:Molecule type: mRNA
A:Residues: 1-48 <OLW>
A:Cross-references: EMBL:Z11544; NID:G49563; PIDN:CAA77643.1; PID:G49564
C:Genetics:
A:Introns: 35/1
A:Superfamily: sperm histone
C:Keywords: chromosomal protein; DNA binding; DNA condensation; nucleosome core; spermat

Query Match 66.7%; Score 34; DB 2; Length 48;
Best Local Similarity 66.7%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCRSSRTR 9
DB 36 CCRRYTRR 44

Search completed: June 28, 2005, 23:32.13
Job time : 11.05 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 04:19:44 ; Search time 116.15 Seconds
(without alignments)
29.797 Million cell updates/sec

Title: US-08-170-344-58

Perfect score: 51

Sequence: 1 CCRSRRTR 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	20	17	US-10-938-249-513
2	51	100.0	24	16	US-10-476-570-44
3	51	100.0	151	14	US-10-177-390-6
4	51	100.0	151	17	US-10-484-063-20
5	51	100.0	151	17	US-10-484-063-27
6	51	100.0	158	17	US-10-858-384-2
7	51	100.0	158	17	US-10-367-057-16
8	51	100.0	171	16	US-10-472-724-2
9	51	100.0	266	9	US-09-367-309A-1
10	51	100.0	273	13	US-10-000-903-4
11	51	100.0	273	17	US-10-899-771-4

12	51	100.0	292	13	US-10-000-903-10	Sequence 10, Appl
13	51	100.0	292	17	US-10-899-771-10	Sequence 10, Appl
14	51	100.0	371	13	US-10-000-903-6	Sequence 6, Appl
15	51	100.0	371	17	US-10-899-771-6	Sequence 6, Appl
16	51	100.0	390	13	US-10-000-903-14	Sequence 14, Appl
17	51	100.0	390	17	US-10-899-771-14	Sequence 14, Appl
18	46	90.2	16	17	US-10-484-063-9	Sequence 9, Appl
19	46	90.2	245	15	US-10-425-114-65786	Sequence 65786, A
20	41	80.4	35	15	US-10-424-599-245237	Sequence 245237,
21	41	80.4	66	16	US-10-425-115-330614	Sequence 330614,
22	41	80.4	111	16	US-10-437-963-135875	Sequence 135875,
23	41	80.4	124	16	US-10-425-115-294572	Sequence 294572,
24	41	80.4	177	15	US-10-425-114-42217	Sequence 42217, A
25	40	78.4	20	11	US-09-855-604-101	Sequence 101, App
26	40	78.4	43	10	US-09-397-945-213	Sequence 93, Appl
27	40	78.4	43	15	US-10-653-595-213	Sequence 213, App
28	40	78.4	43	15	US-10-425-115-304230	Sequence 304230,
29	40	78.4	87	14	US-10-425-115-33740	Sequence 33740, A
30	40	78.4	87	16	US-10-425-115-267647	Sequence 267647,
31	40	78.4	93	16	US-10-767-701-49570	Sequence 49570, A
32	40	78.4	132	16	US-10-437-963-154099	Sequence 154099,
33	40	78.4	137	10	US-09-397-945-211	Sequence 211, App
34	40	78.4	137	15	US-10-653-595-211	Sequence 211, App
35	39	76.5	102	16	US-10-425-115-184761	Sequence 184761,
36	39	76.5	134	16	US-10-437-963-181461	Sequence 181461,
37	39	76.5	146	16	US-10-437-963-148427	Sequence 148427,
38	39	76.5	251	16	US-10-437-963-160036	Sequence 160036,
39	39	76.5	478	16	US-10-437-963-115033	Sequence 115033,
40	39	76.5	686	16	US-10-437-963-196497	Sequence 196497,
41	39	76.5	118	15	US-10-424-599-182287	Sequence 182287,
42	38	74.5	125	15	US-10-425-114-67214	Sequence 67214, A
43	38	74.5	51	16	US-10-437-963-160782	Sequence 160782,
44	37	72.5	66	16	US-10-437-963-175256	Sequence 175256,
45	37	72.5				

ALIGNMENTS

RESULT 1

US-10-938-249-513
; Sequence 513, Application US/10938249
; Publication No. US20050037969A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Hematopoietic
; FILE REFERENCE: 020054-001130US
; CURRENT APPLICATION NUMBER: US/10/938,249
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: US/09/724,553
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/134,114
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,117
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/134,118
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/160,860
; PRIOR FILING DATE: 1999-10-21
; PRIOR APPLICATION NUMBER: US 60/162,498
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/170,453
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: US 60/176,195
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/182,296
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: US 60/196,267
; PRIOR FILING DATE: 2000-04-11

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 543
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 513

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: HPV16 E6 C-terminal

US-10-938-249-513

Query Match 100.0%; Score 51; DB 17; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.75; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCRSRTTR 9

Db 8 CCRSRTTR 16

RESULT 2

US-10-476-570-44

; Sequence 44, Application US/10476570

; Publication No. US20040170644A1

; GENERAL INFORMATION:

; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE

; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE

; APPLICANT: MAILLERS, Bernard

; APPLICANT: BOURGAULT-VILLADA, Isabelle

; APPLICANT: POUVELLE-MORATILLE, Sandra

; APPLICANT: GUILLET, Jean-Gerard

; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7

; TITLE OF INVENTION: Papillomavirus proteins and uses thereof

; FILE REFERENCE: 45636-5071-US

; CURRENT APPLICATION NUMBER: US/10/476,570

; CURRENT FILING DATE: 2003-11-04

; PRIOR APPLICATION NUMBER: PCT/FR02/01533

; PRIOR FILING DATE: 2002-05-03

; PRIOR APPLICATION NUMBER: FR 01 05980

; PRIOR FILING DATE: 2001-05-04

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 44

; LENGTH: 24

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: Description of the artificial sequence: peptide E6 135-158

US-10-476-570-44

Query Match

Best Local Similarity 100.0%; Score 51; DB 16; Length 24;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCRSRTTR 9

Db 12 CCRSRTTR 20

RESULT 3

US-10-177-390-6

; Sequence 6, Application US/10177390

; Publication No. US20030143743A1

; GENERAL INFORMATION:

; APPLICANT: Schuler, Gerold

; APPLICANT: N.V. Antwerp Innovatiecentrum

; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear

; TITLE OF INVENTION: Polynucleotides by Electroporation

; FILE REFERENCE: 021505wo/JH/ml

; CURRENT APPLICATION NUMBER: US/10/177,390

; CURRENT FILING DATE: 2002-06-20

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6

; LENGTH: 151

; TYPE: PRT

; ORGANISM: Human papillomavirus type 16

US-10-177-390-6

Query Match

Best Local Similarity 100.0%; Score 51; DB 14; Length 151;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCRSRTTR 9

Db 139 CCRSRTTR 147

RESULT 4

US-10-484-063-20

; Sequence 20, Application US/10484063

; Publication No. US20050048467A1

; GENERAL INFORMATION:

; APPLICANT: SASTRY, K. JAGANNADHA

; APPLICANT: TORTOLERO-LUNA, GUILLERMO

; APPLICANT: FOLLEN, MICHELE

; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED

; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN

; FILE REFERENCE: UTSC:560US

; CURRENT APPLICATION NUMBER: US/10/484,063

; CURRENT FILING DATE: 2004-01-16

; PRIOR APPLICATION NUMBER: PCT/US02/23198

; PRIOR FILING DATE: 2002-07-19

; PRIOR APPLICATION NUMBER: 60/306,809

; PRIOR FILING DATE: 2001-07-20

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 20

; LENGTH: 151

; TYPE: PRT

; ORGANISM: Human papillomavirus

US-10-484-063-20

Query Match

Best Local Similarity 100.0%; Score 51; DB 17; Length 151;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCRSRTTR 9

Db 139 CCRSRTTR 147

RESULT 5

US-10-484-063-27

; Sequence 27, Application US/10484063

; Publication No. US20050048467A1

; GENERAL INFORMATION:

; APPLICANT: SASTRY, K. JAGANNADHA

; APPLICANT: TORTOLERO-LUNA, GUILLERMO

; APPLICANT: FOLLEN, MICHELE

; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED

; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN

; FILE REFERENCE: UTSC:560US

; CURRENT APPLICATION NUMBER: US/10/484,063

; CURRENT FILING DATE: 2004-01-16

; PRIOR APPLICATION NUMBER: PCT/US02/23198

; PRIOR FILING DATE: 2002-07-19

; PRIOR APPLICATION NUMBER: 60/306,809

; PRIOR FILING DATE: 2001-07-20

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 27

; LENGTH: 151

; TYPE: PRT

; ORGANISM: Human papillomavirus type 16

US-10-484-063-27

Query Match 100.0%; Score 51; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSRRTR 9
DB 139 CCRSRRTR 147

RESULT 6

US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US2005033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match 100.0%; Score 51; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSRRTR 9
DB 146 CCRSRRTR 154

RESULT 7

US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Ananda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match 100.0%; Score 51; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSRRTR 9

DB 146 CCRSRRTR 154

RESULT 8

US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match 100.0%; Score 51; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSRRTR 9
DB 151 CCRSRRTR 159

RESULT 9

US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 51; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSRRTR 9
DB 146 CCRSRRTR 154

RESULT 10
US-10-000-903-4
; Sequence 4, Application US/10000903

Search completed: June 29, 2005, 05:18:16
Job time : 116.15 secs

US-10-000-903-6
; Sequence 6, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-6

Query Match 100.0%; Score 51; DB 13; Length 371;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSSRTR 9
DB 252 CCRSSRTR 260

RESULT 15
US-10-899-771-6
; Sequence 6, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and E6E7 fusion from Human papilloma
; OTHER INFORMATION: virus type 16)
US-10-899-771-6

Query Match 100.0%; Score 51; DB 17; Length 371;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSSRTR 9
DB 252 CCRSSRTR 260

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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:33:36 ; Search time 17.05 Seconds
(without alignments)
39.404 Million cell updates/sec

Title: US-08-170-344-58
Perfect score: 51
Sequence: 1 CCRSRRTR 9

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	21	US-08-934-915-167	Sequence 167, Appl
2	51	100.0	158	US-09-980-523A-2	Sequence 2, Appl
3	51	100.0	162	US-08-316-239B-3	Sequence 3, Appl
4	51	100.0	162	US-08-316-239B-4	Sequence 4, Appl
5	51	100.0	172	US-08-860-165-12	Sequence 12, Appl
6	51	100.0	172	US-09-359-382-12	Sequence 12, Appl
7	51	100.0	266	US-08-860-165-10	Sequence 10, Appl
8	51	100.0	266	US-09-359-382-10	Sequence 10, Appl
9	51	100.0	266	US-09-367-309A-1	Sequence 1, Appl
10	51	100.0	273	US-09-485-885-4	Sequence 4, Appl
11	51	100.0	292	US-09-485-885-10	Sequence 10, Appl
12	51	100.0	371	US-09-485-885-6	Sequence 6, Appl
13	51	100.0	390	US-09-485-885-14	Sequence 14, Appl
14	44	86.3	171	US-08-311-731A-381	Sequence 381, Appl
15	41	80.4	230	US-09-252-991A-33122	Sequence 33122, A
16	40	78.4	109	US-09-252-991A-22787	Sequence 22787, A
17	39	76.5	953	US-09-252-991A-30039	Sequence 30039, A
18	38	74.5	161	US-09-270-767-36971	Sequence 36971, A
19	38	74.5	161	US-09-270-767-52188	Sequence 52188, A
20	38	74.5	350	US-09-949-016-8615	Sequence 8615, Ap
21	38	74.5	719	US-09-252-991A-30052	Sequence 30052, A
22	37	72.5	87	US-09-252-991A-25071	Sequence 25071, A
23	37	72.5	93	US-09-287-849-35	Sequence 35, Appl
24	37	72.5	109	US-09-252-991A-29444	Sequence 29444, A
25	37	72.5	113	US-09-252-991A-29076	Sequence 29076, A
26	37	72.5	136	US-09-252-991A-21156	Sequence 21156, A
27	37	72.5	138	US-09-489-039A-12930	Sequence 12930, A

28	37	72.5	145	4	US-09-252-991A-23153	Sequence 23153, A
29	37	72.5	154	4	US-09-252-991A-30960	Sequence 30960, A
30	37	72.5	207	4	US-09-270-767-32689	Sequence 32689, A
31	37	72.5	207	4	US-09-270-767-47906	Sequence 47906, A
32	37	72.5	309	4	US-09-252-991A-27914	Sequence 27914, A
33	37	72.5	633	4	US-09-252-991A-26229	Sequence 26229, A
34	36	70.6	141	4	US-10-141-645-72	Sequence 72, Appl
35	36	70.6	141	4	US-10-141-645-73	Sequence 73, Appl
36	36	70.6	153	4	US-09-252-991A-26200	Sequence 26200, A
37	36	70.6	156	4	US-09-252-991A-24413	Sequence 24413, A
38	36	70.6	249	4	US-09-252-991A-28972	Sequence 28972, A
39	36	70.6	331	4	US-09-252-991A-24140	Sequence 24140, A
40	36	70.6	446	4	US-09-252-991A-21791	Sequence 21791, A
41	35	68.6	87	4	US-09-252-991A-21662	Sequence 21662, A
42	35	68.6	90	4	US-09-270-767-34477	Sequence 34477, A
43	35	68.6	90	4	US-09-270-767-49694	Sequence 49694, A
44	35	68.6	143	4	US-09-252-991A-31561	Sequence 31561, A
45	35	68.6	144	4	US-09-949-016-11102	Sequence 11102, A

ALIGNMENTS

RESULT 1
US-08-934-915-167
; Sequence 167, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 167:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-167
Query Match 100.0%; Score 51; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.22;

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSRTTR 9
Db 9 CCRSRTTR 17

RESULT 2
US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WOBI AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 51; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSRTTR 9
Db 146 CCRSRTTR 154

RESULT 3
US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNNE-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 100.0%; Score 51; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNNE-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 100.0%; Score 51; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSRTTR 9
Db 146 CCRSRTTR 154

RESULT 4
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNNE-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 100.0%; Score 51; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CCRSRTTR 9
| | | | |
Db 146 CCRSRTTR 154

RESULT 5
US-08-860-165-12
; Sequence 12, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12

Query Match 100.0%; Score 51; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSRTTR 9
| | | | |
Db 84 CCRSRTTR 92

RESULT 6
US-09-359-382-12
; Sequence 12, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-12

Query Match 100.0%; Score 51; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.2; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSRTTR 9
| | | | |
Db 84 CCRSRTTR 92

RESULT 7
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 51; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.7; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSRTTR 9
| | | | |
Db 146 CCRSRTTR 154

RESULT 8
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 51; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.7; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSRTTR 9

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; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-10

Query Match 100.0%; Score 51; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSRTTR 9
Db 271 CCRSRTTR 279

RESULT 12
US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-6

Query Match 100.0%; Score 51; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSRTTR 9
Db 252 CCRSRTTR 260

RESULT 13
US-09-485-885-14
; Sequence 14, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:

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; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; US-09-367-309A-1

Query Match 100.0%; Score 51; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSRTTR 9
Db 146 CCRSRTTR 154

RESULT 10
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-4

Query Match 100.0%; Score 51; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCRSRTTR 9
Db 252 CCRSRTTR 260

RESULT 11
US-09-485-885-10

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; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
; ORGANISM: Homo sapien
US-09-485-885-14

Query Match      100.0%; Score 51; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCRSRRTR 9
Db      271 CCRSRRTR 279

RESULT 14
US-08-311-731A-381
; Sequence 381, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 381:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 171 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium leprae

US-08-311-731A-381
Query Match      86.3%; Score 44; DB 4; Length 171;
Best Local Similarity 88.9%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCRSRRTR 9
Db      4 CCRSSYTRR 12

RESULT 15
US-09-252-991A-33122
; Sequence 33122, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 33122
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-33122

Query Match      80.4%; Score 41; DB 4; Length 230;
Best Local Similarity 87.5%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCRSRRTR 8
Db      97 CCRSCRTR 104

Search completed: June 28, 2005, 23:37:54
Job time : 17.05 secs
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:24:19 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-57
Perfect score: 50
Sequence: 1 SCCRSSRTR 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	20	2	Q36978 human papill
2	50	100.0	103	2	Q919D6 human papill
3	50	100.0	130	2	Q919B4 human papill
4	50	100.0	130	2	Q919B8 human papill
5	50	100.0	130	2	Q919C0 human papill
6	50	100.0	130	2	Q919C2 human papill
7	50	100.0	130	2	Q919C8 human papill
8	50	100.0	130	2	Q919D0 human papill
9	50	100.0	138	2	Q919D2 human papill
10	50	100.0	143	2	Q919B6 human papill
11	50	100.0	143	2	Q919C4 human papill
12	50	100.0	151	2	O12335 human papill
13	50	100.0	151	2	O12336 human papill
14	50	100.0	151	2	Q76TS0 human papill
15	50	100.0	151	2	Q778I6 human papill
16	50	100.0	151	2	Q77E16 human papill
17	50	100.0	151	2	Q77JC7 human papill
18	50	100.0	151	2	Q77ZJ5 human papill
19	50	100.0	151	2	Q80963 human papill
20	50	100.0	151	2	Q80966 human papill
21	50	100.0	151	2	Q89640 human papill
22	50	100.0	151	2	Q89648 human papill
23	50	100.0	151	2	Q89708 human papill
24	50	100.0	151	2	Q89755 human papill
25	50	100.0	151	2	Q89852 human papill
26	50	100.0	151	2	Q89887 human papill
27	50	100.0	151	2	Q8B564 human papill
28	50	100.0	151	2	Q8B564 human papill
29	50	100.0	151	2	Q8B564 human papill
30	50	100.0	151	2	Q8B564 human papill
31	50	100.0	151	2	Q8B564 human papill

32 50 100.0 151 2 Q9W931 human papill
33 50 100.0 151 2 Q9WMP2 human papill
34 50 100.0 151 2 Q9WMP3 human papill
35 50 100.0 151 2 Q9WMP4 human papill
36 50 100.0 151 2 Q9WMP5 human papill
37 50 100.0 158 1 V86 HPV16
38 50 100.0 158 2 Q8JMU8 human papill
39 50 100.0 158 2 Q8QHN0 human papill
40 50 100.0 158 2 Q8QHP5 human papill
41 50 100.0 158 2 Q8QHT0 human papill
42 50 100.0 158 2 Q8QRD5 human papill
43 50 100.0 158 2 Q8QRD6 human papill
44 50 100.0 158 2 Q8QRD7 human papill
45 50 100.0 158 2 Q8QRD8 human papill

ALIGNMENTS

RESULT 1

Q36978 PRELIMINARY; PRT; 20 AA.
AC Q36978;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DE Mutant early transforming protein E6 (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RA Alvarez-Salas L.M., Wilczynski S.P., Burger R.A., Monk B.J.,
RA DiPaolo J.A.;
RT "Polymorphism of the HPV-16 E6 gene of cervical carcinoma."
RL Int. J. Oncol. 7:261-266(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Alvarez-Salas L.M., DiPaolo J.A.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF014803; AAB87615.1;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2357 MW; 23DA169D44DF4932 CRC64;

Query Match 100.0%; Score 50; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.099;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCCRSSRTR 9
Db 12 SCCRSSRTR 20

RESULT 2

Q919D6 PRELIMINARY; PRT; 103 AA.
ID Q919D6;
AC Q919D6;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404692; AAL01342.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR PFam; PF00518; E6; 1.
DR NON_TER 1
SQ SEQUENCE 103 AA; 12422 MW; 6F90CBAP1F25449B CRC64;

Query Match 100.0%; Score 50; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCCRSTR 9
Db 90 SCCRSTR 98

RESULT 3
Q919B4
ID Q919B4 PRELIMINARY; PRT; 130 AA.
AC Q919B4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404703; AAL01363.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR PFam; PF00518; E6; 1.
DR NON_TER 1
SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227EBDDC CRC64;

Query Match 100.0%; Score 50; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCCRSTR 9
Db 117 SCCRSTR 125

RESULT 4
Q919B8
ID Q919B8 PRELIMINARY; PRT; 130 AA.
AC Q919B8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16

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RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404701; AAL01359.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR PFam; PF00518; E6; 1.
DR NON_TER 1
SQ SEQUENCE 130 AA; 15775 MW; 92D3C07BF96B092F CRC64;

Query Match 100.0%; Score 50; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCCRSTR 9
Db 117 SCCRSTR 125

RESULT 5
Q919C0
ID Q919C0 PRELIMINARY; PRT; 130 AA.
AC Q919C0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404700; AAL01357.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR PFam; PF00518; E6; 1.
DR NON_TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 50; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCCRSTR 9
Db 117 SCCRSTR 125

RESULT 6
Q919C2
ID Q919C2 PRELIMINARY; PRT; 130 AA.
AC Q919C2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404699; AAL01355.1; -.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:33:36 ; Search time 17.05 Seconds
(without alignments)
39.404 Million cell updates/sec

Title: US-08-170-344-56
Perfect score: 54
Sequence: 1 CMSCRSR 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA*
1: /cgm2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgm2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgm2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgm2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgm2_6/ptodata/1/iaa/PTCUS_COMB.pep.*
6: /cgm2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	54	100.0	21	US-08-934-915-167	Sequence 167, App
2	54	100.0	158	US-09-980-523A-2	Sequence 2, Appl
3	54	100.0	162	US-08-316-239B-3	Sequence 3, Appl
4	54	100.0	162	US-08-316-239B-4	Sequence 4, Appl
5	54	100.0	172	US-08-860-165-12	Sequence 12, Appl
6	54	100.0	172	US-09-359-382-12	Sequence 12, Appl
7	54	100.0	266	US-08-860-165-10	Sequence 10, Appl
8	54	100.0	266	US-09-359-382-10	Sequence 10, Appl
9	54	100.0	266	US-09-367-309A-1	Sequence 1, Appl
10	54	100.0	273	US-09-485-885-4	Sequence 4, Appl
11	54	100.0	292	US-09-485-885-10	Sequence 10, Appl
12	54	100.0	371	US-09-485-885-6	Sequence 6, Appl
13	54	100.0	390	US-09-485-885-14	Sequence 14, Appl
14	42	77.8	154	US-09-252-991A-25612	Sequence 25612, A
15	42	77.8	389	US-09-252-991A-31590	Sequence 31590, A
16	39	72.2	141	US-10-141-645-72	Sequence 72, Appl
17	39	72.2	141	US-10-141-645-73	Sequence 73, Appl
18	39	72.2	208	US-09-252-991A-25609	Sequence 25609, A
19	38	70.4	206	US-09-252-991A-22768	Sequence 22768, A
20	38	70.4	449	US-09-252-991A-23908	Sequence 23908, A
21	37	66.5	113	US-09-252-991A-29076	Sequence 29076, A
22	36	66.7	17	US-08-469-260A-425	Sequence 425, App
23	36	66.7	17	US-08-488-446-425	Sequence 425, App
24	36	66.7	17	US-08-467-344A-425	Sequence 425, App
25	36	66.7	17	US-08-424-550B-425	Sequence 425, App
26	36	66.7	73	US-09-270-767-35372	Sequence 35372, A
27	36	66.7	73	US-09-270-767-50589	Sequence 50589, A

28	36	66.7	84	4	US-09-198-452A-1276	Sequence 1276, Ap
29	36	66.7	329	4	US-09-252-991A-18070	Sequence 18070, A
30	36	66.7	953	4	US-09-252-991A-30039	Sequence 30039, A
31	35	64.8	44	4	US-09-270-767-38870	Sequence 38870, A
32	35	64.8	44	4	US-09-270-767-54087	Sequence 54087, A
33	35	64.8	147	4	US-09-252-991A-17724	Sequence 17724, A
34	35	64.8	167	4	US-09-252-991A-20715	Sequence 20715, A
35	35	64.8	168	4	US-09-252-991A-32502	Sequence 32502, A
36	35	64.8	187	4	US-09-673-395A-148	Sequence 148, App
37	35	64.8	197	4	US-09-252-991A-32518	Sequence 32518, A
38	35	64.8	210	4	US-09-198-452A-641	Sequence 641, App
39	35	64.8	218	4	US-09-252-991A-31933	Sequence 31933, A
40	35	64.8	245	4	US-09-270-767-35096	Sequence 35096, A
41	35	64.8	245	4	US-09-270-767-50313	Sequence 50313, A
42	35	64.8	248	4	US-09-252-991A-29249	Sequence 29249, A
43	35	64.8	287	4	US-09-949-016-9099	Sequence 9099, Ap
44	35	64.8	292	3	US-09-439-313-532	Sequence 532, App
45	35	64.8	292	4	US-09-636-215-532	Sequence 532, App

ALIGNMENTS

RESULT 1
US-08-934-915-167
; Sequence 167, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 167:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-167
Query Match 100.0%; Score 54; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.38;

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CMSCCRSSR 9
Db 6 CMSCCRSSR 14

RESULT 2
US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO81 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 54; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CMSCCRSSR 9
Db 143 CMSCCRSSR 151

RESULT 3
US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 100.0%; Score 54; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CMSCCRSSR 9
Db 143 CMSCCRSSR 151

RESULT 4
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 100.0%; Score 54; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 100.0%; Score 54; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CMSCCRSSR 9
Db 143 CMSCCRSSR 151

RESULT 4
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 100.0%; Score 54; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:24:19 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-56
Perfect score: 54
Sequence: 1 CMSCCRSSR 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	103	2 Q919D6	Q919d6 human papil
2	54	100.0	130	2 Q919B4	Q919b4 human papil
3	54	100.0	130	2 Q919B8	Q919b8 human papil
4	54	100.0	130	2 Q919C0	Q919c0 human papil
5	54	100.0	130	2 Q919C2	Q919c2 human papil
6	54	100.0	130	2 Q919C8	Q919c8 human papil
7	54	100.0	130	2 Q919D0	Q919d0 human papil
8	54	100.0	138	2 Q919D2	Q919d2 human papil
9	54	100.0	143	2 Q919B6	Q919b6 human papil
10	54	100.0	143	2 Q919C4	Q919c4 human papil
11	54	100.0	151	2 O12335	O12335 human papil
12	54	100.0	151	2 O12336	O12336 human papil
13	54	100.0	151	2 Q76TS0	Q76ts0 human papil
14	54	100.0	151	2 Q77E16	Q77e16 human papil
15	54	100.0	151	2 Q77E16	Q77e16 human papil
16	54	100.0	151	2 Q77JC7	Q77jc7 human papil
17	54	100.0	151	2 Q77ZJ5	Q77zj5 human papil
18	54	100.0	151	2 Q80963	Q80963 human papil
19	54	100.0	151	2 Q80966	Q80966 human papil
20	54	100.0	151	2 Q89640	Q89640 human papil
21	54	100.0	151	2 Q89648	Q89648 human papil
22	54	100.0	151	2 Q89708	Q89708 human papil
23	54	100.0	151	2 Q89755	Q89755 human papil
24	54	100.0	151	2 Q89852	Q89852 human papil
25	54	100.0	151	2 Q89887	Q89887 human papil
26	54	100.0	151	2 Q8B564	Q8b564 human papil
27	54	100.0	151	2 Q8B564	Q8b564 human papil
28	54	100.0	151	2 Q8BB19	Q8bb19 human papil
29	54	100.0	151	2 Q8BB20	Q8bb20 human papil
30	54	100.0	151	2 Q8BB21	Q8bb21 human papil
31	54	100.0	151	2 Q9W8C3	Q9w8c3 human papil
			151	2 Q9W931	Q9w931 human papil

32	54	100.0	151	2 Q9WMP2	Q9wmp2 human papil
33	54	100.0	151	2 Q9WMP3	Q9wmp3 human papil
34	54	100.0	151	2 Q9WMP4	Q9wmp4 human papil
35	54	100.0	151	2 Q9WMP5	Q9wmp5 human papil
36	54	100.0	158	1 V56 HPV16	P03126 human papil
37	54	100.0	158	2 Q8JMU8	Q8jmu8 human papil
38	54	100.0	158	2 Q8QHNO	Q8qhn0 human papil
39	54	100.0	158	2 Q8QHPS	Q8qhp5 human papil
40	54	100.0	158	2 Q8QHT0	Q8qht0 human papil
41	54	100.0	158	2 Q8QRD5	Q8qrd5 human papil
42	54	100.0	158	2 Q8QRD6	Q8qrd6 human papil
43	54	100.0	158	2 Q8QRD7	Q8qrd7 human papil
44	54	100.0	158	2 Q8QRD8	Q8qrd8 human papil
45	54	100.0	158	2 Q8QRD9	Q8qrd9 human papil

ALIGNMENTS

RESULT 1

Q919D6 PRELIMINARY; PRT; 103 AA.
AC Q919D6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404692; AAL01342.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 103 AA; 12422 MW; 6F90CBAF1F25449B CRC64;

Query Match Similarity 100.0%; Score 54; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.81; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 CMSCCRSSR 9

Db 88 CMSCCRSSR 96

RESULT 2

Q919B4 PRELIMINARY; PRT; 130 AA.
AC Q919B4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).

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DR EMBL; AF404703; AAL01363.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227BEDDC CRC64;
Query Match 100.0%; Score 54; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CMSCCRSSR 9
Db 115 CMSCCRSSR 123

RESULT 3
Q919B8 ID Q919B8 PRELIMINARY; PRT; 130 AA.
AC Q919B8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404701; AAL01359.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15775 MW; 92D3C07BF96B092F CRC64;
Query Match 100.0%; Score 54; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CMSCCRSSR 9
Db 115 CMSCCRSSR 123

RESULT 4
Q919C0 ID Q919C0 PRELIMINARY; PRT; 130 AA.
AC Q919C0
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404700; AAL01357.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
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DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
Query Match 100.0%; Score 54; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CMSCCRSSR 9
Db 115 CMSCCRSSR 123

RESULT 5
Q919C2 ID Q919C2 PRELIMINARY; PRT; 130 AA.
AC Q919C2
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404699; AAL01355.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
Query Match 100.0%; Score 54; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CMSCCRSSR 9
Db 115 CMSCCRSSR 123

RESULT 6
Q919C8 ID Q919C8 PRELIMINARY; PRT; 130 AA.
AC Q919C8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404696; AAL01349.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;
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DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;
Query Match 100.0%; Score 50; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SCCRSTR 9
DB 117 SCCRSTR 125
RESULT 7
Q919C8 PRELIMINARY; PRT; 130 AA.
AC Q919C8;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040696; AAL01349.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;
Query Match 100.0%; Score 50; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SCCRSTR 9
DB 117 SCCRSTR 125
RESULT 8
Q919D0 PRELIMINARY; PRT; 130 AA.
AC Q919D0;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040695; AAL01347.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR Pfam; PF00518; E6; 1.
DR

FT NON TER 1
SQ SEQUENCE 130 AA; 15735 MW; 9EFB30EEDCA21AF3 CRC64;
Query Match 100.0%; Score 50; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SCCRSTR 9
DB 117 SCCRSTR 125
RESULT 9
Q919D2 PRELIMINARY; PRT; 138 AA.
AC Q919D2;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040694; AAL01345.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 138 AA; 16696 MW; 481ESA9A0895FC2 CRC64;
Query Match 100.0%; Score 50; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SCCRSTR 9
DB 125 SCCRSTR 133
RESULT 10
Q919B6 PRELIMINARY; PRT; 143 AA.
AC Q919B6;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040702; AAL01361.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;

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Query Match      100.0%; Score 50; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SCCRSSRTR 9
      |||||
Db      130 SCCRSSRTR 138

RESULT 11
Q919C4      PRELIMINARY;      PRT;      143 AA.
AC O12335;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874 (2002).
DR EMBL; AF404698; AAL01353.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;

Query Match      100.0%; Score 50; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SCCRSSRTR 9
      |||||
Db      130 SCCRSSRTR 138

RESULT 12
Q12335      PRELIMINARY;      PRT;      151 AA.
AC O12335;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208 (1997).
DR EMBL; AF003015; AAB70732.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18238 MW; BEF32A8B016CC88B CRC64;

Query Match      100.0%; Score 50; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SCCRSSRTR 9
      |||||
Db      138 SCCRSSRTR 146

RESULT 13
Q12336      PRELIMINARY;      PRT;      151 AA.
AC O12336;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208 (1997).
DR EMBL; AF003016; AAB70733.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;

Query Match      100.0%; Score 50; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SCCRSSRTR 9
      |||||
Db      138 SCCRSSRTR 146

RESULT 14
Q76TS0      PRELIMINARY;      PRT;      151 AA.
AC Q76TS0;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34114; AAA91661.1; -.
DR EMBL; U34125; AAA91672.1; -.
DR EMBL; U34130; AAA91677.1; -.
DR EMBL; U34131; AAA91678.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.

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DR GO:0003677; F:DNA binding; IEA.
DR InterPro:IPR001334; E6.
DR Pfam:PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;

Query Match      100.0%; Score 50; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. NO. 0.65;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCCRSTR 9
Db 138 SCCRSTR 146

RESULT 15
Q77816
ID Q77816 PRELIMINARY; PRT; 151 AA.
AC Q77816;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Heimerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388056; CAB45104.1; -
DR EMBL; AJ388061; CAB45114.1; -
DR EMBL; AJ388066; CAB45124.1; -
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro:IPR001334; E6.
DR Pfam:PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18334 MW; FF8F2A2FCBBA6C02 CRC64;

Query Match      100.0%; Score 50; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. NO. 0.65;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCCRSTR 9
Db 138 SCCRSTR 146
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Job time : 55.1 secs

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A;Accession: S09235
A;Molecule type: mRNA
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A;Cross-references: UNIPROT:P17696; EMBL:X51467; NID:962761; PIDN:CAA35830.1; PID:962762
R;Joubert, F.J.; Viljoen, C.C.
Hoppe-Seyler's Z. Physiol. Chem. 360, 1075-1090, 1979
A;Title: The amino-acid sequence of the subunits of two reduced and S-carboxymethylated
A;Reference number: A91679; MUID:80070629; PMID:511106
A;Accession: A01679
A;Molecule type: protein
A;Residues: 22-83, N' <JOU>
C;Comment: The functional molecule consists of two nonidentical chains, C9S3 chain 1 and
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C;Keywords: heterodimer; venom
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Qy 1 CMSCRSR 9
Db 75 CVKCKTDR 83
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S11926
cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) - Ruminococcus flavefaciens
N;Alternate names: cellobioextrinase
C;Species: Ruminococcus flavefaciens
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 04-Mar-2000
C;Accession: S11926; S08674
R;Wang, W.; Thomson, J.A.
Mol. Gen. Genet. 222, 265-269, 1990
A;Title: Nucleotide sequence of the cels gene encoding a cellobioextrinase of Ruminococcus
A;Reference number: S11926; MUID:91109710; PMID:2129544
A;Accession: S11926
A;Molecule type: DNA
A;Residues: 1-352 <WAN>
A;Cross-references: EMBL:X51944
C;Genetics:
A;Gene: cels
A;Start codon: TTG
C;Superfamily: Ruminococcus flavefaciens cellulose 1,4-beta-cellobiosidase
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
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Best Local Similarity 55.6%; Pred. No. 2.8e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 CMSCRSR 9
Db 43 CRTCKRKR 51
RESULT 9
T20315
hypothetical protein D1081.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20315
R;Dobson, R.
submitted to the EMBL Data Library, July 1996
A;Reference number: Z19256
A;Accession: T20315
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-421 <WIL>

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A;Experimental source: clone D1081
C;Genetics:
A;Gene: CESP:D1081.4
A;Map position: 1
A;Introns: 25/2; 40/3; 72/3; 114/3; 139/3; 167/3; 227/2; 326/1; 352/3; 376/2; 403/3
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Best Local Similarity 71.4%; Pred. No. 3.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CMSCRSR 7
Db 181 CLSCCAS 187
RESULT 10
T12494
hypothetical protein DKFZp434C091.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: T12494
R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z17525
A;Accession: T12494
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-438 <POU>
A;Cross-references: UNIPROT:Q9Y4N9; EMBL:AL080170
A;Experimental source: adult testis; clone DKFZp434C091
C;Genetics:
A;Note: DKFZp434C091.1
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Best Local Similarity 55.6%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CMSCRSR 9
Db 8 CGGCCRAAR 16
RESULT 11
T48256
hypothetical protein T1E22.110 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48256
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,
submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24489
A;Accession: T48256
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-651 <BEV>
A;Cross-references: UNIPROT:Q9LZ90; EMBL:AL162874
A;Experimental source: cultivar Columbia; BAC clone T1E22
C;Genetics:
A;Map position: 5
A;Note: T1E22.110
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Best Local Similarity 62.5%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CMSCRSR 8
Db 448 CSACCROS 455
RESULT 12

Tl0666
 hypothetical protein F6E21.40 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C:Accession: Tl0666
 R:Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancroft, I.; et al. 1999
 submitted to the Protein Sequence Database, June 1999
 A:Reference number: Z16533
 A:Accession: Tl0666
 A:Molecule type: DNA
 A:Residues: 1-670 <BEV>
 A:Cross-references: UNIPROT:O9M090; EMBL:AL049914; GSPDB:GN00062; ATSP:F6E21.40
 A:Experimental source: cultivar Columbia; BAC clone F6E21
 C:Genetics:
 A:Map position: 4
 A:Introns: 47/3; 87/1; 123/3; 203/3; 230/3; 255/3; 284/3; 305/1; 335/3; 347/3; 370/3; 390/3
 C:Superfamily: Schizosaccharomyces pombe negative regulator of mitosis skb1

Query Match 66.7%; Score 36; DB 2; Length 670;
 Best Local Similarity 85.7%; Pred. No. 4e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 M5CCRS 8
 Db 141 V5CCRS 147

RESULT 13
 T26577
 hypothetical protein Y2H9A.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T26577
 R:Wallis, J.
 submitted to the EMBL Data Library, December 1998
 A:Reference number: Z20237
 A:Accession: T26577
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-898 <WIL>
 A:Cross-references: EMBL:AL021448; PIDN:CAA16276.1; GSPDB:GN00023; CESP:Y2H9A.1
 A:Experimental source: clone Y2H9A
 C:Genetics:
 A:Gene: CESP:Y2H9A.1
 A:Map position: 5
 A:Introns: 95/1; 180/3; 372/2; 473/3; 590/3; 724/3; 768/3; 819/3

Query Match 66.7%; Score 36; DB 2; Length 898;
 Best Local Similarity 71.4%; Pred. No. 4.6e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CM5CCRS 7
 Db 322 CKTCCRS 328

RESULT 14
 T49879
 hypothetical protein T211.110 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
 C:Accession: T49879
 R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Leach, G.; et al. 2000
 submitted to the Protein Sequence Database, April 2000
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 A:Experimental source: cultivar Columbia; BAC clone T211
 C:Genetics:

A:Gene: ATSP:T211.110
 A:Map position: 5
 A:Introns: 411/2; 456/2; 504/3; 604/3; 685/3; 731/3; 768/3; 786/1; 822/3; 865/3; 895/3

Query Match 66.7%; Score 36; DB 2; Length 1075;
 Best Local Similarity 71.4%; Pred. No. 5.1e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CM5CCRS 7
 Db 252 CLSCTS 258

RESULT 15
 H84839
 late embryogenesis abundant M10 protein [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: H84839
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Axtell, E.K.; et al. 1999
 submitted to the EMBL Data Library, December 1999
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Accession: H84839
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-107 <STO>
 A:Cross-references: UNIPROT:O81483; GB:AE002093; NID:g3894195; PIDN:AACT78544.1; GSPDB:GNI84839
 C:Genetics:
 A:Gene: At2g41280
 A:Map position: 2

Query Match 64.8%; Score 35; DB 2; Length 107;
 Best Local Similarity 71.4%; Pred. No. 2.1e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CM5CCRS 7
 Db 81 CIYCCRS 87

Search completed: June 28, 2005, 23:32:12
 Job time : 12.05 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 04:19:44 ; Search time 116.15 Seconds
(without alignments)
29.797 Million cell updates/sec

Title: US-08-170-344-56
Perfect score: 54
Sequence: 1 CMSCCRSR 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	16	17 US-10-484-063-9	Sequence 9, Appli
2	54	100.0	20	17 US-10-938-249-513	Sequence 513, App
3	54	100.0	24	16 US-10-476-570-44	Sequence 4, Appl
4	54	100.0	151	14 US-10-177-390-6	Sequence 20, Appl
5	54	100.0	151	17 US-10-484-063-20	Sequence 27, Appl
6	54	100.0	151	17 US-10-484-063-27	Sequence 2, Appli
7	54	100.0	158	17 US-10-858-384-2	Sequence 16, Appl
8	54	100.0	158	17 US-10-367-057-16	Sequence 2, Appli
9	54	100.0	171	16 US-10-472-724-2	Sequence 1, Appli
10	54	100.0	266	9 US-09-367-309A-1	Sequence 4, Appli
11	54	100.0	273	13 US-10-000-903-4	

12	54	100.0	273	17 US-10-899-771-4	Sequence 4, Appli
13	54	100.0	292	13 US-10-000-903-10	Sequence 10, Appl
14	54	100.0	292	17 US-10-899-771-10	Sequence 10, Appl
15	54	100.0	371	13 US-10-000-903-6	Sequence 6, Appli
16	54	100.0	371	17 US-10-899-771-6	Sequence 6, Appli
17	54	100.0	390	13 US-10-000-903-14	Sequence 14, Appl
18	54	100.0	390	17 US-10-899-771-14	Sequence 14, Appl
19	49	90.7	10	17 US-10-484-063-10	Sequence 10, Appl
20	41	75.9	118	16 US-10-425-115-214017	Sequence 124017,
21	41	75.9	341	16 US-10-437-963-192283	Sequence 192283,
22	41	75.9	377	16 US-10-739-930-11071	Sequence 11071, A
23	41	75.9	747	15 US-10-425-114-38701	Sequence 38701, A
24	41	75.9	817	15 US-10-425-114-38290	Sequence 38290, A
25	41	75.9	941	15 US-10-424-599-210074	Sequence 210074,
26	41	75.9	11300	16 US-10-250-304A-2	Sequence 2, Appli
27	40	74.1	43	10 US-09-397-945-213	Sequence 213, App
28	40	74.1	43	15 US-10-653-595-213	Sequence 213, App
29	40	74.1	61	9 US-09-864-781-36259	Sequence 36259, A
30	40	74.1	137	10 US-09-397-945-211	Sequence 211, App
31	40	74.1	137	15 US-10-653-595-211	Sequence 211, App
32	40	74.1	210	15 US-10-424-599-214145	Sequence 214145,
33	40	74.1	245	15 US-10-425-114-65786	Sequence 65786, A
34	40	74.1	1345	13 US-10-108-605-249	Sequence 249, App
35	40	74.1	1368	15 US-10-263-929-149	Sequence 149, App
36	40	74.1	1368	17 US-10-494-921-57	Sequence 57, Appl
37	39	72.2	50	14 US-10-050-882-89	Sequence 89, Appl
38	39	72.2	67	17 US-10-808-187-1685	Sequence 1685, Ap
39	39	72.2	141	14 US-10-141-645-72	Sequence 72, Appl
40	39	72.2	141	14 US-10-141-645-73	Sequence 73, Appl
41	38	70.4	45	17 US-10-808-187-193	Sequence 193, App
42	38	70.4	70	15 US-10-424-599-202673	Sequence 202673,
43	38	70.4	73	16 US-10-425-115-295668	Sequence 295668,
44	38	70.4	93	16 US-10-425-115-265982	Sequence 265982,
45	38	70.4	136	16 US-10-425-115-357597	Sequence 357597,

ALIGNMENTS

RESULT 1
US-10-484-063-9
; Sequence 9, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-9

Query Match 100.0%; Score 54; DB 17; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CMSCCRSR 9
Db 6 CMSCCRSR 14

Query Match 100.0%; Score 54; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CMSCCRSSR 9
Db 136 CMSCCRSSR 144

RESULT 6
US-10-484-063-27
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-15
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-484-063-27

Query Match 100.0%; Score 54; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CMSCCRSSR 9
Db 136 CMSCCRSSR 144

RESULT 7
US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGALT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match 100.0%; Score 54; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CMSCCRSSR 9
Db 143 CMSCCRSSR 151

RESULT 8
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: Curaseq1ist version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match 100.0%; Score 54; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CMSCCRSSR 9
Db 143 CMSCCRSSR 151

RESULT 9
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match 100.0%; Score 54; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CMSCCRSSR 9
Db 148 CMSCCRSSR 156

RESULT 10

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US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JTM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match          100.0%; Score 54; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CMSCCRSSR 9
Db 143 CMSCCRSSR 151

RESULT 11
US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4

Query Match          100.0%; Score 54; DB 13; Length 273;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CMSCCRSSR 9
Db 249 CMSCCRSSR 257

RESULT 12
US-10-899-771-4
; Sequence 4, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Dalemans, Wilfried L.J.

US-09-367-309A-1
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein (protein D from Haemophilus
; OTHER INFORMATION: Influenzae B and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-4

Query Match          100.0%; Score 54; DB 17; Length 273;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CMSCCRSSR 9
Db 249 CMSCCRSSR 257

RESULT 13
US-10-000-903-10
; Sequence 10, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-10

Query Match          100.0%; Score 54; DB 13; Length 292;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CMSCCRSSR 9
Db 268 CMSCCRSSR 276

RESULT 14
US-10-899-771-10
; Sequence 10, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Dalemans, Wilfried L.J.
```

APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; FILE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein (Clyta from Streptococcus
; OTHER INFORMATION: pneumoniae and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-10

Query Match 100.0%; Score 54; DB 17; Length 292;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CMSCCRSR 9
Db 268 CMSCCRSR 276

RESULT 15

US-10-000-903-6
; Sequence 6, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-6

Query Match 100.0%; Score 54; DB 13; Length 371;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CMSCCRSR 9
Db 249 CMSCCRSR 257

Search completed: June 29, 2005, 05:18:16
Job time : 117.15 secs

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Qy      1 CMSCCRSSR 9
Db      81 CMSCCRSSR 89

RESULT 7
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860.165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match      100.0%; Score 54; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CMSCCRSSR 9
Db      143 CMSCCRSSR 151

RESULT 8
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359.382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860.165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match      100.0%; Score 54; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CMSCCRSSR 9
Db      81 CMSCCRSSR 151

RESULT 5
US-08-860-165-12
; Sequence 12, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860.165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12

Query Match      100.0%; Score 54; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CMSCCRSSR 9
Db      81 CMSCCRSSR 89

RESULT 6
US-09-359-382-12
; Sequence 12, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359.382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860.165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-12

Query Match      100.0%; Score 54; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-10

Query Match      100.0%; Score 54; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CMSCCRSR 9
Db 268 CMSCCRSR 276

RESULT 12
US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-6

Query Match      100.0%; Score 54; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CMSCCRSR 9
Db 249 CMSCCRSR 257

RESULT 13
US-09-485-885-14
; Sequence 14, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:

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; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-10

Query Match      100.0%; Score 54; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CMSCCRSR 9
Db 143 CMSCCRSR 151

RESULT 10
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-4

Query Match      100.0%; Score 54; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CMSCCRSR 9
Db 249 CMSCCRSR 257

RESULT 11
US-09-485-885-10

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Qy 1 TTDLVCYEQ 9
Db 19 TTDLVCYEQ 27

RESULT 11
US-08-075-541D-42
; Sequence 42, Application US/08075541D
; Patent No. 6183745
; GENERAL INFORMATION:
; APPLICANT: TINDLE, ROBERT
; APPLICANT: FERNANDO, GERMAIN
; APPLICANT: FRAZER, IAN
; TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
; TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZ JACOBS & NADEL, P.C.
; STREET: 1601 MARKET STREET, 36TH FLOOR
; CITY: PHILADELPHIA
; STATE: PENNSYLVANIA
; COUNTRY: USA
; ZIP: 19103-2398
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/075,541D
; FILING DATE: 10-JUN-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU Pk 3876
; FILING DATE: 12-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: pct/au91/00575
; FILING DATE: 12-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: NADEL, ALAN S
; REGISTRATION NUMBER: 27,363
; REFERENCE/DOCKET NUMBER: 8795-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-567-2020
; TELEFAX: 215-567-2991
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-075-541D-42

Query Match 100.0%; Score 53; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLVCYEQ 9
Db 19 TTDLVCYEQ 27

RESULT 12
US-09-382-616A-1
; Sequence 1, Application US/09382616A
; Patent No. 620746
; GENERAL INFORMATION:
; APPLICANT: Fisher, Christopher
; APPLICANT: He, Wanxia
; TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
; FILE REFERENCE: 28341/6216

; CURRENT APPLICATION NUMBER: US/09/382,616A
; CURRENT FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/382,616
; PRIOR FILING DATE: 1999-08-25
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Papillomavirus sylvilagi
US-09-382-616A-1

Query Match 100.0%; Score 53; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLVCYEQ 9
Db 19 TTDLVCYEQ 27

RESULT 13
US-08-944-368A-4
; Sequence 4, Application US/08944368A
; Patent No. 6228368
; GENERAL INFORMATION:
; APPLICANT: Gissman, et al.
; TITLE OF INVENTION: Papilloma Virus Capsomere Vaccine
; TITLE OF INVENTION: Formulations and Methods of Use
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 233 South Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,368A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27013/34028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-944-368A-4

Query Match 100.0%; Score 53; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLVCYEQ 9
Db 19 TTDLVCYEQ 27

RESULT 14
US-09-820-764-4

; Sequence 4, Application US/09820764
; Patent No. 6352696
; GENERAL INFORMATION:
; APPLICANT: BURGER, Alexander
; TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
; FORMULATIONS AND METHODS OF USE
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/820,764
; FILING DATE: 30-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/026,896
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Sandercock, Colin G.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37067/102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-820-764-4

Query Match 100.0%; Score 53; DB 3; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLYCYEQ 9
| | | | |
Db 19 TTDLYCYEQ 27

RESULT 15
US-09-613-303-8
; Sequence 8, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: fusion sequence
US-09-613-303-8

Query Match 100.0%; Score 53; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTDLYCYEQ 9
| | | | |
Db 19 TTDLYCYEQ 27

Search completed: June 28, 2005, 21:33:31
Job time : 17 secs

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; APPLICANT: Bruck, Claudine
; APPLICANT: Cabazon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-14

Query Match      100.0%; Score 54; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CMSCCRSSR 9
Db 268 CMSCCRSSR 276

RESULT 14
US-09-252-991A-25612
; Sequence 25612, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25612
; LENGTH: 154
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25612

Query Match      77.8%; Score 42; DB 4; Length 154;
Best Local Similarity 66.7%; Pred. No. 62;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CMSCCRSSR 9
Db 86 CCACCRSR 94

RESULT 15
US-09-252-991A-31590
; Sequence 31590, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
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; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31590
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31590
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Query Match      77.8%; Score 42; DB 4; Length 389;
Best Local Similarity 77.8%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 CMSCCRSSR 9
Db 169 CTSCCRLSR 177
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Search completed: June 28, 2005, 23:37:53
Job time : 17.05 secs
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GenCore version 5.1.1.6
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QM protein - protein search, using sw model

Run on: June 28, 2005, 21:24:19 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-55
Perfect score: 52
Sequence: 1 HLDKKQRFH 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	52	100.0	84	2	Q80882	Q80882 human papil
2	52	100.0	90	2	Q80883	Q80883 human papil
3	52	100.0	90	2	Q80884	Q80884 human papil
4	52	100.0	90	2	Q80885	Q80885 human papil
5	52	100.0	91	2	Q80887	Q80887 human papil
6	52	100.0	103	2	Q819D6	Q819D6 human papil
7	52	100.0	130	2	Q819B4	Q819B4 human papil
8	52	100.0	130	2	Q819B8	Q819B8 human papil
9	52	100.0	130	2	Q819C0	Q819C0 human papil
10	52	100.0	130	2	Q819C2	Q819C2 human papil
11	52	100.0	130	2	Q819C8	Q819C8 human papil
12	52	100.0	130	2	Q819D0	Q819D0 human papil
13	52	100.0	138	2	Q819D2	Q819D2 human papil
14	52	100.0	143	2	Q819B6	Q819B6 human papil
15	52	100.0	143	2	Q819C4	Q819C4 human papil
16	52	100.0	151	2	Q12335	Q12335 human papil
17	52	100.0	151	2	Q12336	Q12336 human papil
18	52	100.0	151	2	Q76TS0	Q76TS0 human papil
19	52	100.0	151	2	Q778I6	Q778I6 human papil
20	52	100.0	151	2	Q77E16	Q77E16 human papil
21	52	100.0	151	2	Q77JC7	Q77JC7 human papil
22	52	100.0	151	2	Q77ZJ5	Q77ZJ5 human papil
23	52	100.0	151	2	Q80963	Q80963 human papil
24	52	100.0	151	2	Q80966	Q80966 human papil
25	52	100.0	151	2	Q89640	Q89640 human papil
26	52	100.0	151	2	Q89648	Q89648 human papil
27	52	100.0	151	2	Q89708	Q89708 human papil
28	52	100.0	151	2	Q89755	Q89755 human papil
29	52	100.0	151	2	Q89852	Q89852 human papil
30	52	100.0	151	2	Q89887	Q89887 human papil
31	52	100.0	151	2	Q8B564	Q8B564 human papil

32	52	100.0	151	2	Q8BB19	Q8BB19 human papil
33	52	100.0	151	2	Q8BB20	Q8BB20 human papil
34	52	100.0	151	2	Q8BB21	Q8BB21 human papil
35	52	100.0	151	2	Q8W8C3	Q8W8C3 human papil
36	52	100.0	151	2	Q8W931	Q8W931 human papil
37	52	100.0	151	2	Q8WMP2	Q8WMP2 human papil
38	52	100.0	151	2	Q8WMP3	Q8WMP3 human papil
39	52	100.0	151	2	Q8WMP4	Q8WMP4 human papil
40	52	100.0	151	2	Q8WMP5	Q8WMP5 human papil
41	52	100.0	158	1	VE6.HPV16	P03126 human papil
42	52	100.0	158	2	Q8JMU8	Q8JMU8 human papil
43	52	100.0	158	2	Q8QHN0	Q8QHN0 human papil
44	52	100.0	158	2	Q8QHP5	Q8QHP5 human papil
45	52	100.0	158	2	Q8QHT0	Q8QHT0 human papil

ALIGNMENTS

RESULT 1
Q80882 .
ID Q80882 PRELIMINARY; PRT; 84 AA.
AC Q80882;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14511; AAB60565.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 84
SQ SEQUENCE 84 AA; 10177 MW; 5AB6B896468E1CAA CRC64;
Query Match 100.0%; Score 52; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;
Qy 1 HLDKKQRFH 9
Db 74 HLDKKQRFH 82
RESULT 2
Q80883 .
ID Q80883 PRELIMINARY; PRT; 90 AA.
AC Q80883;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14512; AAB60566.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.

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DR GO: 0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 10904 MW; 5D3ADF843AD6060B CRC64;
Query Match 100.0%; Score 52; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HLDKKQRFH 9
Db 77 HLDKKQRFH 85
RESULT 3
Q80884 PRELIMINARY; PRT; 90 AA.
AC Q80884;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14513; AAB60567.2; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 11021 MW; 47F42BBEFAFACCC01 CRC64;
Query Match 100.0%; Score 52; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HLDKKQRFH 9
Db 77 HLDKKQRFH 85
RESULT 4
Q80885 PRELIMINARY; PRT; 90 AA.
AC Q80885;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14514; AAB60568.2; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 103 AA; 12422 MW; 6F90CBAF1F25449B CRC64;
DR GO: 0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 10964 MW; BC2531643ACBA76C CRC64;
Query Match 100.0%; Score 52; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HLDKKQRFH 9
Db 77 HLDKKQRFH 85
RESULT 5
Q80887 PRELIMINARY; PRT; 91 AA.
AC Q80887;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14516; AAB60570.1; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 91
SQ SEQUENCE 91 AA; 11136 MW; 22FDF3EA185ACBA7 CRC64;
Query Match 100.0%; Score 52; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 HLDKKQRFH 9
Db 77 HLDKKQRFH 85
RESULT 6
Q919D6 PRELIMINARY; PRT; 103 AA.
AC Q919D6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RL "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF0404632; AAL01342.1; -.
DR GO: 0042025; C:host cell nucleus; IEA.
DR GO: 0003677; F:DNA binding; IEA.
DR InterPro; IPR00518; E6; 1.
FT NON_TER 1
FT NON_TER 103
SQ SEQUENCE 103 AA; 12422 MW; 6F90CBAF1F25449B CRC64;
```

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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:28:02 ; Search time 11.05 Seconds
(without alignments)
78.367 Million cell updates/sec

Title: US-08-170-344-57

Perfect score: 50

Sequence: 1 SCCRSSRTR 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR_79.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	158	1 W6WLHS	protein E6 - human
2	37	74.0	212	2 T47947	hypothetical prote
3	37	74.0	837	2 A42112	mucin-like peptide
4	37	74.0	870	2 T25338	hypothetical prote
5	36	72.0	152	2 T34649	hypothetical prote
6	36	72.0	214	2 T48499	hypothetical prote
7	36	72.0	303	2 AE3504	tryptophan synthas
8	36	72.0	1905	2 IS1553	plexin - African c
9	35	70.0	98	2 IS4366	dopamine D4 recept
10	35	70.0	114	2 D72600	hypothetical prote
11	35	70.0	141	2 T70575	probable PPE prote
12	35	70.0	151	2 S60314	hair keratin cyste
13	35	70.0	166	2 S69692	hypothetical prote
14	35	70.0	229	2 S60454	glucose starvation
15	35	70.0	371	2 G97530	probable zinc-bind
16	35	70.0	414	2 T45639	hypothetical prote
17	35	70.0	670	2 T10666	hypothetical prote
18	34	68.0	222	2 T26209	hypothetical prote
19	34	68.0	313	2 D98202	transcription regu
20	34	68.0	409	2 C97527	hypothetical prote
21	34	68.0	438	2 T12494	hypothetical prote
22	34	68.0	546	2 T48222	hypothetical prote
23	34	68.0	716	2 T47449	hypothetical prote
24	34	68.0	811	2 E97040	phage related prot
25	34	68.0	1258	2 T29041	hypothetical prote
26	33	67.0	271	2 T01767	hypothetical prote
27	33	66.0	125	1 VSWTA2	alpha-2-thionin -
28	33	66.0	133	1 VSBH2	alpha-hordothionin
29.	33	66.0	136	2 S22977	beta-hordothionin

ALIGNMENTS

RESULT 1

W6WLHS

Protein E6 - human papillomavirus type 16

C:Species: human papillomavirus type 16

C>Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03682; T10427

R:Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virology 145, 181-185, 1985

A>Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03682

A:Molecule type: DNA

A:Residues: 1-158 <SEE>

A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A>Title: A negative element in the human poapillomavirus type 16 genome acts at the level

A:Reference number: Z17014; MUID:91162763; PMID:1848319

A:Accession: T10427

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-158 <KEN>

A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

A:Gene: E6

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:37-73/Region: zinc finger CCCC motif

F:110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 50; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.31; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 SCCRSSRTR 9

Db 145 SCCRSSRTR 153

RESULT 2

T47947

hypothetical protein F2A19.150 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C:Accession: T47947

R:De Haan, M.; Maarse, A.C.; Grivell, L.A.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.X.; Quet

A:Reference number: Z24480

A:Accession: T47947

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-212 <DEH>

A;Cross-references: UNIPROT:Q9M313; EMBL:AL1132962
 A;Experimental source: Cultivar Columbia; BAC clone F2A19
 C;Genetics:
 A;Map position: 3
 A;Note: F2A19.150
 F:132-183/Domain: RING finger homology <RRN>

Query Match 74.0%; Score 37; DB 2; Length 212;
 Best Local Similarity 75.0%; Pred. No. 43;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCRSSRTR 9
 |||||
 Db 50 CCRASRLR 57

RESULT 3
 A42112
 mucin-like peptide MLP 2677 - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Mar-2004
 C;Accession: A42112
 J;Xu, G.; Huan, L.J.; Khatri, I.A.; Wang, D.; Bennick, A.; Forstner, G.G.;
 J. Biol. Chem. 267, 5401-5407, 1992
 A;Title: cDNA for the carboxyl-terminal region of a rat intestinal mucin-like peptide.
 A;Reference number: A42112; MUID:92184794; PMID:1371999
 A;Accession: A42112
 A;Status: preliminary
 A;Molecule type: nucleic acid; protein
 A;Residues: 1-837 <XUI>
 A;Experimental source: intestine
 A;Note: sequence inconsistent with the nucleotide translation
 A;Note: sequence extracted from NCBI backbone (NCBIP:87420)
 F:582-650/Domain: von Willebrand factor type C repeat homology <WVC>

Query Match 74.0%; Score 37; DB 2; Length 837;
 Best Local Similarity 75.0%; Pred. No. 1e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SCCRSSRT 8
 |||||
 Db 777 SCCREERT 784

RESULT 4
 T25338
 hypothetical protein ZK1037.11 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T25338; T27667
 R;Mortimore, B.
 submitted to the EMBL Data Library, November 1996
 A;Reference number: Z20018
 A;Accession: T25338
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-870 <W12>
 A;Cross-references: UNIPROT:Q9XTQ4; EMBL:Z82057; PIDN:CAB04861.1; GSPDB:GN00023; CESP:ZK1037.11
 A;Experimental source: clone T26H8
 R;Baaham, V.
 submitted to the EMBL Data Library, October 1996
 A;Reference number: Z20401
 A;Accession: T27667
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-870 <W12>
 A;Cross-references: EMBL:Z81142; PIDN:CAB03512.1; GSPDB:GN00023; CESP:ZK1037.11
 A;Experimental source: clone ZK1037
 C;Genetics:
 A;Gene: CESP:ZK1037.11
 A;Map position: 5
 A;Introns: 161/1; 162/3; 212/3; 233/3; 301/3; 517/2; 562/3; 578/1; 825/2

Query Match 74.0%; Score 37; DB 2; Length 870;
 Best Local Similarity 85.7%; Pred. No. 1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCCRSSR 7
 |||||
 Db 279 SCCKSSR 285

RESULT 5
 T34649
 hypothetical protein SCIA11.02c SCIA11.02c - Streptomyces coelicolor (fragment)
 C;Species: Streptomyces coelicolor
 C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
 C;Accession: T34649
 R;Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, January 1999
 A;Reference number: Z21551
 A;Accession: T34649
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-152 <SEB>
 A;Cross-references: EMBL:AL035205; PIDN:CAA22742.1; GSPDB:GN00070; SCOEDB:SCIA11.02c
 A;Experimental source: strain A3(2)
 C;Genetics:
 A;Gene: SCOEDB:SCIA11.02c

Query Match 72.0%; Score 36; DB 2; Length 152;
 Best Local Similarity 75.0%; Pred. No. 51;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SCCRSSRT 8
 :|||
 Db 18 ACCSSRT 25

RESULT 6
 DB4899
 hypothetical protein At2g46160 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C;Accession: DB4899
 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon, L.;
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: DB4899
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-214 <STO>
 A;Cross-references: UNIPROT:O82353; GB:AE002093; NID:g3702333; PIDN:AACG2890.1; GSPDB:GN00023

Query Match 72.0%; Score 36; DB 2; Length 214;
 Best Local Similarity 75.0%; Pred. No. 63;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCRSSRTR 9
 |||||
 Db 59 CCRDSRRR 66

RESULT 7
 AE3504
 cryptophan synthase (EC 4.2.1.20) [imported] - Brucella melitensis (strain 16M)
 C;Species: Brucella melitensis
 C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 03-Jun-2002
 C;Accession: AE3504
 R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mufer, C.; Los, T.; Ivanova, I.

.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen *Brucella melitens*
A:Reference number: AD3252; PMID:11756688
A:Accession: AE3504
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-303 <KUR>
A:Cross-references: GB:AE008917; PIDN:AAL53200.1; PID:g17984074; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BME12019
A:Map position: 1
A:Superfamily: tryptophan synthase alpha chain; tryptophan synthase alpha chain homology
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 72.0%; Score 36; DB 2; Length 303;
Best Local Similarity 75.0%; Pred. No. 78;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SCCRST 8
Db 10 ACCRLSRT 17

RESULT 8
151553
Plexin - African clawed frog
C:Species: *Xenopus laevis* (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: 151553
R:Ohta, K.; Mizutani, A.; Kawakami, A.; Murakami, Y.; Kasuya, Y.; Takagi, S.; Tanaka, H.
Neuron 14, 1189-1199, 1995
A:Title: Plexin: a novel neuronal cell surface molecule that mediates cell adhesion via
A:Reference number: 151553; MUID:95329274; PMID:7605632
A:Accession: 151553
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1905 <OHT>
A:Cross-references: UNIPROT:Q91823; GB:D38175; NID:961514; PIDN:BAA07374.1; PID:g961515
C:Keywords: duplication

Query Match 72.0%; Score 36; DB 2; Length 1905;
Best Local Similarity 75.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SCCRST 8
Db 1506 SCCRSPOT 1513

RESULT 9
154366
dopamine D4 receptor - human
C:Species: *Homo sapiens* (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: 154366
R:Northen, M.M.; Cichon, S.; Hemmer, S.; Hebebrand, J.; Remschmidt, H.; Lehmkuhl, G.; Pou
Hum. Mol. Genet. 3, 2207-2212, 1994
A:Title: Human dopamine D4 receptor gene: frequent occurrence of a null allele and obser
A:Reference number: 154366; MUID:95187162; PMID:7881421
A:Accession: 154366
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-98 <RES>
A:Cross-references: UNIPROT:Q16303; GB:S76942; NID:9913280; PIDN:AAB33728.1; PID:g913281
A:Superfamily: vertebrate rhodopsin
C:Keywords: neurotransmitter receptor

Query Match 70.0%; Score 35; DB 2; Length 98;
Best Local Similarity 85.7%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCRSRT 8
Db 83 CCRSST 89

RESULT 10

D72600

hypothetical protein APE1268 - *Aeropyrum pernix* (strain K1)

C:Species: *Aeropyrum pernix*

C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004

C:Accession: D72600

R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Tanaka, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Takah

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Takah

DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, *Aeropyr*

A:Reference number: A72450; MUID:99310339; PMID:10382966

A:Accession: D72600

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-114 <KAW>

A:Cross-references: UNIPROT:Q9YCI9; DDBJ:AP000061; NID:g5104821; PIDN:BAA80258.1; PID:d10

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE1268

Query Match 70.0%; Score 35; DB 2; Length 114;
Best Local Similarity 75.0%; Pred. No. 62;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCRSRT 9
Db 10 CCRSLSR 17

RESULT 11

C70575

probable PPE protein - *Mycobacterium tuberculosis* (strain H37RV)

C:Species: *Mycobacterium tuberculosis*

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999

C:Accession: C70575

R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: C70575

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-141 <COL>

A:Cross-references: GB:Z95324; GB:AL123456; NID:g3261760; PIDN:CAB08586.1; PID:e315469; I

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: PPE

Query Match

Best Local Similarity 62.5%; Score 35; DB 2; Length 141;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SCCRST 8
Db 134 TCCRAGRT 141

RESULT 12

S60314

hair keratin cysteine rich protein - sheep

C:Species: *Ovis orientalis aries*, *Ovis ammon aries* (domestic sheep)

C:Date: 12-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004

C:Accession: S60314

R:Fratini, A.; Powell, B.C.; Hynd, P.I.; Keough, R.A.; Rogers, G.E.

J. Invest. Dermatol. 102, 178-185, 1994

A>Title: Dietary cysteine regulates the levels of mRNAs encoding a family of cysteine-rich proteins
 A,Reference number: S60314; MUID:94149288; PMID:7508963
 A,Accession: S60314
 A,Status: preliminary
 A,Molecule type: mRNA
 A,Residues: 1-151 <FRA>
 A,Cross-references: UNIPROT:Q28576; EMBL:X73462; NID:g512030; PIDN:CAA51841.1; PID:g512030
 C,Superfamily: ultra-high-sulfur keratin

Query Match 70.0%; Score 35; DB 2; Length 151;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCCRSS 6
 |||||
 DB 73 SCCRSS 78

RESULT 13

S69692
 hypothetical protein YDR396w - yeast (Saccharomyces cerevisiae)
 C,Species: Saccharomyces cerevisiae
 C,Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004
 A,Accession: S69692
 R,Dietrich, F. S.
 submitted to the EMBL Data Library, July 1995

A,Description: The sequence of S. cerevisiae cosmid 9481, 9509, 9926, 9461, and lambda
 A,Reference number: S69665
 A,Accession: S69692
 A,Molecule type: DNA
 A,Residues: 1-166 <DIE>

A,Cross-references: UNIPROT:Q13522; EMBL:U32274; NID:g927313; PID:g2194162; GSPDB:GN0000
 C,Genetics:
 A,Gene: MIPS:YDR396w
 A,Cross-references: SGD:S0002804
 A,Map position: 4R
 C,Superfamily: Saccharomyces hypothetical protein YDR396w

Query Match 70.0%; Score 35; DB 2; Length 166;
 Best Local Similarity 100.0%; Pred. No. 78;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCCRSS 6
 |||||
 DB 51 SCCRSS 56

RESULT 14

S60454
 glucose starvation-induced protein (clone pZSS3) - maize (fragment)
 C,Species: Zea mays (maize)
 C,Date: 27-Apr-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 R,Chevallier, C.; Bourgeois, E.; Pradet, A.; Raymond, P.
 Plant Mol. Biol. 28, 473-485, 1995
 A>Title: Molecular cloning and characterization of six cDNAs expressed during glucose starvation
 A,Reference number: S60453; MUID:95359405; PMID:7632917
 A,Accession: S60454
 A,Molecule type: mRNA
 A,Residues: 1-229 <CHE>

A,Cross-references: UNIPROT:Q41855; EMBL:X82617; NID:g575425; PIDN:CAA57939.1; PID:g575425

Query Match 70.0%; Score 35; DB 2; Length 229;
 Best Local Similarity 62.5%; Pred. No. 94;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCCRSSRT 8
 :|||:|:
 DB 59 ACCRASRS 66

RESULT 15

G97530

probable zinc-binding alcohol dehydrogenase [imported] - Agrobacterium tumefaciens (strain C,Species: Agrobacterium tumefaciens
 C,Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C,Accession: G97530
 R,Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
 A>Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
 A,Reference number: A97359; MUID:21608551; PMID:11743194
 A,Accession: G97530
 A,Status: preliminary
 A,Molecule type: DNA
 A,Residues: 1-371 <KUR>

A,Cross-references: UNIPROT:Q8UFI9; GB:AE007869; PIDN:AAK87200.1; PID:g15156478; GSPDB:G97530
 C,Genetics:
 A,Gene: AGR_C_2601
 A,Map position: circular chromosome
 C,Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

Query Match 70.0%; Score 35; DB 2; Length 371;
 Best Local Similarity 85.7%; Pred. No. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCRSSRT 8
 |||||
 DB 3 CCRPSRT 9

Search completed: June 28, 2005, 23:32:13
 Job time : 12.05 secs

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OM protein - protein search, using sw model

Run on: June 29, 2005, 04:19:44 ; Search time 116.15 Seconds
(without alignments)
29.797 Million cell updates/sec

Title: US-08-170-344-57

Perfect score: 50

Sequence: 1 SCRRSRR 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/FCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/FCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	16	17	US-10-484-063-9
2	50	100.0	20	17	US-10-938-249-513
3	50	100.0	24	16	US-10-476-570-44
4	50	100.0	151	14	US-10-177-390-6
5	50	100.0	151	17	US-10-484-063-20
6	50	100.0	151	17	US-10-484-063-27
7	50	100.0	158	17	US-10-858-384-2
8	50	100.0	158	17	US-10-367-057-16
9	50	100.0	171	16	US-10-472-724-2
10	50	100.0	266	9	US-09-367-309A-1
11	50	100.0	273	13	US-10-000-903-4

Query Match Sequence 9, Appli 100.0%; Score 50; DB 17; Length 16;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCRRSRR 9

Db 8 SCRRSRR 16

12 50 100.0 273 17 US-10-899-771-4 Sequence 4, Appli
13 50 100.0 292 13 US-10-000-903-10 Sequence 10, Appli
14 50 100.0 292 17 US-10-899-771-10 Sequence 10, Appli
15 50 100.0 371 13 US-10-000-903-6 Sequence 6, Appli
16 50 100.0 371 17 US-10-899-771-6 Sequence 6, Appli
17 50 100.0 390 13 US-10-000-903-14 Sequence 14, Appli
18 50 100.0 390 17 US-10-899-771-14 Sequence 14, Appli
19 44 88.0 43 10 US-09-397-945-213 Sequence 213, App
20 44 88.0 43 15 US-10-653-595-213 Sequence 213, App
21 44 88.0 137 10 US-09-397-945-211 Sequence 211, App
22 44 88.0 137 15 US-10-653-595-211 Sequence 211, App
23 42 84.0 125 15 US-10-425-114-67214 Sequence 67214, A
24 42 84.0 245 15 US-10-425-114-65786 Sequence 65786, A
25 41 82.0 35 15 US-10-424-599-245237 Sequence 245237,
26 39 78.0 102 16 US-10-425-115-184761 Sequence 184761,
27 39 78.0 478 16 US-10-437-963-115033 Sequence 115033,
28 39 78.0 686 16 US-10-437-963-196497 Sequence 196497,
29 38 76.0 134 16 US-10-437-963-181461 Sequence 181461,
30 38 76.0 188 15 US-10-425-114-44271 Sequence 44271, A
31 38 76.0 231 16 US-10-437-963-105833 Sequence 105833,
32 38 76.0 251 16 US-10-437-963-160036 Sequence 160036,
33 37 74.0 51 16 US-10-437-963-160782 Sequence 160782,
34 37 74.0 66 16 US-10-425-115-330614 Sequence 330614,
35 37 74.0 69 16 US-10-425-115-244446 Sequence 244446,
36 37 74.0 165 16 US-10-437-963-199754 Sequence 199754,
37 36 72.0 46 16 US-10-425-115-250250 Sequence 250250,
38 36 72.0 61 9 US-09-864-761-36259 Sequence 36259, A
39 36 72.0 71 16 US-10-437-963-173711 Sequence 173711,
40 36 72.0 100 16 US-10-437-963-135435 Sequence 135435,
41 36 72.0 101 16 US-10-425-115-310834 Sequence 310834,
42 36 72.0 111 16 US-10-437-963-135875 Sequence 135875,
43 36 72.0 124 16 US-10-425-115-294572 Sequence 294572,
44 36 72.0 131 16 US-10-425-115-310833 Sequence 310833,
45 36 72.0 138 16 US-10-425-115-186241 Sequence 186241,

ALIGNMENTS

RESULT 1
US-10-484-063-9
; Sequence 9, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-9

Query Match 100.0%; Score 50; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCCRSTR 9
Db 138 SCCRSTR 146

RESULT 6
US-10-484-063-27
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-484-063-27

Query Match 100.0%; Score 50; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCCRSTR 9
Db 138 SCCRSTR 146

RESULT 7
US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match 100.0%; Score 50; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCCRSTR 9
Db 145 SCCRSTR 153

RESULT 8
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match 100.0%; Score 50; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 6.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCCRSTR 9
Db 145 SCCRSTR 153

RESULT 9
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match 100.0%; Score 50; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCCRSTR 9
Db 150 SCCRSTR 158

RESULT 10

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US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODRICK I.
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match      100.0%; Score 50; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCCRSTR 9
Db 145 SCCRSTR 153

RESULT 11
US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4

Query Match      100.0%; Score 50; DB 13; Length 273;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCCRSTR 9
Db 251 SCCRSTR 259

RESULT 12
US-10-899-771-4
; Sequence 4, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine

```

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US-09-367-309A-1
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: Influenzae B and B6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-4

Query Match      100.0%; Score 50; DB 17; Length 273;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCCRSTR 9
Db 251 SCCRSTR 259

RESULT 13
US-10-000-903-10
; Sequence 10, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-10

Query Match      100.0%; Score 50; DB 13; Length 292;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCCRSTR 9
Db 270 SCCRSTR 278

RESULT 14
US-10-899-771-10
; Sequence 10, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.

```

APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
FILE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
FILE REFERENCE: B45124
CURRENT APPLICATION NUMBER: US/10/899,771
CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-08-20
PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 292
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chimaeric protein (Clyta from Streptococcus
OTHER INFORMATION: pneumoniae and B6 from Human papilloma virus type
OTHER INFORMATION: 16)
US-10-899-771-10

Query Match 100.0%; Score 50; DB 17; Length 292;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCCRSTR 9
Db 270 SCCRSTR 278

RESULT 15

US-10-000-903-6
Sequence 6, Application US/10000903
Publication No. US20020182221A1
GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Bernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 371
TYPE: PRT
ORGANISM: Homo sapien
US-10-000-903-6

Query Match 100.0%; Score 50; DB 13; Length 371;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCCRSTR 9
Db 251 SCCRSTR 259

Search completed: June 29, 2005, 05:18:16
Job time : 116.15 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:33:36 ; Search time 17.05 Seconds
(without alignments)
39.404 Million cell updates/sec

Title: US-08-170-344-57
Perfect score: 50
Sequence: 1 SCRRSTR 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	21	2	US-08-934-915-167
2	50	100.0	158	4	US-09-980-523A-2
3	50	100.0	162	1	US-08-316-239B-3
4	50	100.0	162	1	US-08-316-239B-4
5	50	100.0	172	3	US-08-860-165-12
6	50	100.0	172	3	US-09-359-382-12
7	50	100.0	266	3	US-08-860-165-10
8	50	100.0	266	3	US-09-359-382-10
9	50	100.0	266	4	US-09-367-309A-1
10	50	100.0	273	3	US-09-485-885-4
11	50	100.0	292	3	US-09-485-885-10
12	50	100.0	371	3	US-09-485-885-6
13	50	100.0	390	3	US-09-485-885-14
14	41	82.0	136	4	US-09-252-991A-21156
15	41	82.0	230	4	US-09-252-991A-33122
16	39	78.0	147	4	US-09-252-991A-17724
17	39	78.0	171	4	US-08-311-731A-381
18	39	78.0	953	4	US-09-252-991A-30039
19	38	76.0	113	4	US-09-252-991A-29076
20	38	76.0	138	4	US-09-489-039A-12930
21	38	76.0	154	4	US-09-252-991A-30960
22	37	74.0	161	4	US-09-270-767-36971
23	37	74.0	161	4	US-09-270-767-52188
24	37	74.0	207	4	US-09-270-767-32689
25	37	74.0	207	4	US-09-270-767-47906
26	36	72.0	153	4	US-09-252-991A-26200
27	36	72.0	224	4	US-09-252-991A-18341

Query Match 100.0%; Score 50; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.31;

28	36	72.0	446	4	US-09-252-991A-21791	Sequence 21791, A
29	35	70.0	44	4	US-09-270-767-58297	Sequence 58297, A
30	35	70.0	47	2	US-08-660-789-6	Sequence 6, Appli
31	35	70.0	47	3	US-09-074-114-6	Sequence 6, Appli
32	35	70.0	87	4	US-09-252-991A-25071	Sequence 25071, A
33	35	70.0	108	4	US-09-489-039A-9392	Sequence 9392, Ap
34	35	70.0	109	4	US-09-252-991A-22787	Sequence 22787, A
35	35	70.0	109	4	US-09-252-991A-29444	Sequence 29444, A
36	35	70.0	140	4	US-09-270-767-35721	Sequence 35721, A
37	35	70.0	140	4	US-09-270-767-50938	Sequence 50938, A
38	35	70.0	150	4	US-09-252-991A-24700	Sequence 24700, A
39	35	70.0	168	4	US-09-252-991A-32502	Sequence 32502, A
40	35	70.0	202	4	US-09-252-991A-18240	Sequence 18240, A
41	35	70.0	202	4	US-09-252-991A-28110	Sequence 28110, A
42	35	70.0	210	4	US-09-252-991A-28014	Sequence 28014, A
43	35	70.0	214	4	US-09-270-767-42972	Sequence 42972, A
44	35	70.0	249	4	US-09-252-991A-28972	Sequence 28972, A
45	35	70.0	331	4	US-09-252-991A-24140	Sequence 24140, A

ALIGNMENTS

RESULT 1
US-08-934-915-167
; Sequence 167, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 167:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-167

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCCRSTR 9
Db 8 SCCRSTR 16

RESULT 2
US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGALT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO81 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 50; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCCRSTR 9
Db 145 SCCRSTR 153

RESULT 3
US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 100.0%; Score 50; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 100.0%; Score 50; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCCRSTR 9
Db 145 SCCRSTR 153

RESULT 4
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 100.0%; Score 50; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 SCCRSTR 9
Db 83 SCCRSTR 91

RESULT 7
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 50; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCCRSTR 9
Db 145 SCCRSTR 153

RESULT 8
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 50; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCCRSTR 9
Db 83 SCCRSTR 91

RESULT 5
US-08-860-165-12
; Sequence 12, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12

Query Match 100.0%; Score 50; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCCRSTR 9
Db 83 SCCRSTR 91

RESULT 6
US-09-359-382-12
; Sequence 12, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-12

Query Match 100.0%; Score 50; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```

; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485.885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-10

Query Match      100.0%; Score 50; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 2.6; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY      1 SCCRSSRTR 9
Db      270 SCCRSSRTR 278

RESULT 12
US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485.885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-6

Query Match      100.0%; Score 50; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 3.1; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY      1 SCCRSSRTR 9
Db      251 SCCRSSRTR 259

RESULT 13
US-09-485-885-14
; Sequence 14, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:

```

```

; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODRICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367.309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
; US-09-367-309A-1

Query Match      100.0%; Score 50; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.4; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY      1 SCCRSSRTR 9
Db      145 SCCRSSRTR 153

RESULT 10
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485.885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-485-885-4

Query Match      100.0%; Score 50; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.4; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY      1 SCCRSSRTR 9
Db      251 SCCRSSRTR 259

RESULT 11
US-09-485-885-10

```

; APPLICANT: Bruck, Claudine
; APPLICANT: Cabazon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-14

Query Match 100.0%; Score 50; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SCCRSSRTR 9
Db 270 SCCRSSRTR 278
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RESULT 14

US-09-252-991A-21156
; Sequence 21156, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21156
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21156

Query Match 82.0%; Score 41; DB 4; Length 136;
Best Local Similarity 77.8%; Pred. No. 27;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SCCRSSRTR 9
Db 67 SCCASRTR 75
|||:||||

RESULT 15

US-09-252-991A-33122
; Sequence 33122, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 33122
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-33122

Query Match 82.0%; Score 41; DB 4; Length 230;
Best Local Similarity 87.5%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCRSSRTR 9
Db 97 CCRSSRTR 104
|||||

Search completed: June 28, 2005, 23:37:54
Job time : 18.05 secs

“Page Blank (uspto)”

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:28:02 ; Search time 11.05 Seconds
(without alignments)
78.367 Million cell updates/sec

Title: US-08-170-344-56
Perfect score: 54
Sequence: 1 CMSCCRSSR 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	158	1 W6WLHS	protein E6 - human
2	45	83.3	870	2 T25338	hypothetical prote
3	42	77.8	747	2 T33488	hypothetical prote
4	39	72.2	640	2 T08179	LRG5 protein - Chl
5	37	68.5	101	2 J00877	cyc02 protein prec
6	37	68.5	591	2 C71460	hypothetical prote
7	36	66.7	86	1 V6EP9A	venom protein C983
8	36	66.7	352	2 S11926	cellulose 1.4-beta
9	36	66.7	421	2 T30315	hypothetical prote
10	36	66.7	438	2 T12494	hypothetical prote
11	36	66.7	651	2 T48256	hypothetical prote
12	36	66.7	670	2 T10666	hypothetical prote
13	36	66.7	898	2 T26577	hypothetical prote
14	36	66.7	1075	2 T49879	hypothetical prote
15	35	64.8	107	2 H84839	late embryogenesis
16	35	64.8	151	2 S60314	hair keratin cyste
17	35	64.8	166	2 S69692	hypothetical prote
18	35	64.8	194	2 I39526	hypothetical prote
19	35	64.8	280	2 T09504	LiM-protein FHL3,
20	35	64.8	280	2 H72593	hypothetical prote
21	35	64.8	309	2 T34080	hypothetical prote
22	35	64.8	371	2 G97530	probable zinc-bind
23	35	64.8	442	2 H72266	astB/chuk-related
24	35	64.8	460	2 A31897	muscarinic acetyl
25	35	64.8	460	2 I51837	muscarinic recepto
26	35	64.8	460	2 S09508	muscarinic acetyl
27	35	64.8	460	2 A24325	muscarinic acetyl
28	35	64.8	460	2 A29514	muscarinic acetyl
29	35	64.8	730	2 B85013	hypothetical prote

30 35 64.8 730 2 T10539
31 35 64.8 969 1 A39490
32 35 64.8 2408 2 T24483
33 34 63.0 63 1 V6EP92
34 34 63.0 129 2 A90507
35 34 63.0 139 2 S54085
36 34 63.0 147 2 T30606
37 34 63.0 158 1 W6WL18
38 34 63.0 174 1 JQ1625
39 34 63.0 186 2 A45910
40 34 63.0 189 2 S39864
41 34 63.0 190 2 T34341
42 34 63.0 222 2 E84560
43 34 63.0 229 2 S60454
44 34 63.0 277 2 D97497
45 34 63.0 295 2 A44984

hypothetical prote
subtilisin-like pr
hypothetical prote
venom protein C983
hypothetical prote
probable membrane
hypothetical prote
E6 protein - human
small hydrophobic
ultra-high-sulfur
late competence op
hypothetical prote
hypothetical prote
glucose starvation
pteridine reductas
collagen - nematod

ALIGNMENTS

RESULT 1

W6WLHS
protein E6 - human papillomavirus type 16
C:Species: human papillomavirus type 16
C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C:Accession: A03682; T10427
R:Seedorf, K.; Kramer, G.; Duret, M.; Suhai, S.; Rowekamp, W.G.
Virology 145, 181-185, 1985
A>Title: Human papillomavirus type 16 DNA sequence.
A:Reference number: A22355; MUID:85246220; PMID:2990099
A:Accession: A03682
A:Molecule type: DNA
A:Residues: 1-158 <SEE>
A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A>Title: A negative element in the human poapillomavirus type 16 genome acts at the level
A:Reference number: 217014; MUID:91162763; PMID:1848319
A:Accession: T10427
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-158 <KEN>
A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
C:Genetics:
A:Gene: E6
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:37-73/Region: zinc finger CCCC motif
F:110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 54; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CMSCCRSSR 9
Db 143 CMSCCRSSR 151

RESULT 2

T25338
hypothetical protein ZK1037.11 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T25338; T27667
R:Mortimore, B.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20018
A:Accession: T25338
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-870 <WIL>

A;Cross-references: UNIPROT:Q9XTQ4; EMBL:Z82057; PIDN:CAB04861.1; GSPDB:GN00023; CESP:ZK1037.11
A;Experimental source: clone T26H8
R;Basham, V.
submitted to the EMBL Data Library, October 1996
A;Accession: T27667
A;Reference number: Z20401
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-870 <W12>
A;Cross-references: EMBL:Z81142; PIDN:CAB03512.1; GSPDB:GN00023; CESP:ZK1037.11
A;Experimental source: clone ZK1037
C;Genetics:
A;Gene: CESP:ZK1037.11
A;Map position: 5
A;Introns: 161/1; 162/3; 212/3; 233/3; 301/3; 517/2; 562/3; 578/1; 825/2

Query Match 83.3%; Score 45; DB 2; Length 870;
Best Local Similarity 77.8%; Pred. No. 28;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CMSCCRSSR 9
| | | | |
Db 277 CCSCCKSSR 285
| | | | |

RESULT 3
T33488
hypotheical protein C36C9.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33488
R;Fulton, B.; Martin, J.; O'Brien, D.
submitted to the EMBL Data Library, October 1998
A;Description: The sequence of C. elegans cosmid C36C9.
A;Reference number: Z21357
A;Accession: T33488
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-747 <FUL>
A;Cross-references: UNIPROT:Q9TZL0; EMBL:AF098986; PIDN:AAC67425.1; GSPDB:GN00028; CESP:
A;Experimental source: strain Bristol N2; clone C36C9
C;Genetics:
A;Gene: CESP:C36C9.2
A;Map position: X
A;Introns: 171/3; 427/1; 563/1; 627/2; 686/1

Query Match 77.8%; Score 42; DB 2; Length 747;
Best Local Similarity 75.0%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CMSCCRSS 8
| | | | |
Db 436 CLSCCRGS 443
| | | | |

RESULT 4
T08179
LRG5 protein - Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08179
R;Gloeckner, G.; Beck, C.F.
submitted to the EMBL Data Library, October 1996
A;Description: Molecular characterization of a gene (LRG5) involved in blue light signal
A;Reference number: Z16399
A;Accession: T08179
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-840 <LO>
A;Cross-references: UNIPROT:Q96397; EMBL:U73817; NID:g1644369; PID:g1644370
C;Genetics:
A;Gene: LRG5

Query Match 68.5%; Score 37; DB 2; Length 591;
Best Local Similarity 62.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CMSCCRSS 8
| | | | |
Db 393 CFSCCRGS 400
| | | | |

RESULT 7
V6EP9A
venom protein C9S3 chain 1 precursor - eastern green mamba
C;Species: Dendroaspis angusticeps (eastern green mamba)
C;Date: 19-Feb-1984 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004
C;Accession: S09235; A01679
R;Rowan, E.G.; Ducancel, F.; Doljansky, Y.; Harvey, A.L.; Boulain, J.C.; Manez, A.

Query Match 72.2%; Score 39; DB 2; Length 640;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CMSCCRSSR 9
| | | | |
Db 573 CCRCRCGRS 581
| | | | |

RESULT 5
JQ0877
cycO2 protein precursor - Madagascar periwinkle
C;Species: Catharanthus roseus (Madagascar periwinkle)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C;Accession: JQ0877
R;Kodama, H.; Ito, M.; Hattori, T.; Nakamura, K.; Komanine, A.
submitted to JIPID, February 1991
A;Description: Isolation of genes that are preferentially expressed at the G1/S boundary
A;Reference number: JQ0877
A;Accession: JQ0877
A;Molecule type: mRNA
A;Residues: 1-101 <KOD>
A;Cross-references: UNIPROT:P25923
A;Experimental source: strain B, cell suspension culture
C;Genetics:
A;Gene: cycO2
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-101/Product: cycO2 protein #status predicted <MAT>

Query Match 68.5%; Score 37; DB 2; Length 101;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CMSCCRSS 8
| | | | |
Db 57 CVRCRCRGA 64
| | | | |

RESULT 6
C71460
hypotheical protein CT875 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C;Accession: C71460
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marache, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trach
A;Reference number: A71570; MUID:9900809; PMID:9784136
A;Accession: C71460
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-591 <ARN>
A;Cross-references: UNIPROT:O84883; GB:AE001361; GB:AE001273; NID:g3329348; PIDN:AAC6847;
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: CT875

Query Match 68.5%; Score 37; DB 2; Length 591;
Best Local Similarity 62.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CMSCCRSS 8
| | | | |
Db 393 CFSCCRGS 400
| | | | |

RESULT 7
V6EP9A
venom protein C9S3 chain 1 precursor - eastern green mamba
C;Species: Dendroaspis angusticeps (eastern green mamba)
C;Date: 19-Feb-1984 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004
C;Accession: S09235; A01679
R;Rowan, E.G.; Ducancel, F.; Doljansky, Y.; Harvey, A.L.; Boulain, J.C.; Manez, A.

A:Reference number: A38502; MUID:91135017; PMID:1847266

A:Accession: A38502

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-158 <VOL>

A:Cross-references: UNIPROT:P24835; GB:M62849; EMBL:M38185; NID:g3333245; PIDN:AAA47050.1

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; transforming protein; zinc finger

F:32-68/Region: zinc finger CCCC motif

F:105-141/Region: zinc finger CCCC motif

Query Match 73.1%; Score 38; DB 1; Length 158;

Best Local Similarity 66.7%; Pred. No. 3.3;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9

Db 120 HLNSKRRFH 128

RESULT 7

EWLPR

E6 protein - human papillomavirus type ME180 (provirus)

C:Species: human papillomavirus type ME180

A>Note: host Homo sapiens (man)

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C:Accession: C40509

R:Reuter, S.; Delius, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.

J. Virol. 65, 5564-5568, 1991

A>Title: Characterization of a novel human papillomavirus DNA in the cervical carcinoma

A:Reference number: A40509; MUID:91374616; PMID:1716694

A:Accession: C40509

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-158 <REU>

C:Cross-references: UNIPROT:P27962; GB:M73258

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:32-68/Region: zinc finger CCCC motif

F:105-141/Region: zinc finger CCCC motif

Query Match 73.1%; Score 38; DB 1; Length 158;

Best Local Similarity 66.7%; Pred. No. 3.3;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9

Db 120 HLNSKRRFH 128

RESULT 8

EWLPR

E6 protein - rhesus papillomavirus (type 1)

C:Species: rhesus papillomavirus

C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004

C:Accession: A38503

R:Ostrow, R.S.; LaBresh, K.V.; Faraas, A.J.

Virolgy 181, 424-429, 1991

A>Title: Characterization of the complete RHPV 1 genomic sequence and an integration loc

A:Reference number: A38503; MUID:91135018; PMID:1847267

A:Accession: A38503

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-191 <OST>

C:Cross-references: UNIPROT:P22159; EMBL:M37717

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; transforming protein; zinc finger

F:60-96/Region: zinc finger CCCC motif

F:133-169/Region: zinc finger CCCC motif

Query Match 73.1%; Score 38; DB 1; Length 191;

Best Local Similarity 66.7%; Pred. No. 4;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9

Db 148 HVDQQRHF 156

RESULT 9

H81311

transcription-repair coupling factor Cj1085c [imported] - Campylobacter jejuni (strain NC

C:Species: Campylobacter jejuni

C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C:Accession: H81311

R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling

C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell

Nature 403, 665-668, 2000

A>Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hys

A:Reference number: A81250; MUID:20150912; PMID:10688204

A:Accession: H81311

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-978 <PAR>

A:Cross-references: UNIPROT:Q9PNK9; GB:AL139077; GB:AL111168; NID:g968444; PIDN:CAB7334

A:Experimental source: serotype O2, strain NCTC 11168

C:Genetics:

A:Gene: mfd; Cj1085c

C:Superfamily: transcription-repair coupling protein

Query Match 71.2%; Score 37; DB 2; Length 978;

Best Local Similarity 75.0%; Pred. No. 36;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 8

Db 101 HLDKKQRFH 108

RESULT 10

S36515

E6 protein - human papillomavirus type 34

C:Species: human papillomavirus type 34

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: S36515

R:Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36515

A:Molecule type: DNA

A:Residues: 1-148

A:Cross-references: UNIPROT:P36811; EMBL:X74476; NID:g396989; PIDN:CAAS2555.1; PID:g3969

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 69.2%; Score 36; DB 2; Length 148;

Best Local Similarity 55.6%; Pred. No. 7.7;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9

Db 119 HVDENKRFH 127

RESULT 11

S36527

E6 protein - human papillomavirus type 53

C:Species: human papillomavirus type 53

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C:Accession: S36527

R:Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36527

A:Molecule type: DNA
A:Residues: 1-154
A:Cross-references: UNIPROT:P36815; EMBL:X74482; NID:G937046; PIDN:CAAS2591.1; PID:G937046
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 69.2%; Score 36; DB 2; Length 154;
Best Local Similarity 66.7%; Pred. No. 8;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9
| | | | |
Db 122 HCDYKKRFH 130

RESULT 12
T00065
hypotheical protein KIAA0442 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C:Accession: T00065
R:ishikawa, K.; Nagase, T.; Nakajima, D.; Seki, N.; Ohira, M.; Miyajima, N.; Tanaka, A.;
DNA Res. 4, 307-313, 1997
A:Title: Prediction of the coding sequences of unidentified human genes. VIII. 78 new cd
A:Reference number: Z14084; MUID:98116655; PMID:9455477
A:Accession: T00065
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1172 <ISH>
A:Cross-references: UNIPROT:Q8WXX7; EMBL:AB007902; NID:g2662164; PIDN:BAA23714.1; PID:g2662164
A:Experimental source: brain
C:Genetics:
A:Note: KIAA0442

Query Match 69.2%; Score 36; DB 2; Length 1172;
Best Local Similarity 55.6%; Pred. No. 70;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9
| | | | |
Db 1061 HLDKERLH 1069

RESULT 13
S36561
E6 protein - human papillomavirus type 45
C:Species: human papillomavirus type 45
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36561
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36561
A:Molecule type: DNA
A:Residues: 1-158
A:Cross-references: UNIPROT:P21735; EMBL:X74479; NID:G937022; PIDN:CAAS2573.1; PID:G937022
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 67.3%; Score 35; DB 2; Length 158;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9
| | | | |
Db 120 HLDKKRFH 128

RESULT 14
F87644
transcription regulator, TetR family [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: F87644
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.;
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: F87644
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-411 <STO>
A:Cross-references: UNIPROT:Q9A3L1; GB:AE005673; NID:gl3424868; PIDN:AAK25154.1; GSPDB:G
C:Genetics:
A:Gene: CC3192

Query Match 67.3%; Score 35; DB 2; Length 411;
Best Local Similarity 85.7%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 7
| | | | |
Db 156 HLDKKQRFH 162

RESULT 15
G82923
multiple banded antigen homolog UU172 [imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C:Accession: G82923
R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A:Reference number: A82870
A:Accession: G82923
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-499 <GLA>
A:Cross-references: GB:AE002117; GB:AF222894; NID:G6899132; PIDN:AAF30579.1; GSPDB:GN001
A:Experimental source: serovar 3; biovar 1
C:Genetics:
A:Gene: UU172
A:Genetic code: SGC3

Query Match 67.3%; Score 35; DB 2; Length 499;
Best Local Similarity 55.6%; Pred. No. 45;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9
| | | | |
Db 427 NLDKEQKYH 435

Search completed: June 28, 2005, 23:32:11
Job time : 12.05 secs

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Query Match      100.0%; Score 54; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CMSCCRSSR 9
DB      115 CMSCCRSSR 123

RESULT 7
Q919D0      PRELIMINARY; PRT; 130 AA.
AC Q919D0;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404695; AAL01347.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR PFam; PF00518; E6; 1.
FT NON TER
SQ SEQUENCE 130 AA; 15735 MW; 9EPB30EEDCA21AF3 CRC64;

Query Match      100.0%; Score 54; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CMSCCRSSR 9
DB      115 CMSCCRSSR 123

RESULT 8
Q919D2      PRELIMINARY; PRT; 138 AA.
AC Q919D2;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404694; AAL01345.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR PFam; PF00518; E6; 1.
FT NON TER
SQ SEQUENCE 138 AA; 16696 MW; 481E5AEA90895FC2 CRC64;

Query Match      100.0%; Score 54; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 1;

QY      1 CMSCCRSSR 9
DB      115 CMSCCRSSR 123

Query Match      100.0%; Score 54; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.98;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CMSCCRSSR 9
DB      128 CMSCCRSSR 136

Query Match      100.0%; Score 54; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CMSCCRSSR 9
DB      123 CMSCCRSSR 131

Query Match      100.0%; Score 54; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CMSCCRSSR 9
DB      123 CMSCCRSSR 131

RESULT 9
Q919B6      PRELIMINARY; PRT; 143 AA.
AC Q919B6;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404702; AAL01361.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR PFam; PF00518; E6; 1.
FT NON TER
SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;

Query Match      100.0%; Score 54; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CMSCCRSSR 9
DB      128 CMSCCRSSR 136

RESULT 10
Q919C4      PRELIMINARY; PRT; 143 AA.
AC Q919C4;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404698; AAL01353.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR PFam; PF00518; E6; 1.
FT NON TER
SQ SEQUENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;

Query Match      100.0%; Score 54; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CMSCCRSSR 9

```

Db 128 CMSCCRSSR 136
|||||||
RESULT 11
O12335
ID O12335 PRELIMINARY; PRT; 151 AA.
AC O12335;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Girardo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003015; AAB70732.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18238 MW; BFF32A8B016CC88B CRC64;
Query Match 100.0%; Score 54; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CMSCCRSSR 9
|||||||
Db 136 CMSCCRSSR 144
RESULT 12
O12336
ID O12336 PRELIMINARY; PRT; 151 AA.
AC O12336;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Girardo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003016; AAB70733.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;
Query Match 100.0%; Score 54; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CMSCCRSSR 9
|||||||

Db 136 CMSCCRSSR 144
RESULT 13
Q76TS0
ID Q76TS0 PRELIMINARY; PRT; 151 AA.
AC Q76TS0;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yanada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RA Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34114; AAA91661.1; -;
DR EMBL; U34125; AAA91672.1; -;
DR EMBL; U34130; AAA91677.1; -;
DR EMBL; U34131; AAA91678.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;
Query Match 100.0%; Score 54; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CMSCCRSSR 9
|||||||
Db 136 CMSCCRSSR 144
RESULT 14
Q778I6
ID Q778I6 PRELIMINARY; PRT; 151 AA.
AC Q778I6;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AJ388056; CAB45104.1; -;
DR EMBL; AJ388061; CAB45114.1; -;
DR EMBL; AJ388066; CAB45124.1; -;
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.

```

DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18334 MW;  F98F2A2FCEBA6C02 CRC64;

Query Match
Best Local Similarity 100.0%; Score 54; DB 2; Length 151;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CMSCCRSSR 9
Db 136 CMSCCRSSR 144

RESULT 15
Q77E16
ID Q77E16 PRELIMINARY; PRT; 151 AA.
AC Q77E16;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE E6 oncoprotein (E6 protein).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OC NCBI_TaxID=10581;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M.; Vaeteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AF469197; AAO15691.1; -.
DR EMBL; AJ388063; CAB45118.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CF1F CRC64;

Query Match
Best Local Similarity 100.0%; Score 54; DB 2; Length 151;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CMSCCRSSR 9
Db 136 CMSCCRSSR 144

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Search completed: June 28, 2005, 23:28:13
Job time : 55.1 secs

The Page Blank (uspto)

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:28:02 ; Search time 11.05 Seconds
(without alignments)
78.367 Million cell updates/sec

Title: US-08-170-344-55
Perfect score: 52
Sequence: 1 HLDKKQRFH 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	158	1 W6WLS	protein E6 - human
2	48	92.3	149	1 W6WL31	E6 protein - human
3	40	76.9	149	1 W6WL35	E6 protein - human
4	40	76.9	155	1 W6WL56	E6 protein - human
5	39	75.0	158	1 W6WL18	E6 protein - human
6	38	73.1	158	1 W6WL39	E6 protein - human
7	38	73.1	158	1 W6WLP	E6 protein - human
8	38	73.1	191	1 W6WLR1	E6 protein - rhesu
9	37	71.2	978	2 H81311	transcription-repa
10	36	69.2	148	2 S36515	E6 protein - human
11	36	69.2	154	2 S36527	E6 protein - human
12	36	69.2	1172	2 T00065	hypothetical prote
13	35	67.3	158	2 S36561	E6 protein - human
14	35	67.3	411	2 P87644	transcription regu
15	35	67.3	499	2 G82923	multiple banded an
16	35	67.3	535	2 S11097	cold acclimation p
17	35	67.3	578	2 T15958	hypothetical prote
18	35	67.3	632	2 E88712	protein C17H12.12
19	34	65.4	144	2 D98172	gamma carboxymuon
20	34	65.4	144	2 A13114	gamma carboxymuon
21	34	65.4	166	2 C70746	hypothetical prote
22	34	65.4	179	2 H81682	conserved hypotet
23	34	65.4	182	2 A72854	probable histidino
24	34	65.4	220	2 S78395	ribosomal protein
25	34	65.4	305	2 C39240	finger protein mfg
26	34	65.4	311	2 T44610	cytochrome aa3 con
27	34	65.4	370	2 S52699	hypothetical prote
28	34	65.4	385	2 AE3402	ribonuclease III (
29	34	65.4	450	2 T23528	hypothetical prote

30	34	65.4	461	2 T28006	hypothetical prote
31	34	65.4	622	2 I48733	protein kinase rck
32	34	65.4	622	2 A34711	kinase-related pro
33	34	65.4	629	2 T31626	hypothetical prote
34	34	65.4	707	2 S68858	finger protein - m
35	34	65.4	858	2 A02272	protein serine-thr
36	34	65.4	1509	2 T19486	hypothetical prote
37	33	63.5	90	2 A23735	gonadoliberin prec
38	33	63.5	90	2 I51095	gonadoliberin prec
39	33	63.5	113	2 PC2231	hobo-like transpos
40	33	63.5	118	2 T02052	hypothetical prote
41	33	63.5	136	2 E83730	transcription regu
42	33	63.5	149	1 W6WL33	E6 protein - human
43	33	63.5	149	1 W6WL58	E6 protein - human
44	33	63.5	150	2 S36544	E6 protein - human
45	33	63.5	151	1 W6WL51	E6 protein - human

ALIGNMENTS

RESULT 1

W6WLS

protein E6 - human papillomavirus type 16

C:Species: human papillomavirus type 16

C>Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03682; T10427

R:Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virology 145, 181-185, 1985

A>Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03682

A:Molecule type: DNA

A:Residues: 1-158 <SEE>

A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

J.Kennedy, I.M.; Haddow, J.K.; Clements, J.B.

R. Virol. 65, 2093-2097, 1991

A>Title: A negative element in the human poapillomavirus type 16 genome acts at the level

A:Reference number: Z17014; MUID:91162763; PMID:1848319

A:Accession: T10427

A>Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-158 <KEN>

A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

A:Gene: E6

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:37-73/Region: zinc finger CCCC motif

F:110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 52; DB 1; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.0052;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9

Db 125 HLDKKQRFH 133

|||||

RESULT 2

W6WL31

E6 protein - human papillomavirus type 31

C:Species: human papillomavirus type 31

A>Note: host Homo sapiens (man)

C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004

C:Accession: A32444

R:Goldsbrough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.

Virology 171, 306-311, 1989

A>Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associ

A:Reference number: A94398; MUID:89299478; PMID:2545036

A:Accession: A32444

A>Status: translation not shown

A:Molecule type: DNA
A:Residues: 1-149 <GOL>
A:Cross-references: UNIPROT:P17386; GB:J04353; NID:G333048; PIDN:AAA46950.1; PID:G459916
C:Comment: This protein may be involved in the oncogenic potential of this virus.
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match 92.3%; Score 48; DB 1; Length 149;
Best Local Similarity 88.9%; Pred. No. 0.031;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLDKKQRFH 9
|||:|:|
DB 118 HLDKKQRFH 126

RESULT 3
W6WL35
E6 protein - human papillomavirus type 35
C:Species: human papillomavirus type 35
A:Note: host Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: E40824; S36521
R:Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776, 1992
A:Title: The phylogenetic relationship and complete nucleotide sequence of human papillomavirus type 35
A:Reference number: A40824; MUID:92124753; PMID:1310198
A:Accession: E40824
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-149 <MAR>
A:Cross-references: UNIPROT:P27228; GB:M74117; NID:G333050; PIDN:AAA46966.1; PID:G333051
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36521
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-149
A:Cross-references: EMBL:X74477; NID:G396997; PIDN:CAA52561.1; PID:G396998
A:Experimental source: strain 35H
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match 76.9%; Score 40; DB 1; Length 149;
Best Local Similarity 66.7%; Pred. No. 1.2;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLDKKQRFH 9
|||:|:|
DB 118 HLDKKQRFH 126

RESULT 4
W6WL56
E6 protein - human papillomavirus type 56
C:Species: human papillomavirus type 56
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: A33377; S36579
R:Loerincz, A.T.; Quinn, A.P.; Goldsborough, M.D.; McAllister, P.; Temple, G.F.
J. Gen. Virol. 70, 3099-3104, 1989
A:Title: Human papillomavirus type 56: a new virus detected in cervical cancers.
A:Reference number: A33377; MUID:90063558; PMID:2553440
A:Accession: A33377
A:Molecule type: DNA
A:Residues: 1-155 <LOE>
A:Cross-references: UNIPROT:P24836
R:Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36579
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-155
A:Cross-references: EMBL:X74483; NID:G397053; PIDN:CAA52596.1; PID:G397054
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; transforming protein; zinc finger
F:33-69/Region: zinc finger CCCC motif
F:106-142/Region: zinc finger CCCC motif

Query Match 76.9%; Score 40; DB 1; Length 155;
Best Local Similarity 66.7%; Pred. No. 1.3;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLDKKQRFH 9
|||:|:|
DB 121 HCDKRRRFH 129

RESULT 5
W6WL18
E6 protein - human papillomavirus type 18
C:Species: human papillomavirus type 18
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: A26165; G26251
R:Seedorf, K.; Oltersdorf, T.; Kraemmer, G.; Roewekamp, W.
EMBO J. 6, 139-144, 1987
A:Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 16)
A:Reference number: A91068; MUID:87218459; PMID:3034571
A:Accession: A26165
A:Molecule type: DNA
A:Residues: 1-158 <SSE>
A:Cross-references: UNIPROT:P06463; GB:X04773; NID:G60876; PIDN:CAA28466.1; PID:G60877
R:Cole, S.T.; Danos, O. 608, 1987
J. Mol. Biol. 193, 599-608, 1987
A:Title: Nucleotide sequence and comparative analysis of the human papillomavirus type 18
A:Reference number: A92937; MUID:87283882; PMID:3039146
A:Accession: G26251
A:Molecule type: DNA
A:Residues: 1-158 <COL>
A:Cross-references: GB:X05015; NID:G60975; PIDN:CAA28664.1; PID:G60976
R:Matlashewski, G.; Banks, L.; Wu-Liao, J.; Spence, P.; Pim, D.; Crawford, L.
J. Gen. Virol. 67, 1909-1916, 1986
A:Title: The expression of human papillomavirus type 18 E6 protein in bacteria and the p
A:Reference number: A92791; MUID:86306665; PMID:3018129
A:Contents: annotation; identification of the protein
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; transforming protein; zinc finger
F:32-68/Region: zinc finger CCCC motif
F:105-141/Region: zinc finger CCCC motif

Query Match 75.0%; Score 39; DB 1; Length 158;
Best Local Similarity 66.7%; Pred. No. 2.1;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLDKKQRFH 9
|||:|:|
DB 120 HLNEKRRFH 128

RESULT 6
W6WL39
E6 protein - human papillomavirus type 39
C:Species: human papillomavirus type 39
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: A38502
R:Volpers, C.; Streeck, R.E.
Virology 181, 419-423, 1991
A:Title: Genome organization and nucleotide sequence of human papillomavirus type 39.


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Query Match      100.0%; Score 52; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9
Db 70 HLDKKQRFH 78

RESULT 7
Q919B4 ID Q919B4 PRELIMINARY; PRT; 130 AA.
AC Q919B4;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040703; AAL01363.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR PFam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227BEDDC CRC64;

Query Match      100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9
Db 97 HLDKKQRFH 105

RESULT 8
Q919B8 ID Q919B8 PRELIMINARY; PRT; 130 AA.
AC Q919B8;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040701; AAL01359.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR PFam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15775 MW; 92D3C07BF96B092F CRC64;

Query Match      100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9
Db 97 HLDKKQRFH 105

RESULT 9
Q919C0 ID Q919C0 PRELIMINARY; PRT; 130 AA.
AC Q919C0;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040700; AAL01357.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR PFam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match      100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9
Db 97 HLDKKQRFH 105

RESULT 10
Q919C2 ID Q919C2 PRELIMINARY; PRT; 130 AA.
AC Q919C2;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment)
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040699; AAL01355.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR PFam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match      100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9
Db 97 HLDKKQRFH 105
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Db 97 HLDKKQRFH 105
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RESULT 11

Q919C8 PRELIMINARY; PRT; 130 AA.
AC Q919C8; 130 AA.
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404696; AAL01347.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER
SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9
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Db 97 HLDKKQRFH 105
|||||

RESULT 12

Q919D0 PRELIMINARY; PRT; 130 AA.
AC Q919D0; 130 AA.
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404695; AAL01347.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER
SQ SEQUENCE 130 AA; 15735 MW; 9EPB30EDCA21AF3 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9
|||||

Db 97 HLDKKQRFH 105
|||||

RESULT 13

Q919D2 PRELIMINARY; PRT; 138 AA.
AC Q919D2; 138 AA.
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404694; AAL01345.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER
SQ SEQUENCE 138 AA; 16696 MW; 481E5AEA90895FC2 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9
|||||

Db 105 HLDKKQRFH 113
|||||

RESULT 14

Q919B6 PRELIMINARY; PRT; 143 AA.
AC Q919B6; 143 AA.
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404702; AAL01361.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER
SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;

Query Match 100.0%; Score 52; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9
|||||

Db 110 HLDKKQRFH 118
|||||

RESULT 15

Q919C4

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ID Q919C4 PRELIMINARY; PRT; 143 AA.
AC Q919C4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RL Int. J. Cancer 97:868-874 (2002).
DR EMBL; AF404698; AAL01353.1; --
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;

Query Match 100.0%; Score 52; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9
Db 110 HLDKKQRFH 118

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Search completed: June 28, 2005, 23:28:13
 Job time : 56.1 secs

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OM protein - protein search, using sw model

Run on: June 29, 2005, 04:19:44 ; Search time 116.15 Seconds
(without alignments)
29.797 Million cell updates/sec

Title: US-08-170-344-55
Perfect score: 52
Sequence: 1 HLDKKQRFH 9

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Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0
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Listing first 45 summaries

Database : Published Applications AA:
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5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	52	100.0	14	16	US-10-476-570-42
2	52	100.0	20	16	US-10-476-570-41
3	52	100.0	22	16	US-10-476-570-56
4	52	100.0	22	17	US-10-858-384-10
5	52	100.0	23	16	US-10-476-570-40
6	52	100.0	151	14	US-10-177-390-6
7	52	100.0	151	17	US-10-484-063-20
8	52	100.0	151	17	US-10-484-063-27
9	52	100.0	158	17	US-10-858-384-2
10	52	100.0	158	17	US-10-367-057-16
11	52	100.0	171	16	US-10-472-724-2
					Sequence 42, Appl
					Sequence 41, Appl
					Sequence 56, Appl
					Sequence 10, Appl
					Sequence 40, Appl
					Sequence 6, Appl
					Sequence 20, Appl
					Sequence 27, Appl
					Sequence 2, Appl
					Sequence 16, Appl
					Sequence 2, Appl

12	52	100.0	266	9	US-09-367-309A-1	Sequence 1, Appli
13	52	100.0	273	13	US-10-000-903-4	Sequence 4, Appli
14	52	100.0	273	17	US-10-899-771-4	Sequence 4, Appli
15	52	100.0	292	13	US-10-000-903-10	Sequence 10, Appl
16	52	100.0	292	17	US-10-899-771-10	Sequence 10, Appl
17	52	100.0	371	13	US-10-000-903-6	Sequence 6, Appli
18	52	100.0	371	17	US-10-899-771-6	Sequence 6, Appli
19	52	100.0	390	13	US-10-000-903-14	Sequence 14, Appl
20	52	100.0	390	17	US-10-899-771-14	Sequence 14, Appl
21	44	84.6	10	14	US-10-239-313A-538	Sequence 538, App
22	39	75.0	158	16	US-10-800-023-27	Sequence 27, Appl
23	39	75.0	172	16	US-10-472-724-6	Sequence 6, Appli
24	39	75.0	278	13	US-10-000-903-21	Sequence 21, Appl
25	39	75.0	278	17	US-10-899-771-21	Sequence 21, Appl
26	39	75.0	383	13	US-10-000-903-23	Sequence 23, Appl
27	39	75.0	383	17	US-10-899-771-23	Sequence 23, Appl
28	37	71.2	15	14	US-10-283-423-181	Sequence 181, App
29	37	71.2	15	14	US-10-213-821-181	Sequence 181, App
30	37	71.2	978	15	US-10-282-122A-54504	Sequence 54504, A
31	36	69.2	229	16	US-10-425-115-291659	Sequence 291659, A
32	36	69.2	231	9	US-09-925-301-1336	Sequence 1336, Ap
33	36	69.2	960	17	US-10-732-923-8156	Sequence 8156, Ap
34	36	69.2	1266	16	US-10-723-860-4398	Sequence 4398, Ap
35	36	69.2	1281	15	US-10-363-616-334	Sequence 334, App
36	35	67.3	51	17	US-10-926-683-1426	Sequence 1426, App
37	35	67.3	165	15	US-10-424-599-250631	Sequence 250631, A
38	35	67.3	299	15	US-10-378-083-14	Sequence 14, Appl
39	35	67.3	509	14	US-10-156-761-8929	Sequence 8929, Ap
40	35	67.3	535	17	US-10-732-923-2363	Sequence 2363, Ap
41	35	67.3	895	16	US-10-472-078-6	Sequence 6, Appli
42	35	67.3	897	16	US-10-472-078-4	Sequence 4, Appli
43	35	67.3	1005	14	US-10-193-764-41	Sequence 41, Appl
44	35	67.3	1011	14	US-10-193-764-39	Sequence 39, Appl
45	35	67.3	1215	16	US-10-437-963-129618	Sequence 129618, A

ALIGNMENTS

RESULT 1
US-10-476-570-42
; Sequence 42, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from B6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 14
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide B6 124-138
US-10-476-570-42

Query Match 100.0%; Score 52; DB 16; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0081;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9
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 Db 1 HLDKKQRFH 9

RESULT 2

US-10-476-570-41
 ; Sequence 41, Application US/10476570
 ; Publication No. US20040170644A1
 ; GENERAL INFORMATION:
 ; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
 ; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
 ; APPLICANT: MAILLIERE, Bernard
 ; APPLICANT: BOURGAULT-VILLADA, Isabelle
 ; APPLICANT: POUVELLE-MORATILLE, Sandra
 ; APPLICANT: GUILLET, Jean-Gerard
 ; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
 ; TITLE OF INVENTION: papillomavirus proteins and uses thereof
 ; FILE REFERENCE: 45636-5071-US
 ; CURRENT APPLICATION NUMBER: US/10/476,570
 ; CURRENT FILING DATE: 2003-11-04
 ; PRIOR APPLICATION NUMBER: PCT/FR02/01533
 ; PRIOR FILING DATE: 2002-05-03
 ; PRIOR APPLICATION NUMBER: FR 01 05980
 ; PRIOR FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 41
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of the artificial sequence: peptide E6 121-140
 US-10-476-570-41

Query Match 100.0%; Score 52; DB 16; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9
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 Db 5 HLDKKQRFH 13

RESULT 3

US-10-476-570-56
 ; Sequence 56, Application US/10476570
 ; Publication No. US20040170644A1
 ; GENERAL INFORMATION:
 ; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
 ; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
 ; APPLICANT: MAILLIERE, Bernard
 ; APPLICANT: BOURGAULT-VILLADA, Isabelle
 ; APPLICANT: POUVELLE-MORATILLE, Sandra
 ; APPLICANT: GUILLET, Jean-Gerard
 ; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
 ; TITLE OF INVENTION: papillomavirus proteins and uses thereof
 ; FILE REFERENCE: 45636-5071-US
 ; CURRENT APPLICATION NUMBER: US/10/476,570
 ; CURRENT FILING DATE: 2003-11-04
 ; PRIOR APPLICATION NUMBER: PCT/FR02/01533
 ; PRIOR FILING DATE: 2002-05-03
 ; PRIOR APPLICATION NUMBER: FR 01 05980
 ; PRIOR FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 56
 ; LENGTH: 22
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of the artificial sequence: peptide E6 118-139
 US-10-476-570-56

Query Match 100.0%; Score 52; DB 16; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9
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 Db 8 HLDKKQRFH 16

RESULT 4

US-10-858-384-10
 ; Sequence 10, Application US/10858384
 ; Publication No. US20050033025A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHOPPIN, JEANNINE
 ; APPLICANT: BOURGAULT VILLADA, ISABELLE
 ; APPLICANT: GUILLET, JEAN-GERARD
 ; APPLICANT: CONNAN, FRANCINE
 ; APPLICANT: FERRIES, ESTELLE
 ; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
 ; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
 ; FILE REFERENCE: 0508-1037-1
 ; CURRENT APPLICATION NUMBER: US/10/858,384
 ; CURRENT FILING DATE: 2004-06-02
 ; PRIOR APPLICATION NUMBER: FR 9907012
 ; PRIOR FILING DATE: 1999-06-03
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 10
 ; LENGTH: 22
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
 ; OTHER INFORMATION: for E6 of HPV
 US-10-858-384-10

Query Match 100.0%; Score 52; DB 17; Length 22;
 Best Local Similarity 100.0%; Pred. No. 0.013;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9
 |||||
 Db 8 HLDKKQRFH 16

RESULT 5

US-10-476-570-40
 ; Sequence 40, Application US/10476570
 ; Publication No. US20040170644A1
 ; GENERAL INFORMATION:
 ; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
 ; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
 ; APPLICANT: MAILLIERE, Bernard
 ; APPLICANT: BOURGAULT-VILLADA, Isabelle
 ; APPLICANT: POUVELLE-MORATILLE, Sandra
 ; APPLICANT: GUILLET, Jean-Gerard
 ; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
 ; TITLE OF INVENTION: papillomavirus proteins and uses thereof
 ; FILE REFERENCE: 45636-5071-US
 ; CURRENT APPLICATION NUMBER: US/10/476,570
 ; CURRENT FILING DATE: 2003-11-04
 ; PRIOR APPLICATION NUMBER: PCT/FR02/01533
 ; PRIOR FILING DATE: 2002-05-03
 ; PRIOR APPLICATION NUMBER: FR 01 05980
 ; PRIOR FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 40
 ; LENGTH: 23
 ; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: Description of the artificial sequence: peptide E6 118-140
US-10-476-570-40

Query Match 100.0%; Score 52; DB 16; Length 23;

Best Local Similarity 100.0%; Pred. No. 0.013; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 HLDKKQRFH 9

Db 8 HLDKKQRFH 16

RESULT 6

US-10-177-390-6

; Sequence 6, Application US/10177390

; Publication No. US20030143743A1

; GENERAL INFORMATION:

; APPLICANT: Schuler, Gerold

; APPLICANT: N.V. Antwerp Innovatiecentrum

; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear

; TITLE OF INVENTION: Polynucleotides by Electroporation

; FILE REFERENCE: 021505wo/H/ml

; CURRENT APPLICATION NUMBER: US/10/177,390

; CURRENT FILING DATE: 2002-06-20

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6

; LENGTH: 151

; TYPE: PRT

; ORGANISM: Human papillomavirus type 16

US-10-177-390-6

Query Match

Best Local Similarity 100.0%; Score 52; DB 14; Length 151;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9

Db 118 HLDKKQRFH 126

RESULT 7

US-10-484-063-20

; Sequence 20, Application US/10484063

; Publication No. US20050048467A1

; GENERAL INFORMATION:

; APPLICANT: SASTRY, K. JAGANNADHA

; APPLICANT: TORTOLERO-LUNA, GUILLERMO

; APPLICANT: FOLLEN, MICHELE

; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED

; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN

; FILE REFERENCE: UTSC:560US

; CURRENT APPLICATION NUMBER: US/10/484,063

; CURRENT FILING DATE: 2004-01-16

; PRIOR APPLICATION NUMBER: PCT/US02/23198

; PRIOR FILING DATE: 2002-07-19

; PRIOR APPLICATION NUMBER: 60/306,809

; PRIOR FILING DATE: 2001-07-20

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 20

; LENGTH: 151

; TYPE: PRT

; ORGANISM: Human papillomavirus

US-10-484-063-20

Query Match

Best Local Similarity 100.0%; Score 52; DB 17; Length 151;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9

Db 118 HLDKKQRFH 126

RESULT 8

US-10-484-063-27

; Sequence 27, Application US/10484063

; Publication No. US20050048467A1

; GENERAL INFORMATION:

; APPLICANT: SASTRY, K. JAGANNADHA

; APPLICANT: TORTOLERO-LUNA, GUILLERMO

; APPLICANT: FOLLEN, MICHELE

; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED

; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN

; FILE REFERENCE: UTSC:560US

; CURRENT APPLICATION NUMBER: US/10/484,063

; CURRENT FILING DATE: 2004-01-16

; PRIOR APPLICATION NUMBER: PCT/US02/23198

; PRIOR FILING DATE: 2002-07-19

; PRIOR APPLICATION NUMBER: 60/306,809

; PRIOR FILING DATE: 2001-07-20

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 27

; LENGTH: 151

; TYPE: PRT

; ORGANISM: Human papillomavirus type 16

US-10-484-063-27

Query Match

Best Local Similarity 100.0%; Score 52; DB 17; Length 151;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9

Db 118 HLDKKQRFH 126

RESULT 9

US-10-858-384-2

; Sequence 2, Application US/10858384

; Publication No. US20050033025A1

; GENERAL INFORMATION:

; APPLICANT: CHOPPIN, JEANNINE

; APPLICANT: BOURGAULT VILLADA, ISABELLE

; APPLICANT: GUILLET, JEAN-GERARD

; APPLICANT: CONNAN, FRANCINE

; APPLICANT: FERRIES, ESTELLE

; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 PROTEIN

; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE

; FILE REFERENCE: 0508-1037-1

; CURRENT APPLICATION NUMBER: US/10/858,384

; CURRENT FILING DATE: 2004-06-02

; PRIOR APPLICATION NUMBER: FR 9907012

; PRIOR FILING DATE: 1999-06-03

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 2

; LENGTH: 158

; TYPE: PRT

; ORGANISM: Human Papillomavirus

US-10-858-384-2

Query Match

Best Local Similarity 100.0%; Score 52; DB 17; Length 158;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9

Db 125 HLDKKQRFH 133

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RESULT 10
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match      100.0%; Score 52; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.093;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRPH 9
Db 125 HLDKKQRPH 133

RESULT 11
US-10-472-724-2
; Sequence 24, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match      100.0%; Score 52; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRPH 9
Db 130 HLDKKQRPH 138

RESULT 12
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM

```

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; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match      100.0%; Score 52; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRPH 9
Db 125 HLDKKQRPH 133

RESULT 13
US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4

Query Match      100.0%; Score 52; DB 13; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRPH 9
Db 231 HLDKKQRPH 239

RESULT 14
US-10-899-771-4
; Sequence 4, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976

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; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-4

```

```

Query Match      100.0%; Score 52; DB 17; Length 273;
Best Local Similarity 100.0%; Pred.No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 HLDKKQRFH 9
        |||||
Db      231 HLDKKQRFH 239

```

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RESULT 15
US-10-000-903-10
; Sequence 10, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezón Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-10

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Query Match      100.0%; Score 52; DB 13; Length 292;
Best Local Similarity 100.0%; Pred.No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 HLDKKQRFH 9
        |||||
Db      250 HLDKKQRFH 258

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Search completed: June 29, 2005, 05:18:15
Job time : 116.15 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 28, 2005, 21:33:36 ; Search time 17.05 Seconds
(without alignments)
39.404 Million cell updates/sec

Title: US-08-170-344-55
Perfect score: 52
Sequence: 1 HLDKKQRFH 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	9	3	US-08-159-339A-223
2	52	100.0	20	4	Sequence 223, App
3	52	100.0	22	4	Sequence 278, App
4	52	100.0	158	4	Sequence 10, Appl
5	52	100.0	162	1	Sequence 2, Appl
6	52	100.0	162	1	Sequence 3, Appl
7	52	100.0	172	3	Sequence 4, Appl
8	52	100.0	172	3	Sequence 12, Appl
9	52	100.0	182	1	Sequence 12, Appl
10	52	100.0	266	3	Sequence 10, Appl
11	52	100.0	266	3	Sequence 10, Appl
12	52	100.0	266	3	Sequence 10, Appl
13	52	100.0	273	3	Sequence 1, Appl
14	52	100.0	292	3	Sequence 4, Appl
15	52	100.0	371	3	Sequence 10, Appl
16	52	100.0	390	3	Sequence 6, Appl
17	47	90.4	21	2	Sequence 14, Appl
18	40	76.9	10	1	Sequence 166, App
19	39	75.0	158	2	Sequence 5, Appl
20	39	75.0	158	3	Sequence 10, Appl
21	39	75.0	271	1	Sequence 19, Appl
22	39	75.0	278	3	Sequence 14, Appl
23	39	75.0	383	3	Sequence 21, Appl
24	37	71.2	362	4	Sequence 23, Appl
25	35	67.3	51	4	Sequence 17504, A
26	35	67.3	51	4	Sequence 4563, Ap
27	35	67.3	535	2	Sequence 1426, Ap
					Sequence 2, Appl

28 35 67.3 538 4 US-09-489-039A-11091 Sequence 11091, A
29 35 67.3 805 4 US-09-252-991A-32752 Sequence 32752, A
30 35 67.3 1005 4 US-09-206-942-41 Sequence 41, Appl
31 35 67.3 1011 4 US-09-206-942-39 Sequence 39, Appl
32 34 65.4 181 4 US-09-270-767-40463 Sequence 40463, A
33 34 65.4 181 4 US-09-270-767-55679 Sequence 55679, A
34 34 65.4 352 4 US-09-252-991A-17455 Sequence 17455, A
35 33 63.5 90 1 US-08-341-219-24 Sequence 24, Appl
36 33 63.5 90 3 US-08-912-314A-24 Sequence 24, Appl
37 33 63.5 124 4 US-09-270-767-33151 Sequence 33151, A
38 33 63.5 130 1 US-08-485-455D-67 Sequence 67, Appl
39 33 63.5 130 2 US-08-482-130C-67 Sequence 67, Appl
40 33 63.5 130 2 US-08-484-211C-67 Sequence 67, Appl
41 33 63.5 130 3 US-08-906-769-67 Sequence 67, Appl
42 33 63.5 130 3 US-08-906-616-67 Sequence 67, Appl
43 33 63.5 130 3 US-08-817-795-67 Sequence 67, Appl
44 33 63.5 130 3 US-08-485-443B-67 Sequence 67, Appl
45 33 63.5 130 3 US-08-639-075A-67 Sequence 67, Appl

ALIGNMENTS

RESULT 1
US-08-159-339A-223
; Sequence 223, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 223:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-223

Query Match 100.0%; Score 52; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9
| | | | | | | | |
Db 1 HLDKKQRFH 9

RESULT 2

US-09-601-729-278
; Sequence 278, Application US/09601729

; Patent No. 6683052

; GENERAL INFORMATION:

; APPLICANT: THIAM, KADER

; APPLICANT: AURIAULT, CLAUDE

; APPLICANT: GRAS-MASSE, HELENE

; APPLICANT: LOING, ESTELLE

; APPLICANT: VERWAERDE, CLAUDIE

; APPLICANT: GUILLET, JEAN GERARD

; TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES
; TITLE OF INVENTION: THEROF IN PHARMACEUTICAL COMPOSITIONS

; FILE REFERENCE: USB-97-AU-IN

; CURRENT APPLICATION NUMBER: US/09/601,729

; CURRENT FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: PCT/FR99/00259

; PRIOR FILING DATE: 1999-02-05

; PRIOR APPLICATION NUMBER: 98 01439

; PRIOR FILING DATE: 1998-02-06

; NUMBER OF SEQ ID NOS: 281

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 278

; LENGTH: 20

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

; OTHER INFORMATION: peptide

US-09-601-729-278

Query Match 100.0%; Score 52; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0045;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9
| | | | | | | | | |
Db 5 HLDKKQRFH 13

RESULT 3

US-09-980-523A-10

; Sequence 10, Application US/09980523A

; Patent No. 6783763

; GENERAL INFORMATION:

; APPLICANT: CHOPPIN, JEANNINE

; APPLICANT: BOURGAULT VILLADA, ISABELLE

; APPLICANT: GUILLET, JEAN-GERARD

; APPLICANT: CONNAN, FRANCINE

; APPLICANT: FERRIES, ESTELLE

; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE

; TITLE OF INVENTION: PARTICULARLY IN VACCINATION

; FILE REFERENCE: WO81 AO INS

; CURRENT APPLICATION NUMBER: US/09/980,523A

; CURRENT FILING DATE: 2002-04-29

; PRIOR APPLICATION NUMBER: PCT/FR00/01513

; PRIOR FILING DATE: 2000-05-31

; PRIOR APPLICATION NUMBER: FR 99/07012

; PRIOR FILING DATE: 1999-06-03

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 10
; LENGTH: 22
; TYPE: PRT

; ORGANISM: Human Papillomavirus
US-09-980-523A-10

Query Match 100.0%; Score 52; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9
| | | | | | | | |
Db 8 HLDKKQRFH 16

RESULT 4

US-09-980-523A-2

; Sequence 2, Application US/09980523A

; Patent No. 6783763

; GENERAL INFORMATION:

; APPLICANT: CHOPPIN, JEANNINE

; APPLICANT: BOURGAULT VILLADA, ISABELLE

; APPLICANT: GUILLET, JEAN-GERARD

; APPLICANT: CONNAN, FRANCINE

; APPLICANT: FERRIES, ESTELLE

; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7

; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE

; TITLE OF INVENTION: PARTICULARLY IN VACCINATION

; FILE REFERENCE: WO81 AO INS

; CURRENT APPLICATION NUMBER: US/09/980,523A

; CURRENT FILING DATE: 2002-04-29

; PRIOR APPLICATION NUMBER: PCT/FR00/01513

; PRIOR FILING DATE: 2000-05-31

; PRIOR APPLICATION NUMBER: FR 99/07012

; PRIOR FILING DATE: 1999-06-03

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 158

; TYPE: PRT

; ORGANISM: Human Papillomavirus

US-09-980-523A-2

Query Match 100.0%; Score 52; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLDKKQRFH 9
| | | | | | | | |
Db 125 HLDKKQRFH 133

RESULT 5

US-08-316-239B-3

; Sequence 3, Application US/08316239B

; Patent No. 5679509

; GENERAL INFORMATION:

; APPLICANT: Wheeler, Cosette M.

; APPLICANT: Parmenter, Cheryl A.

; TITLE OF INVENTION: Methods and a Diagnostic Aid for

; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an

; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and

; TITLE OF INVENTION: Cervical Cancer

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jagtiani & Associates

; STREET: 6126 Rocky Way Court

; CITY: Centreville

; STATE: VA

; COUNTRY: USA

; ZIP: 20120-3400

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jagtiani, Ajay A.
REGISTRATION NUMBER: 35,205
REFERENCE/DOCKET NUMBER: UNME-0001
TELEPHONE: (703) 817-9453
TELEFAX: (703) 803-9387
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 100.0%; Score 52; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLDKKQRFH 9
DB 125 HLDKKQRFH 133

RESULT 6

US-08-316-239B-4
Sequence 4, Application US/08316239B
Patent No. 5679509
GENERAL INFORMATION:
APPLICANT: Wheeler, Cosette M.
APPLICANT: Parmenter, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
TITLE OF INVENTION: Cervical Cancer
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Jagtiani & Associates
STREET: 6126 Rocky Way Court
CITY: Centreville
STATE: VA
COUNTRY: USA
ZIP: 20120-3400

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jagtiani, Ajay A.
REGISTRATION NUMBER: 35,205
REFERENCE/DOCKET NUMBER: UNME-0001
TELEPHONE: (703) 817-9453
TELEFAX: (703) 803-9387
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant

TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 100.0%; Score 52; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLDKKQRFH 9
DB 125 HLDKKQRFH 133

RESULT 7

US-08-860-165-12
Sequence 12, Application US/08860165A
Patent No. 6004557
GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PN0157
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 12
LENGTH: 172
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12

Query Match 100.0%; Score 52; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLDKKQRFH 9
DB 63 HLDKKQRFH 71

RESULT 8

US-09-359-382-12
Sequence 12, Application US/09359382
Patent No. 6306397
GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 017227/0148
CURRENT APPLICATION NUMBER: US/09/359,382
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: US 08/860,165
EARLIER FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PN0157/94
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 12
LENGTH: 172

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; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-12

Query Match      100.0%; Score 52; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HLDKKQRFH 9
Db      63 HLDKKQRFH 71

RESULT 9
US-08-117-083-10
; Sequence 10, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Bourasnell, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
; OTHER INFORMATION: /note="Xaa refers to stop codon in
; OTHER INFORMATION: the open reading frame."
US-08-117-083-10

Query Match      100.0%; Score 52; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HLDKKQRFH 9
Db      86 HLDKKQRFH 94

RESULT 10
US-08-860-165-10
; Sequence 1, Application US/09367309A
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; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match      100.0%; Score 52; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HLDKKQRFH 9
Db      125 HLDKKQRFH 133

RESULT 11
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match      100.0%; Score 52; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HLDKKQRFH 9
Db      125 HLDKKQRFH 133

RESULT 12
US-09-367-309A-1
; Sequence 1, Application US/09367309A
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; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match      100.0%; Score 52; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLDKKQRPH 9
Db 125 HLDKKQRPH 133

RESULT 13
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match      100.0%; Score 52; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLDKKQRPH 9
Db 231 HLDKKQRPH 239

RESULT 14
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6

Query Match      100.0%; Score 52; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLDKKQRPH 9
Db 231 HLDKKQRPH 239

Search completed: June 28, 2005, 23:37:53
Job time : 18.05 secs
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:24:19 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-54

Perfect score: 51

Sequence: 1 LIRCINCOQ 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	81	2 Q80886	Q80886 human papil
2	51	100.0	84	2 Q80882	Q80882 human papil
3	51	100.0	90	2 Q80883	Q80883 human papil
4	51	100.0	90	2 Q80884	Q80884 human papil
5	51	100.0	90	2 Q80885	Q80885 human papil
6	51	100.0	91	2 Q80887	Q80887 human papil
7	51	100.0	99	2 Q19B2	Q19B2 human papil
8	51	100.0	103	2 Q19D6	Q19D6 human papil
9	51	100.0	130	2 Q19B4	Q19B4 human papil
10	51	100.0	130	2 Q19B8	Q19B8 human papil
11	51	100.0	130	2 Q19C0	Q19C0 human papil
12	51	100.0	130	2 Q19C2	Q19C2 human papil
13	51	100.0	130	2 Q19C8	Q19C8 human papil
14	51	100.0	130	2 Q19D0	Q19D0 human papil
15	51	100.0	138	2 Q19D2	Q19D2 human papil
16	51	100.0	143	2 Q19B6	Q19B6 human papil
17	51	100.0	143	2 Q19C4	Q19C4 human papil
18	51	100.0	151	2 Q12335	Q12335 human papil
19	51	100.0	151	2 Q76TS0	Q76TS0 human papil
20	51	100.0	151	2 Q77E16	Q77E16 human papil
21	51	100.0	151	2 Q77E16	Q77E16 human papil
22	51	100.0	151	2 Q77JC7	Q77JC7 human papil
23	51	100.0	151	2 Q77ZJ5	Q77ZJ5 human papil
24	51	100.0	151	2 Q80963	Q80963 human papil
25	51	100.0	151	2 Q80966	Q80966 human papil
26	51	100.0	151	2 Q89640	Q89640 human papil
27	51	100.0	151	2 Q89648	Q89648 human papil
28	51	100.0	151	2 Q89708	Q89708 human papil
29	51	100.0	151	2 Q89755	Q89755 human papil
30	51	100.0	151	2 Q89852	Q89852 human papil
31	51	100.0	151	2 Q89887	Q89887 human papil

32 51 100.0 151 2 Q8B564 human papil
33 51 100.0 151 2 Q8BB19 human papil
34 51 100.0 151 2 Q8BB20 human papil
35 51 100.0 151 2 Q8BB21 human papil
36 51 100.0 151 2 Q8W8C3 human papil
37 51 100.0 151 2 Q8W931 human papil
38 51 100.0 151 2 Q8WMP2 human papil
39 51 100.0 151 2 Q8WMP3 human papil
40 51 100.0 151 2 Q8WMP5 human papil
41 51 100.0 158 1 V86 HPV16 human papil
42 51 100.0 158 2 Q8JMU8 human papil
43 51 100.0 158 2 Q8QHN0 human papil
44 51 100.0 158 2 Q8QHP5 human papil
45 51 100.0 158 2 Q8QHT0 human papil

ALIGNMENTS

RESULT 1
Q80886 PRELIMINARY; PRT; 81 AA.
AC Q80886;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14515; AAB60569.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 81 81
SQ SEQUENCE 81 AA; 9784 MW; DD5FEDBC9F845B97 CRC64;

Query Match Similarity 100.0%; Score 51; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 0.2; 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0

Qy 1 LIRCINCOQ 9
Db 59 LIRCINCOQ 67

RESULT 2
Q80882 PRELIMINARY; PRT; 84 AA.
AC Q80882;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14511; AAB60565.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.

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DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 84
SQ SEQUENCE 84 AA; 10177 MW; 5AB6B896468E1CAA CRC64;
Query Match 100.0%; Score 51; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
Db 56 LIRCINCOK 64

RESULT 3
Q80883 PRELIMINARY; PRT; 90 AA.
AC Q80883;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14512; AAB60566.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 10904 MW; 5D3ADF843AD6060B CRC64;
Query Match 100.0%; Score 51; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
Db 59 LIRCINCOK 67

RESULT 4
Q80884 PRELIMINARY; PRT; 90 AA.
AC Q80884;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14513; AAB60567.2; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.

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FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 11021 MW; 47F42BBEFACCCC01 CRC64;
Query Match 100.0%; Score 51; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
Db 59 LIRCINCOK 67

RESULT 5
Q80885 PRELIMINARY; PRT; 90 AA.
AC Q80885;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14514; AAB60568.2; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 10964 MW; BC2531643ACBA76C CRC64;
Query Match 100.0%; Score 51; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
Db 59 LIRCINCOK 67

RESULT 6
Q80887 PRELIMINARY; PRT; 91 AA.
AC Q80887;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14516; AAB60570.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 91
SQ SEQUENCE 91 AA; 11136 MW; 22FDF3EA185ACHA7 CRC64;

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Query Match 100.0%; Score 51; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
| | | | | | | |
Db 59 LIRCINCOK 67

RESULT 7

Q919B2 PRELIMINARY; PRT; 99 AA.
AC Q919B2; 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF0404704; AAL01342.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 99
SQ SEQUENCE 99 AA; 12005 MW; C2B96025EC370E38 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
| | | | | | | |
Db 76 LIRCINCOK 84

RESULT 8

Q919D6 PRELIMINARY; PRT; 103 AA.
AC Q919D6; 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF0404692; AAL01342.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 103
SQ SEQUENCE 103 AA; 12422 MW; 6F90CBAF1F25449B CRC64;

Query Match 100.0%; Score 51; DB 2; Length 103;

Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
| | | | | | | |
Db 52 LIRCINCOK 60

RESULT 9

Q919B4 PRELIMINARY; PRT; 130 AA.
AC Q919B4; 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF0404703; AAL01363.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 130
SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227EEDDC CRC64;

Query Match 100.0%; Score 51; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
| | | | | | | |
Db 79 LIRCINCOK 87

RESULT 10

Q919B8 PRELIMINARY; PRT; 130 AA.
AC Q919B8; 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF0404701; AAL01359.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 130
SQ SEQUENCE 130 AA; 15775 MW; 92D3C07BF96B092F CRC64;

Query Match 100.0%; Score 51; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 LIRCINCOK 9
    |||||||
Db 79 LIRCINCOK 87

RESULT 11
Q919C0 PRELIMINARY; PRT; 130 AA.
AC Q919C0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404700; AAL01357.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. NO. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
    |||||||
Db 79 LIRCINCOK 87

RESULT 12
Q919C2 PRELIMINARY; PRT; 130 AA.
AC Q919C2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404699; AAL01355.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. NO. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
    |||||||
Db 79 LIRCINCOK 87

RESULT 13
Q919C8 PRELIMINARY; PRT; 130 AA.
AC Q919C8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404696; AAL01349.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15778 MW; 2830147D37880DC9 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. NO. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
    |||||||
Db 79 LIRCINCOK 87

RESULT 14
Q919D0 PRELIMINARY; PRT; 130 AA.
AC Q919D0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404695; AAL01347.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15735 MW; 9EFB30EEDCA21AF3 CRC64;

Query Match 100.0%; Score 51; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. NO. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
    |||||||
Db 79 LIRCINCOK 87

RESULT 15
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Q919D2
 ID Q919D2 PRELIMINARY; PRT; 138 AA.
 AC Q919D2;
 DT 01-DEC-2001 (TREMELrel. 19, Created)
 DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404694; AAL01345.1; --
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON TER 1
 SQ SEQUENCE 138 AA; 16696 MW; 481ESA9A90895FC2 CRC64;
 Query Match 100.0%; Score 51; DB 2; Length 138;
 Best Local Similarity 100.0%; Pred. No. 0.33;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LIRCINCOK 9
 DB 87 LIRCINCOK 95

Search completed: June 28, 2005, 23:28:12
 Job time : 55.1 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:28:02 ; Search time 11.05 Seconds
(without alignments)
78.367 Million cell updates/sec

Title: US-08-170-344-54
Perfect score: 51
Sequence: 1 LIRCINQCK 9
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	158	1 W6WL35	protein E6 - human
2	45	88.2	149	1 W6WL35	E6 protein - human
3	43	84.3	158	1 W6WL18	E6 protein - human
4	43	84.3	158	2 S36561	E6 protein - human
5	42	82.4	149	1 W6WL31	E6 protein - human
6	41	80.4	75	2 E91249	C4-type zinc finger
7	40	78.4	119	2 S47942	ribosomal protein
8	40	78.4	119	2 S50634	ribosomal protein
9	39	76.5	103	2 T08775	hypothetical prote
10	39	76.5	149	1 W6WL33	E6 protein - human
11	39	76.5	149	1 W6WL58	ribosomal protein
12	38	74.5	113	2 T43515	E6 protein - human
13	38	74.5	119	2 T37896	40s ribosomal prot
14	38	74.5	120	2 T39095	40s ribosomal prot
15	38	74.5	230	2 C50266	heterodisulfide re
16	38	74.5	559	2 T33347	hypothetical prote
17	37	72.5	103	2 T26806	hypothetical prote
18	37	72.5	148	2 S36515	E6 protein - human
19	37	72.5	191	1 W6WL11	E6 protein - hesu
20	37	72.5	311	2 B84428	hypothetical prote
21	37	72.5	1932	2 T25525	hypothetical prote
22	36	70.6	120	2 T14466	lipid transfer pro
23	36	70.6	133	2 AB3465	hypothetical prote
24	36	70.6	153	2 S36503	E6 protein - human
25	36	70.6	198	2 S48236	SNW1 protein - yea
26	36	70.6	274	2 T34004	hypothetical prote
27	36	70.6	795	2 T48252	eciferinm3 (CER3)
28	36	70.6	902	2 B84652	hypothetical prote
29	35	68.6	38	2 S07972	regulatory protein

30	35	68.6	133	2 T04081	probable ribosomal
31	35	68.6	134	2 T28417	ORF MSV256 hypothe
32	35	68.6	142	2 S36509	E6 protein - human
33	35	68.6	155	1 W6WL56	E6 protein - human
34	35	68.6	314	2 D96703	hypothetical prote
35	35	68.6	451	2 G01227	recepin - human
36	35	68.6	506	1 A38068	gag polyprotein -
37	35	68.6	695	2 E70923	hypothetical prote
38	35	68.6	797	2 T27518	hypothetical prote
39	35	68.6	950	2 S27473	URB1 protein - sm
40	34	66.7	53	2 AC2031	hypothetical prote
41	34	66.7	63	2 AC8278	hypothetical prote
42	34	66.7	67	2 C98802	conserved hypotet
43	34	66.7	73	2 S24472	gag polyprotein -
44	34	66.7	75	2 S24475	gag polyprotein -
45	34	66.7	89	2 AC2284	hypothetical prote

ALIGNMENTS

RESULT 1

W6WL35
protein E6 - human papillomavirus type 16
C:Species: human papillomavirus type 16
C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C:Accession: A03682; T10427
R:Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
Virology 145, 181-185, 1985
A:Title: Human papillomavirus type 16 DNA sequence.
A:Reference number: A22355; MUID:85246220; PMID:2990099
A:Accession: A03682
A:Molecule type: DNA
A:Residues: 1-158 <SEE>
A:Cross-references: UNIPROT:P03126; GB:K02719; NID:G333031; PIDN:AAA46939.1; PID:G333032
R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level
A:Reference number: 217014; MUID:91162763; PMID:1848319
A:Accession: T10427
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-158 <KEN>
A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
C:Genetics:
A:Gene: E6
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:37-73/Region: zinc finger CCCC motif
F:110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 51; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. NO. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LIRCINQCK 9

Db 107 LIRCINQCK 115

RESULT 2

W6WL35
E6 protein - human papillomavirus type 35
C:Species: human papillomavirus type 35
A:Note: host Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: E40824; S36521
R:Marich, J.E.; Pontaler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776, 1992
A:Title: The phylogenetic relationship and complete nucleotide sequence of human papillon
A:Reference number: A40824; MUID:92124753; PMID:1310198
A:Accession: E40824
A:Status: translation not shown

```
A;Molecule type: DNA
A;Residues: 1-149 <MAP>
A;Cross-references: UNIPROT:P27228; GB:M74117; NID:G333050; PIDN:AAA46966.1; PID:G333051
R;Delius, H.; Hofmann, B.
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36521
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-149 <DEL>
A;Cross-references: EMBL:X74477; NID:G396997; PIDN:CAA52561.1; PID:G396998
A;Experimental source: strain 35H
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif

Query Match      88.2%; Score 45; DB 1; Length 149;
Best Local Similarity 88.9%; Pred. No. 2.6; 1; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 1;

Qy 1 LIRCINQCK 9
    ||||| |||
Db 100 LIRCITCQK 108

RESULT 3
W6WL18
E6 protein - human papillomavirus type 18
C;Species: human papillomavirus type 18
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C;Accession: A26165; G26251
R;Seedorf, K.; Oltersdorf, T.; Kraemmer, G.; Roewekamp, W.
EMBO J. 6, 139-144, 1987
A;Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 16)
A;Reference number: A91068; MUID:87218459; PMID:3034571
A;Accession: A26165
A;Molecule type: DNA
A;Residues: 1-158 <SEE>
A;Cross-references: UNIPROT:P06463; GB:X04773; NID:G60876; PIDN:CAA28466.1; PID:G60877
R;Cole, S.T.; Danos, O.
J. Mol. Biol. 193, 595-608, 1987
A;Title: Nucleotide sequence and comparative analysis of the human papillomavirus type 1
A;Reference number: A92937; MUID:87283882; PMID:3039146
A;Accession: G26251
A;Molecule type: DNA
A;Residues: 1-158 <COL>
A;Cross-references: GB:X05015; NID:G60975; PIDN:CAA28664.1; PID:G60976
R;Matlashewski, G.; Banks, L.; Wu-Liao, J.; Spence, P.; Pim, D.; Crawford, L.
J. Gen. Virol. 67, 1909-1916, 1986
A;Title: The expression of human papillomavirus type 18 E6 protein in bacteria and the p
A;Contents: annotation: identification of the protein
A;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;32-68/Region: zinc finger CCCC motif
F;105-141/Region: zinc finger CCCC motif

Query Match      84.3%; Score 43; DB 1; Length 158;
Best Local Similarity 77.8%; Pred. No. 5.5;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LIRCINQCK 9
    ||||| |||
Db 102 LIRCIRCQK 110

RESULT 4
S36561
E6 protein - human papillomavirus type 45
C;Species: human papillomavirus type 45
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
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```
C;Accession: S36561
R;Delius, H.; Hofmann, B.
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36561
A;Molecule type: DNA
A;Residues: 1-158 <DEL>
A;Cross-references: UNIPROT:P21735; EMBL:X74479; NID:G397022; PIDN:CAA52573.1; PID:G39702;
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match      84.3%; Score 43; DB 2; Length 158;
Best Local Similarity 77.8%; Pred. No. 5.5;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LIRCINQCK 9
    ||||| |||
Db 102 LIRCIRCQK 110

RESULT 5
W6WL31
E6 protein - human papillomavirus type 31
C;Species: human papillomavirus type 31
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: A32444
R;Goldsbrough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.
Virolgy 171, 306-311, 1989
A;Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associated
A;Reference number: A94398; MUID:89299478; PMID:2545036
A;Accession: A32444
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-149 <GOL>
A;Cross-references: UNIPROT:P17386; GB:J04353; NID:G333048; PIDN:AAA46950.1; PID:G459916
C;Comment: This protein may be involved in the oncogenic potential of this virus.
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif

Query Match      82.4%; Score 42; DB 1; Length 149;
Best Local Similarity 77.8%; Pred. No. 7.5;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LIRCINQCK 9
    ||||| |||
Db 100 LIRCITCQK 108

RESULT 6
E91249
C4-type zinc finger protein (TraR family) [imported] - Escherichia coli (strain O157:H7,
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: E91249
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: E91249
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-75 <HAY>
A;Cross-references: UNIPROT:Q8X320; GB:BA000007; PIDN:BA838388.1; PID:gl3364441; GSPDB:G
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs4965

Query Match      80.4%; Score 41; DB 2; Length 75;
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Best Local Similarity 85.7%; Pred. No. 6.6; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 1;
Qy 2 IRCINCQ 8
Db 57 IRCVNCQ 63
RESULT 7
S47942
ribosomal protein S26.e.A, cytosolic - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein G1355; protein YGL189C
C:Species: Saccharomyces cerevisiae
C:Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 09-Jul-2004
C:Accession: S47942; S61129; S64206
R:Wu, M.; Tan, H.
submitted to the EMBL Data Library, June 1994
A:Description: Disruption of RPS26 in Saccharomyces cerevisiae results in the formation
A:Reference number: S47942
A:Accession: S47942
A:Molecule type: DNA
A:Residues: 1-119 <WUM>
A:Cross-references: UNIPROT:P3938; EMBL:U10563; NID:G533506; PIDN:AAA66066.1; PID:G5335
R:Bertani, I.; Coglievina, M.; Zaccaria, F.; Klima, R.; Bruschi, C.V.
submitted to the EMBL Data Library, September 1995
A:Description: The sequence analysis of a 7.9 kb DNA fragment from the left arm of S.cer
ive new Genes.
A:Reference number: S61128
A:Accession: S61128
A:Molecule type: DNA
A:Residues: 1-119 <BER>
A:Cross-references: EMBL:X91489; NID:G1143557; PIDN:CAA62786.1; PID:G1143559
R:Bruschi, C.V.; Coglievina, M.; Bertani, I.; Klima, R.; Zaccaria, P.; Delneri, D.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64183
A:Accession: S64206
A:Molecule type: DNA
A:Residues: 1-119 <BRU>
A:Cross-references: EMBL:Z72711; NID:G1322808; PIDN:CAA96901.1; PID:G1322809; MIPS:YGL18
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:RPS26A
A:Cross-references: SGD:S0003157; MIPS:YGL189C
A:Map position: 7L
C:Superfamily: rat ribosomal protein S26
C:Keywords: cytosol; protein biosynthesis; ribosome
Query Match 78.4%; Score 40; DB 2; Length 119;
Best Local Similarity 62.5%; Pred. No. 13; Mismatches 2; Indels 1; Gaps 0;
Matches 5; Conservative 2;
Qy 2 IRCINCQ 9
Db 21 VRCVNCQ 28
RESULT 8
S50634
ribosomal protein S26.e.B, cytosolic - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YER131W
C:Species: Saccharomyces cerevisiae
C:Date: 28-Jan-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C:Accession: S50634
R:Dieterich, F.S.
submitted to the EMBL Data Library, December 1994
A:Description: The sequence of S. cerevisiae cosmids 9781, 8198, 9115, 9981, and lambda
A:Reference number: S50437
A:Accession: S50634
A:Molecule type: DNA
A:Residues: 1-119 <DIE>
A:Cross-references: UNIPROT:P3939; EMBL:U18916; NID:G1384128; PIDN:AAC03229.1; PID:G603
C:Genetics:
A:Gene: SGD:RPS26B

A:Cross-references: SGD:S0000933; MIPS:YER131W
A:Map position: 5R
C:Superfamily: rat ribosomal protein S26
C:Keywords: cytosol; protein biosynthesis; ribosome
Query Match 78.4%; Score 40; DB 2; Length 119;
Best Local Similarity 62.5%; Pred. No. 13; Mismatches 2; Indels 1; Gaps 0;
Matches 5; Conservative 2;
Qy 2 IRCINCQ 9
Db 21 VRCVNCQ 28
RESULT 9
T08775
hypothetical protein DKFZp586C1620.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T08775
R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, March 1999
A:Reference number: Z16471
A:Accession: T08775
A:Molecule type: mRNA
A:Residues: 1-103 <WAM>
A:Cross-references: UNIPROT:Q9Y3X7; EMBL:AL050144
A:Experimental source: adult uterus; clone DKFZp586C1620
C:Genetics:
A:Note: DKFZp586C1620.1
Query Match 76.5%; Score 39; DB 2; Length 103;
Best Local Similarity 62.5%; Pred. No. 17; Mismatches 3; Indels 0; Gaps 0;
Matches 5; Conservative 3;
Qy 2 IRCINCQ 9
Db 27 VQCINCEK 34
RESULT 10
W6WLJ33
E6 protein - human papillomavirus type 33
C:Species: human papillomavirus type 33
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: A03683
R:Cole, S.T.; Strebeck, R.E.
J. Virol. 58, 991-995, 1986
A:Title: Genome organization and nucleotide sequence of human papillomavirus type 33, whi
A:Reference number: A93020; MUID:86200464; PMID:3009902
A:Accession: A03683
A:Molecule type: DNA
A:Residues: 1-149 <COL>
A:Cross-references: UNIPROT:P06427; GB:M12732; NID:G333049; PIDN:AAA46958.1; PID:G463177
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif
Query Match 76.5%; Score 39; DB 1; Length 149;
Best Local Similarity 77.8%; Pred. No. 22; Mismatches 1; Indels 0; Gaps 0;
Matches 7; Conservative 1;
Qy 1 LIRCINCQ 9
Db 100 LIRCICQ 108
RESULT 11
W6WLJ58
E6 protein - human papillomavirus type 58
C:Species: human papillomavirus type 58
A:Note: host Homo sapiens (man)

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: E36779
R;Kirii, Y.; Iwamoto, S.; Matsukura, T.
Virology 185, 424-427, 1991
A;Title: Human papillomavirus type 58 DNA sequence.
A;Reference number: A36779; MUID:92024102; PMID:1656594
A;Accession: E36779
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-149 <KTR>
A;Cross-references: UNIPROT:P26555; GB:D90400; NID:g222386; PIDN:BAA31845.1; PID:g333709
C;Superfamily: Schizosaccharomyces pombe
C;Keywords: DNA binding; early protein; zinc finger
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif

Query Match 76.5%; Score 39; DB 1; Length 149;
Best Local Similarity 77.8%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
:|||||:
Db 100 LIRCIICOR 108

RESULT 12

ribosomal protein S26 - fission yeast (Schizosaccharomyces pombe) (fragment)
C;Species: Schizosaccharomyces pombe
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43515
R;Kawamukai, M.
submitted to the EMBL Data Library, July 1999
A;Description: S. pombe ribosomal protein S26 homolog.
A;Reference number: Z22530
A;Accession: T43515
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-113 <KAW>
A;Cross-references: UNIPROT:Q9UTG4; EMBL:AB029514; PIDN:BAA82318.1
C;Superfamily: rat ribosomal protein S26

Query Match 74.5%; Score 38; DB 2; Length 113;
Best Local Similarity 62.5%; Pred. No. 26;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IRCINCOK 9
:|||||:
Db 15 VRCINCSR 22

RESULT 13

40S ribosomal protein S26 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37896
R;Rieger, M.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1999
A;Reference number: Z21752
A;Accession: T37896
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-119 <RIE>
A;Cross-references: UNIPROT:Q9UTG4; EMBL:AL117390; PIDN:CAB55852.1; GSPDB:GN000066; SPDB:
A;Experimental source: strain 972h-; cosmid c1805
C;Genetics:
A;Gene: SPDB:SPAC1805.11c
A;Map position: 1
A;Introns: 42/1
C;Superfamily: rat ribosomal protein S26

Query Match 74.5%; Score 38; DB 2; Length 119;

Best Local Similarity 62.5%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IRCINCOK 9
:|||||:
Db 21 VRCINCSR 28

RESULT 14

40S ribosomal protein S26 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39095
R;Wedler, H.; Duesterhoeft, A.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1999
A;Reference number: Z21827
A;Accession: T39095
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-120 <WED>
A;Cross-references: UNIPROT:Q9UT56; EMBL:AL117212; PIDN:CAB55282.1; GSPDB:GN000066; SPDB:
A;Experimental source: strain 972h-; cosmid c806
C;Genetics:
A;Gene: SPDB:SPAC806.03c
A;Map position: 1
C;Superfamily: rat ribosomal protein S26

Query Match 74.5%; Score 38; DB 2; Length 120;
Best Local Similarity 62.5%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IRCINCOK 9
:|||||:
Db 21 VRCINCSR 28

RESULT 15

heterodisulfide reductase subunit C (hdcC-2) [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: C90266
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-y
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
arratt, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: C90266
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-230 <KUR>
A;Cross-references: UNIPROT:Q97212; GB:AE006641; NID:gl3814322; PIDN:AAK41386.1; GSPDB:G
C;Genetics:
A;Gene: hdcC-2

Query Match 74.5%; Score 38; DB 2; Length 230;
Best Local Similarity 66.7%; Pred. No. 43;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
:|||||:
Db 106 LWRVCSCOK 114

Search completed: June 28, 2005, 23:32:10
Job time : 12.05 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 04:19:44 ; Search time 116.15 Seconds
(without alignments)
29.797 Million cell updates/sec

Title: US-08-170-344-54

Perfect score: 51

Sequence: 1 LIRINCQK 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	15	16	US-10-476-570-39
2	51	100.0	20	17	US-10-484-063-8
3	51	100.0	22	16	US-10-476-570-60
4	51	100.0	29	16	US-10-476-570-13
5	51	100.0	151	14	US-10-177-390-6
6	51	100.0	151	17	US-10-484-063-20
7	51	100.0	151	17	US-10-484-063-27
8	51	100.0	158	17	US-10-858-384-2
9	51	100.0	158	17	US-10-367-057-16
10	51	100.0	171	16	US-10-472-724-2
11	51	100.0	266	9	US-09-367-309A-1

12	51	100.0	273	13	US-10-000-903-4	Sequence 4, Appli
13	51	100.0	273	17	US-10-899-771-4	Sequence 4, Appli
14	51	100.0	292	13	US-10-000-903-10	Sequence 10, Appl
15	51	100.0	292	17	US-10-899-771-10	Sequence 10, Appl
16	51	100.0	371	13	US-10-000-903-6	Sequence 6, Appli
17	51	100.0	371	17	US-10-899-771-6	Sequence 6, Appli
18	51	100.0	390	13	US-10-000-903-14	Sequence 14, Appl
19	51	100.0	390	17	US-10-899-771-14	Sequence 14, Appl
20	43	84.3	10	17	US-10-751-845-138	Sequence 138, App
21	43	84.3	27	17	US-10-751-845-153	Sequence 153, App
22	43	84.3	119	17	US-10-751-845-159	Sequence 159, App
23	43	84.3	158	16	US-10-800-023-27	Sequence 27, Appli
24	43	84.3	172	16	US-10-472-724-6	Sequence 6, Appli
25	43	84.3	236	17	US-10-751-845-157	Sequence 157, App
26	43	84.3	237	17	US-10-751-845-158	Sequence 158, App
27	43	84.3	261	17	US-10-751-845-160	Sequence 160, App
28	43	84.3	278	13	US-10-000-903-21	Sequence 21, Appl
29	43	84.3	278	17	US-10-899-771-21	Sequence 21, Appl
30	43	84.3	383	13	US-10-000-903-23	Sequence 23, Appl
31	43	84.3	383	17	US-10-899-771-23	Sequence 23, Appl
32	41	80.4	180	16	US-10-767-701-53503	Sequence 53503, A
33	40	78.4	117	11	US-09-864-408A-3358	Sequence 3358, Ap
34	40	78.4	159	17	US-10-928-992-182	Sequence 182, App
35	40	78.4	237	16	US-10-437-963-144051	Sequence 144051, A
36	40	78.4	265	16	US-10-739-930-11014	Sequence 11014, A
37	39	76.5	161	16	US-10-425-115-317008	Sequence 317008,
38	39	76.5	261	15	US-10-291-172-279	Sequence 279, App
39	39	76.5	261	15	US-10-104-047-2517	Sequence 2517, Ap
40	39	76.5	261	15	US-10-221-278-279	Sequence 279, App
41	39	76.5	288	15	US-10-291-172-655	Sequence 655, App
42	39	76.5	288	15	US-10-221-278-655	Sequence 655, App
43	38	74.5	60	15	US-10-424-599-212183	Sequence 212183,
44	38	74.5	83	16	US-10-425-115-286600	Sequence 286600,
45	38	74.5	654	16	US-10-437-963-156405	Sequence 156405,

ALIGNMENTS

RESULT 1

- US-10-476-570-39
- Sequence 39, Application US/10476570
- Publication No. US20040170644A1
- GENERAL INFORMATION:
- APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
- APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
- APPLICANT: MAILLIERE, Bernard
- APPLICANT: BOURGAULT-VILLADA, Isabelle
- APPLICANT: POUVILLE-MORATILLE, Sandra
- APPLICANT: GUILLET, Jean-Gerard
- TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
- TITLE OF INVENTION: papillomavirus proteins and uses thereof
- FILE REFERENCE: 45636-5071-US
- CURRENT APPLICATION NUMBER: US/10/476,570
- CURRENT FILING DATE: 2003-11-04
- PRIOR APPLICATION NUMBER: PCT/FR02/01533
- PRIOR FILING DATE: 2002-05-03
- PRIOR APPLICATION NUMBER: FR 01 05980
- PRIOR FILING DATE: 2001-05-04
- NUMBER OF SEQ ID NOS: 63
- SOFTWARE: PatentIn Ver. 2.1
- SEQ ID NO 39
- LENGTH: 15
- TYPE: PRT
- ORGANISM: artificial sequence
- FEATURE:
- OTHER INFORMATION: Description of the artificial sequence: peptide E6 101-115

Query Match 100.0%; Score 51; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
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Db 7 LIRCINCOK 15

RESULT 2
US-10-484-063-8
; Sequence 8, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-8

Query Match 100.0%; Score 51; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
| | | | | | | |
Db 11 LIRCINCOK 19

RESULT 3
US-10-476-570-60
; Sequence 60, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 22
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 105-126
US-10-476-570-60

Query Match 100.0%; Score 51; DB 16; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
| | | | | | | |
Db 3 LIRCINCOK 11

RESULT 4
US-10-476-570-13
; Sequence 13, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 29
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 91-119
US-10-476-570-13

Query Match 100.0%; Score 51; DB 16; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
| | | | | | | |
Db 17 LIRCINCOK 25

RESULT 5
US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerps Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6

Query Match 100.0%; Score 51; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
| | | | | | | |
Db 100 LIRCINCOK 108

```

RESULT 6
US-10-484-063-20
; Sequence 20, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-20

Query Match      100.0%; Score 51; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
Db 100 LIRCINCOK 108

RESULT 7
US-10-484-063-27
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-484-063-27

Query Match      100.0%; Score 51; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
Db 100 LIRCINCOK 108

RESULT 8
US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:

```

```

; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match      100.0%; Score 51; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
Db 107 LIRCINCOK 115

RESULT 9
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match      100.0%; Score 51; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
Db 107 LIRCINCOK 115

RESULT 10
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17

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; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match      100.0%; Score 51; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
Db 112 LIRCINCOK 120

RESULT 11
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match      100.0%; Score 51; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
Db 107 LIRCINCOK 115

RESULT 12
US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22

; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4

Query Match      100.0%; Score 51; DB 13; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
Db 213 LIRCINCOK 221

RESULT 13
US-10-899-771-4
; Sequence 4, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: Influenzae B and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-4

Query Match      100.0%; Score 51; DB 17; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
Db 213 LIRCINCOK 221

RESULT 14
US-10-000-903-10
; Sequence 10, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
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; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-10

Query Match      100.0%; Score 51; DB 13; Length 292;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LIRCINCOK 9
Db      232 LIRCINCOK 240

RESULT 15
US-10-899-771-10
; Sequence 10, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; FILE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric protein (Clyta from Streptococcus
; OTHER INFORMATION: pneumoniae and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-10

Query Match      100.0%; Score 51; DB 17; Length 292;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 LIRCINCOK 9
Db      232 LIRCINCOK 240

Search completed: June 29, 2005, 05:18:15
Job time : 117.15 secs
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:33:36 ; Search time 17.05 Seconds
(without alignments)
39.404 Million cell updates/sec

Title: US-08-170-344-54
Perfect score: 51
Sequence: 1 LIRINCQX 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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4: /cgm2_6/ptodata/1/iaa/6B_COMB.pap:*
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6: /cgm2_6/ptodata/1/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	10	3	US-08-159-339A-79
2	51	100.0	20	2	US-08-934-915-185
3	51	100.0	158	4	US-09-980-523A-2
4	51	100.0	162	1	US-08-316-239B-3
5	51	100.0	162	1	US-08-316-239B-4
6	51	100.0	172	3	US-08-860-165-12
7	51	100.0	172	3	US-09-359-382-12
8	51	100.0	266	3	US-08-860-165-10
9	51	100.0	266	3	US-09-359-382-10
10	51	100.0	266	4	US-09-367-309A-1
11	51	100.0	273	3	US-09-485-885-4
12	51	100.0	292	3	US-09-485-885-10
13	51	100.0	371	3	US-09-485-885-6
14	51	100.0	390	3	US-09-485-885-14
15	43	84.3	9	3	US-08-159-339A-569
16	43	84.3	10	3	US-08-159-339A-90
17	43	84.3	158	2	US-08-247-904B-10
18	43	84.3	158	3	US-08-767-942A-19
19	43	84.3	271	1	US-08-117-083-14
20	43	84.3	278	3	US-09-485-885-21
21	43	84.3	383	3	US-09-485-885-23
22	40	78.4	119	4	US-09-732-210-333
23	40	78.4	119	4	US-09-732-210-334
24	40	78.4	119	4	US-09-538-092-255
25	40	78.4	119	4	US-09-538-092-316
26	38	74.5	32	4	US-09-270-767-59109
27	38	74.5	40	4	US-09-270-767-60605

28	38	74.5	44	4	US-09-270-767-45114	Sequence 45114, A
29	38	74.5	84	4	US-09-270-767-43718	Sequence 43718, A
30	36	70.6	71	4	US-09-489-039A-9691	Sequence 9691, Ap
31	36	70.6	269	4	US-09-328-352-5522	Sequence 5522, Ap
32	36	70.6	504	4	US-09-270-767-35938	Sequence 35938, A
33	36	70.6	504	4	US-09-270-767-51155	Sequence 51155, A
34	35	68.6	121	4	US-09-248-796A-19706	Sequence 19706, A
35	35	68.6	133	4	US-09-732-210-1578	Sequence 1578, Ap
36	35	68.6	340	5	PCT-US96-02331-13	Sequence 13, Appl
37	35	68.6	842	5	PCT-US96-02331-15	Sequence 15, Appl
38	34	66.7	35	3	US-09-057-486-2	Sequence 2, Appl
39	34	66.7	55	3	US-09-057-486-1	Sequence 1, Appl
40	34	66.7	71	4	US-09-930-181-6	Sequence 6, Appl
41	34	66.7	72	4	US-09-107-532A-4927	Sequence 4927, Ap
42	34	66.7	79	4	US-09-513-999C-6001	Sequence 6001, Ap
43	34	66.7	91	4	US-09-543-681A-6613	Sequence 6613, Ap
44	34	66.7	92	4	US-09-270-767-40981	Sequence 40981, A
45	34	66.7	92	4	US-09-270-767-56197	Sequence 56197, A

ALIGNMENTS

RESULT 1
US-08-159-339A-79
; Sequence 79, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-79

Query Match 100.0%; Score 51; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCQK 9
| | | | |
Db 2 LIRCINCQK 10

RESULT 2

US-08-934-915-165
; Sequence 165 Application US/08934915
; Patent No. 5932412

; GENERAL INFORMATION:

; APPLICANT: DILLNER, JOAKIM

; APPLICANT: DILLNER, LENA

; APPLICANT: CHENG, HWEI-MING

; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN

; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,

; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,

; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR

; TITLE OF INVENTION: DIAGNOSTIC PURPOSES

; NUMBER OF SEQUENCES: 193

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MASON & ASSOCIATES, P.A.

; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500

; CITY: CLEARWATER

; STATE: FLORIDA

; COUNTRY: U.S.A.

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Microsoft Word 6.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/934,915

; FILING DATE: 22-SEP-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/949,836

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: LOUISE A. Foutch

; REGISTRATION NUMBER: 37,133

; REFERENCE/DOCKET NUMBER: 1946.6

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 813-538-3800

; TELEFAX: 813-538-3820

; TELEX:

; INFORMATION FOR SEQ ID NO: 165:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-934-915-165

Query Match 100.0%; Score 51; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCQK 9
| | | | |
Db 1 LIRCINCQK 9

RESULT 3

US-09-980-523A-2

; Sequence 2, Application US/09980523A

; Patent No. 6783763

; GENERAL INFORMATION:

; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO/1 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 51; DB 4; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.23; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCQK 9

| | | | |

Db 107 LIRCINCQK 115

RESULT 4

US-08-316-239B-3

; Sequence 3, Application US/08316239B

; Patent No. 5679509

; GENERAL INFORMATION:

; APPLICANT: Wheeler, Cosette M.

; TITLE OF INVENTION: Methods and a Diagnostic Aid for

; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an

; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and

; TITLE OF INVENTION: Cervical Cancer

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jagtiani & Associates

; STREET: 6126 Rocky Way Court

; CITY: Centreville

; STATE: VA

; COUNTRY: USA

; ZIP: 20120-3400

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/316,239B

; FILING DATE: 30-SEP-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Jagtiani, Ajay A.

; REGISTRATION NUMBER: 35,205

; REFERENCE/DOCKET NUMBER: UNME-0001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 817-9453

; TELEFAX: (703) 803-9387

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 162 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: not relevant

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; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match      100.0%; Score 51; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
Db 107 LIRCINCOK 115

RESULT 5
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Colette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4

Query Match      100.0%; Score 51; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
Db 107 LIRCINCOK 115

RESULT 6
US-08-860-165-12
; Sequence 12, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
```

```
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12

Query Match      100.0%; Score 51; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
Db 45 LIRCINCOK 53

RESULT 7
US-09-359-382-12
; Sequence 12, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-12

Query Match      100.0%; Score 51; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
Db 45 LIRCINCOK 53

RESULT 8
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
```

; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; PRIOR FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 51; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
Db 107 LIRCINCOK 115

RESULT 9
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; PRIOR FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 51; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
Db 107 LIRCINCOK 115

RESULT 10
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES

; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 51; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
Db 107 LIRCINCOK 115

RESULT 11
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match 100.0%; Score 51; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.39;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
Db 213 LIRCINCOK 221

RESULT 12
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18

; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10

Query Match 100.0%; Score 51; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
Db 232 LIRCINCOK 240

RESULT 13
US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6

Query Match 100.0%; Score 51; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.53;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
Db 213 LIRCINCOK 221

RESULT 14
US-09-485-885-14
; Sequence 14, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5

; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-14

Query Match 100.0%; Score 51; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LIRCINCOK 9
Db 232 LIRCINCOK 240

RESULT 15
US-08-159-339A-569
; Sequence 569, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Cellis, Esteban
; TITLE OF INVENTION: HIA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 569:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-569

Query Match 84.3%; Score 43; DB 3; Length 9;
Best Local Similarity 77.8%; Pred. No. 4.1e+05;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LIRCINCK 9
|||: ||
Db 1 LIRCINCK 9

Search completed: June 28, 2005, 23:37:52
Job time : 18.05 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:24:19 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-53
Perfect score: 54
Sequence: 1 QQYNKPLCD 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	81	2 Q80886	Q80886 human papil
2	54	100.0	84	2 Q80882	Q80882 human papil
3	54	100.0	90	2 Q80883	Q80883 human papil
4	54	100.0	90	2 Q80884	Q80884 human papil
5	54	100.0	90	2 Q80885	Q80885 human papil
6	54	100.0	91	2 Q80887	Q80887 human papil
7	54	100.0	99	2 Q919B2	Q919B2 human papil
8	54	100.0	130	2 Q919B4	Q919B4 human papil
9	54	100.0	130	2 Q919B8	Q919B8 human papil
10	54	100.0	130	2 Q919C0	Q919C0 human papil
11	54	100.0	130	2 Q919C2	Q919C2 human papil
12	54	100.0	130	2 Q919C8	Q919C8 human papil
13	54	100.0	130	2 Q919D0	Q919D0 human papil
14	54	100.0	138	2 Q919D2	Q919D2 human papil
15	54	100.0	143	2 Q919B6	Q919B6 human papil
16	54	100.0	143	2 Q919C4	Q919C4 human papil
17	54	100.0	151	2 Q919C3	Q919C3 human papil
18	54	100.0	151	2 Q919C6	Q919C6 human papil
19	54	100.0	151	2 Q919D1	Q919D1 human papil
20	54	100.0	151	2 Q919D2	Q919D2 human papil
21	54	100.0	151	2 Q919E6	Q919E6 human papil
22	54	100.0	151	2 Q919C7	Q919C7 human papil
23	54	100.0	151	2 Q919C5	Q919C5 human papil
24	54	100.0	151	2 Q90963	Q90963 human papil
25	54	100.0	151	2 Q90966	Q90966 human papil
26	54	100.0	151	2 Q90960	Q90960 human papil
27	54	100.0	151	2 Q90968	Q90968 human papil
28	54	100.0	151	2 Q909708	Q909708 human papil
29	54	100.0	151	2 Q909755	Q909755 human papil
30	54	100.0	151	2 Q909852	Q909852 human papil
31	54	100.0	151	2 Q909887	Q909887 human papil

32 54 100.0 151 2 Q8B564 human papil
33 54 100.0 151 2 Q8BB19 human papil
34 54 100.0 151 2 Q8BB20 human papil
35 54 100.0 151 2 Q8BB21 human papil
36 54 100.0 151 2 Q8B8C3 human papil
37 54 100.0 151 2 Q9W931 human papil
38 54 100.0 151 2 Q9WMP2 human papil
39 54 100.0 151 2 Q9WMP3 human papil
40 54 100.0 151 2 Q9WMP4 human papil
41 54 100.0 151 2 Q9WMP5 human papil
42 54 100.0 158 1 V56 HPV16 human papil
43 54 100.0 158 2 Q8JMU8 human papil
44 54 100.0 158 2 Q8QHN0 human papil
45 54 100.0 158 2 Q8QHP5 human papil

ALIGNMENTS

RESULT 1
Q80886 PRELIMINARY; PRT; 81 AA.
AC Q80886;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haggert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14515; AAB60569.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 81 81
SQ SEQUENCE 81 AA; 9784 MW; DD5FEDBC9F845B97 CRC64;

Query Match Similarity 100.0%; Score 54; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 0.0098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 QQYNKPLCD 9
Db 49 QQYNKPLCD 57

RESULT 2
Q80882 PRELIMINARY; PRT; 84 AA.
AC Q80882;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical;
RA Haggert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14511; AAB60565.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.

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DR GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1. 1
FT NON_TER 84
SQ SEQUENCE 84 AA; 10177 MW; 5AB5B896468E1CAA CRC64;
Query Match 100.0%; Score 54; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.01; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
Db 46 QQYNKPLCD 54

RESULT 3
Q80883 PRELIMINARY; PRT; 90 AA.
AC Q80883;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14512; AAB60566.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1. 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 10904 MW; 5D3ADF843AD6060B CRC64;
Query Match 100.0%; Score 54; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.01; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
Db 49 QQYNKPLCD 57

RESULT 4
Q80884 PRELIMINARY; PRT; 90 AA.
AC Q80884;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14513; AAB60567.2; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1. 1

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FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 11021 MW; 47F42BBEFACCCC01 CRC64;
Query Match 100.0%; Score 54; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.01; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
Db 49 QQYNKPLCD 57

RESULT 5
Q80885 PRELIMINARY; PRT; 90 AA.
AC Q80885;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14514; AAB60568.2; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1. 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 10964 MW; BC2531643ACBA76C CRC64;
Query Match 100.0%; Score 54; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.01; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
Db 49 QQYNKPLCD 57

RESULT 6
Q80887 PRELIMINARY; PRT; 91 AA.
AC Q80887;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14516; AAB60570.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1. 1
FT NON_TER 91
SQ SEQUENCE 91 AA; 11136 MW; 22PDF3EA185ACBA7 CRC64;

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Query Match      100.0%; Score 54; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYNKPLCD 9
DB 49 QOYNKPLCD 57

RESULT 7
Q919B2
ID Q919B2 PRELIMINARY; PRT; 99 AA.
AC Q919B2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040704; AAL01365.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
FT NON TER 99
SQ SEQUENCE 99 AA; 12005 MW; C2B96025EC370E38 CRC64;

Query Match      100.0%; Score 54; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYNKPLCD 9
DB 66 QOYNKPLCD 74

RESULT 8
Q919B4
ID Q919B4 PRELIMINARY; PRT; 130 AA.
AC Q919B4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040703; AAL01363.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
FT NON TER 130
SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227BEDDC CRC64;

Query Match      100.0%; Score 54; DB 2; Length 130;

Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYNKPLCD 9
DB 69 QOYNKPLCD 77

RESULT 9
Q919B8
ID Q919B8 PRELIMINARY; PRT; 130 AA.
AC Q919B8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040701; AAL01359.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
FT NON TER 130
SQ SEQUENCE 130 AA; 15775 MW; 92D3C07BF96B092F CRC64;

Query Match      100.0%; Score 54; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOYNKPLCD 9
DB 69 QOYNKPLCD 77

RESULT 10
Q919C0
ID Q919C0 PRELIMINARY; PRT; 130 AA.
AC Q919C0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040700; AAL01357.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
FT NON TER 130
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match      100.0%; Score 54; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 QQYNKPLCD 9
| | | | | | | |
Db 69 QQYNKPLCD 77

RESULT 11

Q919C2 ID Q919C2 PRELIMINARY; PRT; 130 AA.
AC Q919C2; 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404699; AAL01349.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 54; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
| | | | | | | |
Db 69 QQYNKPLCD 77

RESULT 12

Q919C8 ID Q919C8 PRELIMINARY; PRT; 130 AA.
AC Q919C8; 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404699; AAL01349.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;

Query Match 100.0%; Score 54; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
| | | | | | | |
Db 69 QQYNKPLCD 77

RESULT 13

Q919D0 ID Q919D0 PRELIMINARY; PRT; 130 AA.
AC Q919D0; 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404699; AAL01349.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15735 MW; 9EFB30EEDCA21AF3 CRC64;

Query Match 100.0%; Score 54; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
| | | | | | | |
Db 69 QQYNKPLCD 77

RESULT 14

Q919D2 ID Q919D2 PRELIMINARY; PRT; 138 AA.
AC Q919D2; 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT Cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404699; AAL01349.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 138 AA; 16696 MW; 481E5AEA90895FC2 CRC64;

Query Match 100.0%; Score 54; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
| | | | | | | |
Db 77 QQYNKPLCD 85

RESULT 15

Q919B6
 ID Q919B6 PRELIMINARY; PRT; 143 AA.
 AC Q919B6;
 DT 01-DEC-2001 (TREMELrel. 19, Created)
 DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404702; AAL01361.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON_TER
 SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;

 Query Match 100.0%; Score 54; DB 2; Length 143;
 Best Local Similarity 100.0%; Pred. No. 0.018;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 QQYNKPLCD 9
 Db 82 QQYNKPLCD 90
 |||||
 |||||

Search completed: June 28, 2005, 23:28:12
 Job time : 55.1 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:28:02 ; Search time 11.05 Seconds
(without alignments)
78.367 Million cell updates/sec

Title: US-08-170-344-53

Perfect score: 54

Sequence: 1 QQYNKPLCD 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	158	1	W6LHS
2	38	70.4	1656	2	S54520
3	36	66.7	83	2	S07941
4	36	66.7	102	1	TSYD2
5	36	66.7	412	2	E82310
6	36	66.7	609	2	A71461
7	36	66.7	1289	2	S67200
8	35	64.8	87	2	T10785
9	35	64.8	209	2	J02347
10	35	64.8	354	1	H64235
11	35	64.8	412	1	C37777
12	35	64.8	412	1	G30315
13	35	64.8	438	2	B96759
14	35	64.8	601	2	B81723
15	35	64.8	681	2	I38755
16	35	64.8	907	2	T27317
17	35	64.8	1003	2	S33760
18	35	64.8	1097	2	A56138
19	34	63.0	218	2	S67481
20	34	63.0	355	2	G82247
21	34	63.0	649	2	F85682
22	34	63.0	676	2	T24550
23	34	63.0	782	2	H08823
24	34	63.0	993	2	A38437
25	34	63.0	2269	2	T18472
26	33	61.1	127	2	H64012
27	33	61.1	239	2	A69124
28	33	61.1	253	2	S76761
29	33	61.1	256	2	F86463

ALIGNMENTS

RESULT 1

W6LHS

protein E6 - human papillomavirus type 16

C:Species: human papillomavirus type 16

C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C:Accession: A03682; T10427

R:Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowe&kamp, W.G.

Virolgy 145, 181-185, 1985

A:Title: Human papillomavirus type 16 DNA sequence.

A:Reference number: A22355; MUID:85246220; PMID:2990099

A:Accession: A03682

A:Molecule type: DNA

A:Residues: 1-158 <SEE>

A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

J. Kennedy, I.M.; Haddock, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level

A:Reference number: 217014; MUID:91162763; PMID:1848319

A:Accession: T10427

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-158 <KEN>

A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032

C:Genetics:

A:Gene: E6

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:37-73/Region: zinc finger CCCC motif

F:110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 54; DB 1; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.007; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0;

QY 1 QQYNKPLCD 9

Db 97 QQYNKPLCD 105

RESULT 2

S54520

probable membrane protein YMR162c - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein YMR820.11c

C:Species: Saccharomyces cerevisiae

C:Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004

C:Accession: S54520; S54607

R:Hunt, S.; Bowman, S.

submitted to the EMBL Data Library, May 1995

A:Reference number: S54510

A:Accession: S54520

A:Molecule type: DNA

A:Residues: 1-1656 <HUN>

A;Cross-references: UNIPROT:Q12674; GB:Z49705; EMBL:Z49700; NID:g2825556; PID:g2825567; EM
A;Experimental source: strain AB972
C;Genetics:
A;Gene: MIPS:YMR162c
A;Cross-references: SGD:S0004772
A;Map position: 13R
A;Keywords: transmembrane protein
F;454-470/Domain: transmembrane #status predicted <TM1>
F;510-526/Domain: transmembrane #status predicted <TM2>
F;1323-1339/Domain: transmembrane #status predicted <TM3>
F;1373-1389/Domain: transmembrane #status predicted <TM4>
F;1400-1416/Domain: transmembrane #status predicted <TM5>
F;1436-1452/Domain: transmembrane #status predicted <TM6>
F;1474-1490/Domain: transmembrane #status predicted <TM7>

Query Match 70.4%; Score 38; DB 2; Length 1656;
Best Local Similarity 55.6%; Pred. No. 69;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QYKNKPLCD 9
Db 132 BRFNKPYCD 140

RESULT 3
S07941
protease inhibitor IV - soybean
C;Species: Glycine max (soybean)
C;Date: 02-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: S07941
R;Joudrier, P.E.; Foard, D.E.; Floener, L.A.; Larkins, B.A.
Plant Mol. Biol. 10, 35-42, 1987
A;Title: Isolation and sequence of cDNA encoding the soybean protease inhibitors PI IV a
A;Reference number: S07405
A;Accession: S07941
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-83 <JOU>
A;Cross-references: UNIPROT:P01064; EMBL:M20733; NID:g169946; PIDN:AAA33954.1; PID:g1699
C;Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
F;25-51/Domain: Bowman-Birk inhibitor repeat homology <BB1>
F;52-77/Domain: Bowman-Birk inhibitor repeat homology <BB12>

Query Match 66.7%; Score 36; DB 2; Length 83;
Best Local Similarity 62.5%; Pred. No. 9.7;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QYKNKPLCD 9
Db 19 EYSKPCCD 26

RESULT 4
TISYD2
protease inhibitor (Bowman-Birk) D-II precursor - soybean
C;Species: Glycine max (soybean)
C;Date: 24-Apr-1984 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C;Accession: S32243; J02224; A01303; B01303; S29559
R;Song, J.C.; Baek, J.M.; Kim, S.I.
submitted to the EMBL Data Library, October 1992
A;Description: Molecular cloning of a gemonic DNA encoding the soybean bowman-birk prote
A;Reference number: S32243
A;Accession: S32243
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-102 <SON>
A;Cross-references: UNIPROT:Q43709; EMBL:X68707; NID:g288618; PIDN:CAA48658.1; PID:g2886
R;Baek, J.M.; Song, J.C.; Choi, Y.D.; Kim, S.I.
Biosci. Biotechnol. Biochem. 58, 843-846, 1994
A;Title: Nucleotide sequence homology of cDNAs encoding soybean Bowman-Birk type protein
A;Reference number: JC2224; MUID:94289861; PMID:7764974
A;Accession: JC2224

A;Molecule type: mRNA
A;Residues: 1-102 <BA2>
A;Cross-references: EMBL:X68706; NID:g18571; PIDN:CAA48657.1; PID:g18572
R;Odani, S.; Ikenaka, T.
J. Biochem. 83, 737-745, 1978
A;Title: Studies on soybean trypsin inhibitors. XII. Linear sequences of two soybean dou
A;Reference number: A01303; MUID:78150870; PMID:641033
A;Accession: A01303
A;Molecule type: protein
A;Residues: 28-102 <OD1>
A;Accession: B01303
A;Molecule type: protein
A;Residues: 37-57 <OD2>
R;Chen, P.; Rose, J.; Love, R.; Wei, C.H.; Wang, B.C.
J. Biol. Chem. 267, 1990-1994, 1992
A;Title: Reactive sites of an anticarcinogenic Bowman-Birk proteinase inhibitor are simil
A;Reference number: A42052; MUID:92112932; PMID:1730730
A;Contents: annotation: X-ray crystallography of inhibitor PI-II at 2.5 angstroms
C;Comment: This protein regulates endogenous proteinase during germination, stores sulfi
C;Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
C;Keywords: duplication; seed; serine proteinase inhibitor; storage protein
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-102/Product: proteinase inhibitor (Bowman-Birk) D-II #status experimental <MAT>
F;44-70/Domain: Bowman-Birk inhibitor repeat homology <BB1>
F;71-96/Domain: Bowman-Birk inhibitor repeat homology <BB2>
F;43-97,44-59,47-93,49-57,67-74,71-96,76-84/Disulfide bonds: #status experimental
F;51/Inhibitory site: Arg (trypsin) #status predicted
F;78/Inhibitory site: Arg (trypsin) #status predicted

Query Match 66.7%; Score 36; DB 1; Length 102;
Best Local Similarity 62.5%; Pred. No. 12;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QYKNKPLCD 9
Db 38 EYSKPCCD 45

RESULT 5
B82310
reCA protein VC0543 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: B82310
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
L. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: B82310
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-412 <HEI>
A;Cross-references: GB:AE004140; GB:AE003852; NID:g9654965; PIDN:AAF93711.1; GSPDB:GNO01;
A;Experimental source: serogroup O1; strain N16961; biotype El For
C;Genetics:
A;Gene: VC0543
A;Map position: 1
C;Superfamily: recombination protein recA

Query Match 66.7%; Score 36; DB 2; Length 412;
Best Local Similarity 77.8%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QYKNKPLCD 9
Db 28 QYKNKPOHD 36

RESULT 6
A71461

hypothetical protein CT858 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
R:Accession: A71461
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis
A:Reference number: A71570; MUID:99000809; PMID:9784136
A:Accession: A71461
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-609 <ARN>
A:Cross-references: GB:AE001273; NID:g3329331; PIDN:AA68456.1; PID:g3329331
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: CT858

Query Match 66.7%; Score 36; DB 2; Length 609;
Best Local Similarity 71.4%; Pred. No. 63;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QYKPLC 8
Db 484 QYKPLC 490

RESULT 7
S67200
hypothetical protein YOR296w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein O5623
C:Species: Saccharomyces cerevisiae
C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
R:Accession: S67200
R:Cziepluch, C.; Jauniaux, J.C.; Kordes, E.; Poirey, R.; Pujol, A.; Tobiasch, E. submitted to the Protein Sequence Database, July 1996
A:Reference number: S67194
A:Accession: S67200
A:Molecule type: DNA
A:Residues: 1-1289 <CZI>
A:Cross-references: UNIPROT:Q08748; EMBL:275204; NID:g1420655; PID:g1420656; GSPDB:GN000000
A:Experimental source: strain S288C
C:Genetics:
A:Gene: MIPS:YOR296w
A:Cross-references: SGD:S0005822
A:Map position: 15R
C:Superfamily: Saccharomyces cerevisiae hypothetical protein YOR296w

Query Match 66.7%; Score 36; DB 2; Length 1289;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QYKPLC 9
Db 562 KRYKPLC 570

RESULT 8
T10785
pathogen-induced protein 1 - cucumber
C:Species: Cucumis sativus (cucumber)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
R:Accession: T10785
R:Marro, P.; Metraux, J.P.; Sticher, L. submitted to the EMBL Data Library, March 1997
A:Description: Isolation of a novel cucumber cDNA associated with systemic acquired resistance
A:Reference number: Z17142
A:Accession: T10785
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-87 <MAR>
A:Cross-references: UNIPROT:Q24512; EMBL:U93586; NID:g2406581; PID:g2406582

Query Match 64.8%; Score 35; DB 2; Length 87;

Best Local Similarity 83.3%; Pred. No. 16;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NKPLC 9
Db 53 NKPLC 58

RESULT 9
JQ2347
hypothetical 23.6K protein - turkey herpesvirus
N:Alternate names: ORF2 protein
C:Species: turkey herpesvirus
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
R:Accession: JQ2347
R:Zelnik, V.; Dartail, R.; Audonnet, J.C.; Smith, G.D.; Riviere, M.; Pastorek, J.; Ross, J. Gen. Virol. 74, 2151-2162, 1993
A:Title: The complete sequence and gene organization of the short unique region of herpesvirus turk
A:Reference number: JQ2346; MUID:94014999; PMID:8409940
A:Accession: JQ2347
A:Molecule type: DNA
A:Residues: 1-209 <ZEL>
A:Cross-references: UNIPROT:Q88519; EMBL:X68653; NID:g406783; PIDN:CAA48613.1; PID:g406783
A:Experimental source: strain FC126
C:Superfamily: Marek's disease virus minor virion protein

Query Match 64.8%; Score 35; DB 2; Length 209;
Best Local Similarity 75.0%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QYKPLC 8
Db 174 QYKPLC 181

RESULT 10
H64235
X-Pro aminopeptidase (EC 3.4.11.9) - Mycoplasma genitalium
C:Species: Mycoplasma genitalium
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
R:Accession: H64235
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.; M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J. C.A.; Venter, J.C. Science 270, 397-403, 1995
A:Title: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64200; MUID:96026346; PMID:7569993
A:Accession: H64235
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-354 <TIGR>
A:Cross-references: UNIPROT:P47566; GB:U39715; GB:L43967; NID:g1046026; PID:g1046027; TIC
A:Experimental source: strain G-37.
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: X-Pro aminopeptidase
C:Keywords: aminopeptidase

Query Match 64.8%; Score 35; DB 1; Length 354;
Best Local Similarity 66.7%; Pred. No. 59;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QYKPLC 9
Db 304 QYKPLC 312

RESULT 11
C37777
polyferredoxin 6x2[4Fe-4S] - Methanothermobacter ferrooxidans
C:Species: Methanothermobacter ferrooxidans
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: C37777

R;Steigerwald, V.J.; Beckler, G.S.; Reeve, J.N.
 J. Bacteriol. 172, 4715-4718, 1990
 A:Title: Conservation of hydrogenase and polyferredoxin structures in the hyperthermophilic
 A:Reference number: A37777; MUID:90330590; PMID:2115877
 A:Accession: C37777
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-412 <STP>
 A:Cross-references: UNIPROT:Q49180; GB:M34016; NID:g149803; PIDN:AAAY2833.1; PID:g149806
 C:Superfamily: polyferredoxin 6x2[4Fe-4S]; ferredoxin 2[4Fe-4S] homology
 C:Keywords: electron transfer
 F:2-55/Domain: ferredoxin 2[4Fe-4S] homology <FER1>
 F:68-125/Domain: ferredoxin 2[4Fe-4S] homology <FER2>
 F:139-195/Domain: ferredoxin 2[4Fe-4S] homology <FER3>
 F:209-263/Domain: ferredoxin 2[4Fe-4S] homology <FER4>
 F:277-342/Domain: ferredoxin 2[4Fe-4S] homology <FER5>
 F:358-412/Domain: ferredoxin 2[4Fe-4S] homology <FER6>

Query Match 64.8%; Score 35; DB 1; Length 412;
 Best Local Similarity 75.0%; Pred. No. 68;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QYNKPLCD 9
 ||| |||
 Db 359 QYNPSLCD 366

RESULT 12
 G30315
 polyferredoxin 6x2[4Fe-4S] mvhB - Methanobacterium thermoautotrophicum (strains Delta H
 C:Species: Methanobacterium thermoautotrophicum
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: G30315; H69017; S20413
 R;Reeve, J.N.; Beckler, G.S.; Cram, D.S.; Hamilton, P.T.; Brown, J.W.; Krzycki, J.A.; K
 Proc. Natl. Acad. Sci. U.S.A. 85, 3031-3035, 1989
 A:Title: A hydrogenase-linked gene in Methanobacterium thermoautotrophicum strain delta-
 A:Reference number: A30315; MUID:89240669; PMID:2654933
 A:Accession: G30315
 A:Molecule type: DNA
 A:Residues: 1-388,'A',390-412 <REE>
 A:Cross-references: UNIPROT:Q50784; GB:J04540; NID:g149730
 A:Experimental source: strain Delta H
 A:Note: the sequence is revised in GenBank entry MBPMVHR, release 109.0. (PID:g149734)
 R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
 ; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.
 K1, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
 A:Reference number: A59000; MUID:98037514; PMID:9371463
 A:Accession: H69017
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-95,'G',97-412 <MTH>
 A:Cross-references: GB:A500083; GB:AE000666; NID:g262231; PIDN:AAB85622.1; PID:g262223
 A:Experimental source: strain Delta H
 R;Hedderich, R.; Albracht, S.P.J.; Linder, D.; Koch, J.; Thauer, R.K.
 FEBS Lett. 298, 65-68, 1992
 A:Title: Isolation and characterization of polyferredoxin from Methanobacterium thermoau
 A:Reference number: S20413; MUID:92183831; PMID:1312016
 A:Accession: S20413
 A:Molecule type: protein
 A:Residues: 1-2,'V',4-28 <HED>
 A:Cross-references: PIDN:AAB31772.1; PID:g247131
 A:Experimental source: strain Marburg, DSM 2133
 C:Genetics:
 A:Gene: mvhB; MTH1133
 C:Superfamily: polyferredoxin 6x2[4Fe-4S]; ferredoxin 2[4Fe-4S] homology
 C:Keywords: 4Fe-4S; iron-sulfur protein; metalloprotein
 F:2-55/Domain: ferredoxin 2[4Fe-4S] homology <FER1>
 F:69-125/Domain: ferredoxin 2[4Fe-4S] homology <FER2>
 F:139-195/Domain: ferredoxin 2[4Fe-4S] homology <FER3>
 F:209-264/Domain: ferredoxin 2[4Fe-4S] homology <FER4>
 F:278-343/Domain: ferredoxin 2[4Fe-4S] homology <FER5>

F:359-412/Domain: ferredoxin 2[4Fe-4S] homology <FER6>
 F:9,12,15,47/Binding site: 4Fe-4S cluster (Cys) (covalent) #status experimental
 F:19,34,37,43/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
 F:76,79,82,117/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
 F:86,107,110,113/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
 F:146,149,152,187/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
 F:156,177,180,183/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
 F:216,219,222,256/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
 F:226,246,249,252/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
 F:285,291,335/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
 F:295,325,328,331/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
 F:366,369,372,404/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
 F:376,394,397,400/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 64.8%; Score 35; DB 1; Length 412;
 Best Local Similarity 75.0%; Pred. No. 68;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QYNKPLCD 9
 ||| |||
 Db 360 QYNPALCD 367

RESULT 13
 B96759
 protein serine carboxypeptidase T18K17.4 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 16-Aug-2004
 C:Accession: B96759
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Cressy, T.H.; Dewar, K.;
 ansen, N.P.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
 C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: B96759
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-438 <STO>
 A:Cross-references: UNIPROT:Q9CAU2; GB:AE005173; NID:96598854; PIDN:AAF18708.1; GSPDB:GNC
 C:Genetics:
 A:Gene: T18K17.4
 A:Map position: 1
 C:Superfamily: Serine carboxypeptidase

Query Match 64.8%; Score 35; DB 2; Length 438;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOYNKP 6
 ||| |||
 Db 144 QOYNKP 149

RESULT 14
 B81723
 conserved hypothetical protein TC0248 [imported] - Chlamydia muridarum (strain Nigg)
 C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C:Accession: B81723
 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, I
 , C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
 Nucleic Acids Res. 28, 1397-1406, 2000
 A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
 A:Reference number: A81500; MUID:20150255; PMID:10684935
 A:Accession: B81723
 A:Status: preliminary
 A:Molecule type: DNA

A;Residues: 1-601 <TET>
A;Cross-references: UNIPROT:Q9PL60; GB:AE002292; GB:AE002160; NID:g7190286; PIDN:AAF3911
A;Experimental source: strain Nigg (MoPn)
C;Genetics:
A;Gene: TC0248

Query Match 64.8%; Score 35; DB 2; Length 601;
Best Local Similarity 71.4%; Pred. No. 97;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 2 QYNKPLC 8
| | | | |
Db 476 QYKPC 482

RESULT 15
I38755
transcription factor REST (version 2) - human (fragment)
N;Alternate names: neural-restrictive silencer factor; RE1-silencing transcription facto
C;Species: Homo sapiens (man)
C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
C;Accession: I38755
R;Schoenherr, C.J.; Anderson, D.J.
Science 267, 1360-1363, 1995
A;Title: The neuron-restrictive silencer factor (NRSF): a coordinate repressor of multip
A;Reference number: I38754; MUID:95176234; PMID:7871435
A;Accession: I38755
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-681 <RES>
A;Cross-references: UNIPROT:Q12957; EMBL:U13879; NID:g606947; PIDN:AAC50115.1; PID:g6069
C;Genetics:
A;Gene: GDB:REST; NRSP
A;Cross-references: GDB:702138
A;Map position: 4q12-4q12
C;Keywords: transcription regulation

Query Match 64.8%; Score 35; DB 2; Length 681;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QQYNKPLCD 9
: | | | |
Db 469 RQFNCPCVD 477

Search completed: June 28, 2005, 23:32:09
Job time : 12.05 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 04:19:44 ; Search time 116.15 Seconds
(without alignments)
29.797 Million cell updates/sec

Title: US-08-170-344-53
Perfect score: 54
Sequence: 1 QYKNKPLCD 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	15	16	US-10-476-570-37
2	54	100.0	15	16	US-10-476-570-38
3	54	100.0	20	16	US-10-476-570-35
4	54	100.0	20	17	US-10-484-063-8
5	54	100.0	29	16	US-10-476-570-13
6	54	100.0	29	16	US-10-476-570-55
7	54	100.0	29	17	US-10-858-384-8
8	54	100.0	151	14	US-10-177-390-6
9	54	100.0	151	17	US-10-484-063-20
10	54	100.0	151	17	US-10-484-063-27
11	54	100.0	158	17	US-10-858-384-2

12	54	100.0	158	17	US-10-367-057-16
13	54	100.0	171	16	US-10-472-724-2
14	54	100.0	266	9	US-09-367-309A-1
15	54	100.0	273	13	US-10-000-903-4
16	54	100.0	273	17	US-10-899-771-4
17	54	100.0	292	13	US-10-000-903-10
18	54	100.0	292	17	US-10-899-771-10
19	54	100.0	371	13	US-10-000-903-6
20	54	100.0	371	17	US-10-899-771-6
21	54	100.0	390	13	US-10-000-903-14
22	54	100.0	390	17	US-10-899-771-14
23	49	90.7	10	14	US-10-339-313A-654
24	44	81.5	10	14	US-10-161-097-43
25	40	74.1	234	16	US-10-437-963-133006
26	40	74.1	683	16	US-10-437-963-133028
27	39	72.2	15	16	US-10-476-570-36
28	39	72.2	114	15	US-10-424-599-171491
29	39	72.2	212	16	US-10-425-115-299823
30	39	72.2	253	16	US-10-425-115-246016
31	39	72.2	262	15	US-10-425-114-64511
32	39	72.2	448	15	US-10-425-114-72678
33	39	72.2	572	16	US-10-767-701-45294
34	39	72.2	572	16	US-10-425-115-235491
35	39	72.2	576	16	US-10-437-963-150743
36	39	72.2	603	15	US-10-425-114-62427
37	39	72.2	605	15	US-10-425-114-69012
38	38	70.4	65	15	US-10-424-599-184614
39	38	70.4	509	16	US-10-425-115-211981
40	38	70.4	529	16	US-10-425-115-191031
41	38	70.4	555	16	US-10-425-115-191021
42	38	70.4	1656	15	US-10-369-493-1894
43	37	68.5	79	16	US-10-437-963-135294
44	37	68.5	208	10	US-09-954-342-16
45	37	68.5	240	16	US-10-425-115-226921

ALIGNMENTS

RESULT 1

- Sequence 37, Application US/10476570
- Publication No. US20040170644A1
- GENERAL INFORMATION:
- APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
- APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
- APPLICANT: MAILLIERE, Bernard
- APPLICANT: BOURGAULT-VILLADA, Isabelle
- APPLICANT: POUVELLE-MORATILLE, Sandra
- APPLICANT: GUILLET, Jean-Gerard
- TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
- TITLE OF INVENTION: papillomavirus proteins and uses thereof
- FILE REFERENCE: 45636-5071-US
- CURRENT APPLICATION NUMBER: US/10/476,570
- CURRENT FILING DATE: 2003-11-04
- PRIOR APPLICATION NUMBER: PCT/FR02/01533
- PRIOR FILING DATE: 2002-05-03
- PRIOR APPLICATION NUMBER: FR 01 05980
- PRIOR FILING DATE: 2001-05-04
- NUMBER OF SEQ ID NOS: 63
- SOFTWARE: Patentin Ver. 2.1
- SEQ ID NO 37
- LENGTH: 15
- TYPE: PRT
- ORGANISM: artificial sequence
- FEATURE:

OTHER INFORMATION: Description of the artificial sequence: peptide E6 93-107
US-10-476-570-37

Query Match 100.0%; Score 54; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
| | | | |
Db 5 QQYNKPLCD 13

RESULT 2

US-10-476-570-38
; Sequence 38, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 97-111
US-10-476-570-38

Query Match 100.0%; Score 54; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
| | | | |
Db 1 QQYNKPLCD 9

RESULT 3

US-10-476-570-35
; Sequence 35, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 20
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 91-110
US-10-476-570-35

Query Match 100.0%; Score 54; DB 16; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
| | | | |
Db 7 QQYNKPLCD 15

RESULT 4

US-10-484-063-8
; Sequence 8, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-8

Query Match 100.0%; Score 54; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0088;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
| | | | |
Db 1 QQYNKPLCD 9

RESULT 5

US-10-476-570-13
; Sequence 13, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 29
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 91-119
US-10-476-570-13

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Query Match      100.0%; Score 54; DB 16; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
Db 7 QQYNKPLCD 15

RESULT 6
US-10-476-570-55
; Sequence 55, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; FILE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 29
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 80-108
US-10-476-570-55

Query Match      100.0%; Score 54; DB 16; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
Db 18 QQYNKPLCD 26

RESULT 7
US-10-858-384-8
; Sequence 8, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; FILE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
US-10-858-384-8

Query Match      100.0%; Score 54; DB 17; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
Db 18 QQYNKPLCD 26

RESULT 8
US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerps Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; FILE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6

Query Match      100.0%; Score 54; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
Db 90 QQYNKPLCD 98

RESULT 9
US-10-484-063-20
; Sequence 20, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-20

Query Match      100.0%; Score 54; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
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Db          90 QQYNKPLCD 98
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RESULT 10
US-10-484-063-27
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRI, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-484-063-27

Query Match          100.0%; Score 54; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
|||||
Db 90 QQYNKPLCD 98

RESULT 11
US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIDIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match          100.0%; Score 54; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
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Db 97 QQYNKPLCD 105

RESULT 12
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match          100.0%; Score 54; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.068;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
|||||
Db 97 QQYNKPLCD 105

RESULT 13
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match          100.0%; Score 54; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
|||||
Db 102 QQYNKPLCD 110

RESULT 14
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
```

; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES

; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 54; DB 9; Length 266;
Best Local Similarity 100.0%; Pred.No. 0.11; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQYNKPLCD 9
Db 97 QQYNKPLCD 105

RESULT 15

US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4

Query Match 100.0%; Score 54; DB 13; Length 273;
Best Local Similarity 100.0%; Pred.No. 0.12; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQYNKPLCD 9
Db 203 QQYNKPLCD 211

Search completed: June 29, 2005, 05:18:14
Job time : 116.15 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:33:36 ; Search time 17.05 Seconds
(without alignments)
39.404 Million cell updates/sec

Title: US-08-170-344-53

Perfect score: 54

Sequence: 1 QQYNKPLCD 9

Scoring table: BLOSUM62

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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
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5: /cgn2_6/ptodata/1/iaa/PCITUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	20	2	US-08-934-915-45
2	54	100.0	29	4	US-09-980-523A-8
3	54	100.0	158	4	US-09-980-523A-2
4	54	100.0	162	1	US-08-316-239B-3
5	54	100.0	162	1	US-08-316-239B-4
6	54	100.0	172	3	US-08-860-165-12
7	54	100.0	172	3	US-09-359-382-12
8	54	100.0	266	3	US-08-860-165-10
9	54	100.0	266	3	US-09-359-382-10
10	54	100.0	266	4	US-09-367-309A-1
11	54	100.0	273	3	US-09-485-885-4
12	54	100.0	292	3	US-09-485-885-10
13	54	100.0	371	3	US-09-485-885-6
14	54	100.0	390	3	US-09-485-885-14
15	49	90.7	20	2	US-08-934-915-164
16	45	83.3	9	3	US-08-159-339A-233
17	44	81.5	10	4	US-09-574-749B-43
18	38	70.4	227	4	US-09-270-767-40613
19	38	70.4	227	4	US-09-270-767-55829
20	35	64.8	209	1	US-07-621-193A-2
21	35	64.8	209	1	US-08-018-489C-2
22	35	64.8	676	2	US-08-398-590A-40
23	35	64.8	676	3	US-08-894-997-40
24	35	64.8	676	4	US-09-873-155A-40
25	35	64.8	976	3	US-08-894-997-50
26	35	64.8	976	4	US-09-873-155A-50
27	35	64.8	1088	4	US-09-949-016-6644

28	35	64.8	1147	4	US-09-949-016-8616	Sequence 8616, Ap
29	35	64.8	2644	4	US-09-029-047C-2	Sequence 2, Appl
30	34.5	63.9	465	4	US-09-489-039A-10910	Sequence 10910, A
31	34	63.0	148	1	US-08-565-386-8	Sequence 8, Appl
32	34	63.0	502	4	US-09-248-796A-17327	Sequence 17327, A
33	33	61.1	46	4	US-09-270-767-44293	Sequence 44293, A
34	33	61.1	58	4	US-09-270-767-59624	Sequence 59624, A
35	33	61.1	73	4	US-09-270-767-61424	Sequence 61424, A
36	33	61.1	83	4	US-09-270-767-45891	Sequence 45891, A
37	33	61.1	339	3	US-09-120-365-62	Sequence 62, Appl
38	33	61.1	339	3	US-09-120-365-80	Sequence 80, Appl
39	33	61.1	339	3	US-09-515-039-62	Sequence 62, Appl
40	33	61.1	339	3	US-09-515-039-80	Sequence 80, Appl
41	33	61.1	674	4	US-09-252-991A-31500	Sequence 31500, A
42	32	59.3	51	4	US-09-270-767-37773	Sequence 37773, A
43	32	59.3	84	4	US-09-270-767-52990	Sequence 52990, A
44	32	59.3	84	4	US-09-513-999C-7233	Sequence 7233, Ap
45	32	59.3	87	4	US-09-270-767-39610	Sequence 39610, A

ALIGNMENTS

RESULT 1

US-08-934-915-45
; Sequence 45, Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEI-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-934-915-45

Query Match 100.0%; Score 54; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00084;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
| | | | | | | |
Db 6 QQYNKPLCD 14

RESULT 2

US-09-980-523A-8
; Sequence 8, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO81 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-8

Query Match 100.0%; Score 54; DB 4; Length 29;

Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
| | | | | | | |
Db 18 QQYNKPLCD 26

RESULT 3

US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO81 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 54; DB 4; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
| | | | | | | |
Db 97 QQYNKPLCD 105

RESULT 4

US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
US-08-316-239B-3

Query Match 100.0%; Score 54; DB 1; Length 162;

Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
| | | | | | | |
Db 97 QQYNKPLCD 105

RESULT 5

US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer

```
Query Match      100.0%; Score 47; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNK 9
Db 45 TTLEQQYNK 53

RESULT 7
Q919B2 ID Q919B2 PRELIMINARY; PRT; 99 AA.
AC Q919B2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404704; AAL01363.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 99
FT NON_TER 99
SQ SEQUENCE 99 AA; 12005 MW; C2B96025EC370E38 CRC64;

Query Match      100.0%; Score 47; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNK 9
Db 62 TTLEQQYNK 70

RESULT 8
Q919B4 ID Q919B4 PRELIMINARY; PRT; 130 AA.
AC Q919B4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404703; AAL01363.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227BEDDC CRC64;

Query Match      100.0%; Score 47; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNK 9
Db 65 TTLEQQYNK 73

RESULT 9
Q919B8 ID Q919B8 PRELIMINARY; PRT; 130 AA.
AC Q919B8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404701; AAL01359.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 130 AA; 15775 MW; 92D3C07BF96B092F CRC64;

Query Match      100.0%; Score 47; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNK 9
Db 65 TTLEQQYNK 73

RESULT 10
Q919C0 ID Q919C0 PRELIMINARY; PRT; 130 AA.
AC Q919C0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404700; AAL01357.1; -
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match      100.0%; Score 47; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 TTLEQQYNK 9
 |||||
 Db 65 TTLEQQYNK 73

RESULT 11
 Q919C2 PRELIMINARY; PRT; 130 AA.
 AC Q919C2
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404699; AAL01355.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON_TER 1
 SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNK 9
 |||||
 Db 65 TTLEQQYNK 73

RESULT 12
 Q919C8 PRELIMINARY; PRT; 130 AA.
 AC Q919C8
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404699; AAL01349.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON_TER 1
 SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNK 9
 |||||
 Db 65 TTLEQQYNK 73

RESULT 13
 Q919D0 PRELIMINARY; PRT; 130 AA.
 AC Q919D0
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404699; AAL01347.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON_TER 1
 SQ SEQUENCE 130 AA; 15735 MW; 9EFB30EDCA21AF3 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNK 9
 |||||
 Db 65 TTLEQQYNK 73

RESULT 14
 Q919D2 PRELIMINARY; PRT; 138 AA.
 AC Q919D2
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE E6 protein (Fragment).
 OS Human papillomavirus type 16.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.
 OX NCBI_TaxID=10581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21846229; PubMed=11857370;
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
 RT "Sequence variation and physical state of human papillomavirus type 16
 RT cervical cancer isolates from Australia and New Caledonia.";
 RL Int. J. Cancer 97:868-874(2002).
 DR EMBL; AF404699; AAL01345.1; -.
 DR GO; GO:0042025; C:host cell nucleus; IEA.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR Pfam; PF00518; E6; 1.
 FT NON_TER 1
 SQ SEQUENCE 138 AA; 16696 MW; 481E5AE90895FC2 CRC64;

Query Match 100.0%; Score 47; DB 2; Length 138;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNK 9
 |||||
 Db 73 TTLEQQYNK 81

RESULT 15

Q919C4
ID Q919C4 PRELIMINARY; PRT; 143 AA.
AC Q919C4;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
EL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404698; AAL01353.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 143 AA; 17274 MW; 5FB0F7E1EC6DBA82 CRC64;
Query Match 100.0%; Score 47; DB 2; Length 143;
Best Local Similarity 100.0%; Pred.No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTLEQQYNK 9
Db 78 TTLEQQYNK 86

Search completed: June 28, 2005, 23:28:12
Job time : 56.1 secs

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A:Experimental source: isolate FCBR

Query Match 72.3%; Score 34; DB 2; Length 407;
Best Local Similarity 66.7%; Pred. No. 56;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTLEQQYNK 9
| : : : : :
Db 249 TEIEQYNK 257

RESULT 8

T10487

glutamate dehydrogenase (NADP) (EC 1.4.1.4) - Prevotella ruminicola
C:Species: Prevotella ruminicola

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T10487

R:Wen, Z.T.; Morrison, M.

submitted to the EMBL Data Library, December 1996

A:Reference number: Z17049

A:Accession: T10487

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-444 <WEN>

A:Cross-references: UNIPROT:P95544; EMBL:U82240; NID:gl1772844; PID:gl1772845

A:Experimental source: strain B14

C:Genetics:

A:Note: gdhA

C:Superfamily: glutamate dehydrogenase (NAD(P)+)

C:Keywords: NADP; oxidoreductase

Query Match 72.3%; Score 34; DB 2; Length 444;
Best Local Similarity 62.5%; Pred. No. 62;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTLEQQYNK 9
| : : : : :
Db 30 TIEEYNK 37

RESULT 9

T27581

hypothetical protein ZC455.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C:Accession: T27581

R:Lightning, J.

submitted to the EMBL Data Library, June 1996

A:Reference number: Z20390

A:Accession: T27581

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-526 <WIL>

A:Cross-references: UNIPROT:Q23333; EMBL:Z75554; PIDN:CAA99954.1; GSPDB:GN00023; CESP:ZC

A:Experimental source: clone ZC455

C:Genetics:

A:Gene: CESP:ZC455.3

A:Map position: 5

A:Introns: 47/3; 123/1; 153/1; 389/3

C:Superfamily: glucuronosyltransferase

Query Match 72.3%; Score 34; DB 2; Length 526;
Best Local Similarity 55.6%; Pred. No. 73;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTLEQQYNK 9
| : : : : :
Db 279 TTLDEEYNK 287

RESULT 10

S69702

hypothetical protein YDR419w - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C:Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 09-Jul-2004

C:Accession: S69702

R:Dietrich, F.S.

submitted to the EMBL Data Library, August 1995

A:Description: The sequence of S. cerevisiae lambda 3641 and cosmids 9461, 9831, and 9410

A:Reference number: S69555

A:Accession: S69702

A:Molecule type: DNA

A:Residues: 1-632 <DIE>

A:Cross-references: UNIPROT:Q04049; EMBL:U33007; NID:g927685; PIDN:AAB64856.1; PID:g92766

C:Genetics:

A:Gene: SGD:RAD30

A:Cross-references: SGD:S0002827; MIPS:YDR419w

A:Map position: 4R

Query Match 72.3%; Score 34; DB 2; Length 632;
Best Local Similarity 85.7%; Pred. No. 89;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 LEQQYNK 9
| : : : : :
Db 430 LEQYNK 436

RESULT 11

C70791

probable ponA' protein - Mycobacterium tuberculosis (strain H37Rv)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C:Accession: C70791

R:Cole, S.T.; Bosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: C70791

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-810 <COL>

A:Cross-references: UNIPROT:O69650; GB:AL022121; GB:AL123456; NID:g3261559; PIDN:CAA18004

A:Experimental source: strain H37Rv

C:Genetics:

A:Gene: ponA'

Query Match 72.3%; Score 34; DB 2; Length 810;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTLEQQYNK 9
| : : : : :
Db 134 STLEQQYVK 142

RESULT 12

AG1733

gp49 (Bacteriophage A118) homolog lin2412 [imported] - Listeria innocua (strain Clip1126;
C:Species: Listeria innocua

C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C:Accession: AG1733

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,

; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat

ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A:Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AG1733

A:Status: preliminary

A:Molecule type: DNA

A;Residues: 1-310 <GLA>
A;Cross-references: UNIPROT:Q928X0; GB:AL592022; PIDN:CAC97639.1; PID:g16414934; GSPDB:C
A;Experimental source: strain Clip11262
C;Genetics:
A;Gene: lin2412

Query Match 70.2%; Score 33; DB 2; Length 310;
Best Local Similarity 85.7%; Pred. No. 67;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LEQQYNK 9
|||||:
Db 246 LEQYKNK 252

RESULT 13
AE1364
protein gp49 [Bacteriophage A118] homolog lmo2317 [imported] - Listeria monocytogenes (E
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE1364
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kref, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative Genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AE1364
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-324 <GLA>
A;Cross-references: UNIPROT:Q8Y4W2; GB:NC_003210; PIDN:CAD00395.1; PID:g16411787; GSPDB:
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo2317

Query Match 70.2%; Score 33; DB 2; Length 324;
Best Local Similarity 85.7%; Pred. No. 70;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LEQQYNK 9
|||||:
Db 260 LEQYKNK 266

RESULT 14
T06825
ketol-acid reductoisomerase (EC 1.1.1.86) - garden pea
C;Species: Pisum sativum (garden pea)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T06825
R;Zhu, X.
submitted to the EMBL Data Library, August 1998
A;Reference number: Z15837
A;Accession: T06825
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-581 <ZHU>
A;Cross-references: UNIPROT:O82043; EMBL:Y17796; PIDN:CAA76854.1
A;Experimental source: cv. G2
C;Genetics:
A;Gene: pgaair
C;Superfamily: plant ketol-acid reductoisomerase; ketol-acid reductoisomerase homology
C;Keywords: isoleucine-valine biosynthesis; isomerase; oxidoreductase
F;113-311/Domain: ketol-acid reductoisomerase homology <KAR>

Query Match 70.2%; Score 33; DB 2; Length 581;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQY 7
|||||:
Db 300 TTLEQQY 306

Search completed: June 28, 2005, 23:32:08
Job time : 12.05 secs

Db 290 TTLEQQY 296
|||||:
RESULT 15
S30145
ketol-acid reductoisomerase (EC 1.1.1.86) precursor - Arabidopsis thaliana
N;Alternate names: acetohydroxy acid isomerase
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S30145; S34040; S36884
R;Curien, G.; Dumas, R.; Douce, R.
Plant Mol. Biol. 21, 717-722, 1993
A;Title: Nucleotide sequence and characterization of a cDNA encoding the acetohydroxy aci
A;Reference number: S30145; MUID:93192533; PMID:8448371
A;Accession: S30145
A;Molecule type: mRNA
A;Residues: 1-591 <CUR>
A;Cross-references: UNIPROT:Q05758; EMBL:X68150
R;Dumas, R.
submitted to the EMBL Data Library, July 1992
A;Reference number: S34040
A;Accession: S34040
A;Molecule type: mRNA
A;Residues: 1-284, 'R', 286-591 <DUM>
A;Cross-references: EMBL:X68150; NID:g288062; PIDN:CAA48253.1; PID:g288063
R;Dumas, R.; Curien, G.; Derose, R.T.; Douce, R.
Biochem. J. 294, 821-828, 1993
A;Title: Branched-chain-amino-acid biosynthesis in plants: molecular cloning and characte
s thaliana (thale cress).
A;Reference number: S36884; MUID:93393563; PMID:8379936
A;Accession: S36884
A;Molecule type: DNA
A;Residues: 1-578, 'A', 580-591 <DU2>
A;Cross-references: EMBL:X69880; NID:g402551; PIDN:CAA49506.1; PID:g402552
C;Genetics:
A;Genome: nuclear
A;Introns: 99/3; 130/3; 152/3; 199/3; 275/3; 315/1; 361/3; 417/3; 469/3
C;Superfamily: plant ketol-acid reductoisomerase; ketol-acid reductoisomerase homology
C;Keywords: chloroplast; isoleucine-valine biosynthesis; isomerase; oxidoreductase
F;1-67/Domain: transit peptide (chloroplast) #status predicted <TNP>
F;68-591/Product: ketol-acid reductoisomerase #status predicted <MAT>
F;123-321/Domain: ketol-acid reductoisomerase homology <KAR>

Query Match 70.2%; Score 33; DB 1; Length 591;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQY 7
|||||:
Db 300 TTLEQQY 306

Search completed: June 28, 2005, 23:32:08
Job time : 12.05 secs

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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:24:19 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-51
Perfect score: 45
Sequence: 1 SLYGTTLEQ 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	90	2 Q80883	Q80883 human papil
2	45	100.0	90	2 Q80884	Q80884 human papil
3	45	100.0	90	2 Q80885	Q80885 human papil
4	45	100.0	99	2 Q819B2	Q819B2 human papil
5	45	100.0	103	2 Q819D6	Q819D6 human papil
6	45	100.0	130	2 Q819B4	Q819B4 human papil
7	45	100.0	130	2 Q819D0	Q819D0 human papil
8	45	100.0	151	2 Q812336	O12336 human papil
9	45	100.0	151	2 Q76TS0	Q76TS0 human papil
10	45	100.0	151	2 Q778I6	Q778I6 human papil
11	45	100.0	151	2 Q778I6	Q778I6 human papil
12	45	100.0	151	2 Q80966	Q80966 human papil
13	45	100.0	151	2 Q89640	Q89640 human papil
14	45	100.0	151	2 Q89708	Q89708 human papil
15	45	100.0	151	2 Q89755	Q89755 human papil
16	45	100.0	151	2 Q8B564	Q8B564 human papil
17	45	100.0	151	2 Q8W8C3	Q8W8C3 human papil
18	45	100.0	151	2 Q8W931	Q8W931 human papil
19	45	100.0	151	2 Q8WMP2	Q8WMP2 human papil
20	45	100.0	151	2 Q8WMP4	Q8WMP4 human papil
21	45	100.0	158	1 V86 HPV16	P03126 human papil
22	45	100.0	158	2 Q8JMU8	Q8JMU8 human papil
23	45	100.0	158	2 Q8QHN0	Q8QHN0 human papil
24	45	100.0	158	2 Q8QHP5	Q8QHP5 human papil
25	45	100.0	158	2 Q8QHT0	Q8QHT0 human papil
26	45	100.0	158	2 Q8QRD6	Q8QRD6 human papil
27	45	100.0	158	2 Q8QRD7	Q8QRD7 human papil
28	45	100.0	158	2 Q8QRD8	Q8QRD8 human papil
29	45	100.0	158	2 Q8QRD9	Q8QRD9 human papil
30	45	100.0	158	2 Q8QRE0	Q8QRE0 human papil
31	45	100.0	158	2 Q8QRE1	Q8QRE1 human papil

32 45 100.0 158 2 Q9QDH3 Q9qdh3 human papil
33 45 100.0 158 2 Q9QDH5 Q9qdh5 human papil
34 45 100.0 158 2 Q9QDH7 Q9qdh7 human papil
35 45 100.0 158 2 Q9QDH9 Q9qdh9 human papil
36 45 100.0 161 2 Q819B1 Q819b1 human papil
37 45 100.0 161 2 Q819C6 Q819c6 human papil
38 45 100.0 161 2 Q819D4 Q819d4 human papil
39 42 93.3 81 2 Q80886 Q80886 human papil
40 42 93.3 84 2 Q80882 Q80882 human papil
41 42 93.3 91 2 Q80887 Q80887 human papil
42 42 93.3 130 2 Q819B8 Q819b8 human papil
43 42 93.3 130 2 Q819C0 Q819c0 human papil
44 42 93.3 130 2 Q819C2 Q819c2 human papil
45 42 93.3 130 2 Q819C8 Q819c8 human papil

ALIGNMENTS

RESULT 1
Q80883 PRELIMINARY; PRT; 90 AA.
AC Q80883;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galuira D.F., Youngusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14512; AAB60566.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90 90
SQ SEQUENCE 90 AA; 10904 MW; 5D3ADF843AD6060B CRC64;
Query Match Similarity 100.0%; Score 45; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.074; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SLYGTTTLEQ 9
| | | | | | | | | |
Db 41 SLYGTTTLEQ 49

RESULT 2
Q80884 PRELIMINARY; PRT; 90 AA.
AC Q80884;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galuira D.F., Youngusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14513; AAB60567.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.

DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 11021 MW; 47F42BBEFAACCC01 CRC64;
Query Match 100.0%; Score 45; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SLYGTTLEQ 9
Db 41 SLYGTTLEQ 49
RESULT 3
Q80885
ID Q80885 PRELIMINARY; PRT; 90 AA.
AC Q80885;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Youngusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14514; AAB60568.2; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 90
SQ SEQUENCE 90 AA; 10964 MW; BC2531643ACBA76C CRC64;
Query Match 100.0%; Score 45; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9
Db 41 SLYGTTLEQ 49
RESULT 4
Q919B2
ID Q919B2 PRELIMINARY; PRT; 99 AA.
AC Q919B2;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404704; AAL01365.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.

DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 99
SQ SEQUENCE 99 AA; 12005 MW; C2B96025EC370E38 CRC64;
Query Match 100.0%; Score 45; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.082;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SLYGTTLEQ 9
Db 58 SLYGTTLEQ 66
RESULT 5
Q919D6
ID Q919D6 PRELIMINARY; PRT; 103 AA.
AC Q919D6;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404692; AAL01342.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 103
SQ SEQUENCE 103 AA; 12422 MW; 6F90CBAF1F25449B CRC64;
Query Match 100.0%; Score 45; DB 2; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.086;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SLYGTTLEQ 9
Db 34 SLYGTTLEQ 42
RESULT 6
Q919B4
ID Q919B4 PRELIMINARY; PRT; 130 AA.
AC Q919B4;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF404703; AAL01363.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1

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SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227EEDDC CRC64;
Query Match 100.0%; Score 45; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9
Db 61 SLYGTTLEQ 69

RESULT 7
Q919D0 PRELIMINARY; PRT; 130 AA.
AC Q919D0;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF040695; AAL01347.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR Pfam; PF00518; E6; 1.
FT NON TER 1
SQ SEQUENCE 130 AA; 15735 MW; 9EFB30EEDCA21AF3 CRC64;

Query Match 100.0%; Score 45; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9
Db 61 SLYGTTLEQ 69

RESULT 8
O12336 PRELIMINARY; PRT; 151 AA.
AC O12336;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
DR EMBL; AF003016; AAB70733.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18206 MW; 51C12A8B149C6D8A CRC64;
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Query Match 100.0%; Score 45; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9
Db 82 SLYGTTLEQ 90

RESULT 9
Q76TS0 PRELIMINARY; PRT; 151 AA.
AC Q76TS0;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States populations characterized by nucleotide sequence analysis of the E6, L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34114; AAA91661.1; -.
DR EMBL; U34125; AAA91672.1; -.
DR EMBL; U34130; AAA91677.1; -.
DR EMBL; U34131; AAA91678.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;

Query Match 100.0%; Score 45; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9
Db 82 SLYGTTLEQ 90

RESULT 10
Q77816 PRELIMINARY; PRT; 151 AA.
AC Q77816;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
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DR EMBL; AJ388056; CAB45104.1; -.
DR EMBL; AJ388061; CAB45114.1; -.
DR EMBL; AJ388065; CAB45124.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18334 MW; FF8F2A2FCEBA6C02 CRC64;

Query Match      100.0%; Score 45; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9
Db 82 SLYGTTLEQ 90

RESULT 11
Q77E16 PRELIMINARY; PRT; 151 AA.
AC Q77E16;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 oncoprotein (E6 protein).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]_
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AF469197; AAO15691.1; -.
DR EMBL; AJ388063; CAB45118.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CF1F CRC64;

Query Match      100.0%; Score 45; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9
Db 82 SLYGTTLEQ 90

RESULT 12
Q80966 PRELIMINARY; PRT; 151 AA.
AC Q80966; O12650; O12651; O12652; O12926; O12927; Q80962;
AC Q80964; Q80965;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]_

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RP SEQUENCE FROM N.A.
RX MEDLINE=97437474; PubMed=9292007;
RA Tonnesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
RA Beth-Giraldo E., Giraldo G.;
RT "Sequence variations and viral genomic state of human papillomavirus
RT type 16 in penile carcinomas from Ugandan patients.";
RL J. Gen. Virol. 78:2199-2208(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Terai M., Ma Z., Burk R.D.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20112892; PubMed=10644829;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
RT "Analysis of human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
RL J. Gen. Virol. 81:317-325(2000).
DR EMBL; AF003014; AAB70731.1; -.
DR EMBL; AF003017; AAB70734.1; -.
DR EMBL; AF472508; AAO15697.1; -.
DR EMBL; AJ388068; CAB45128.1; -.
DR EMBL; AF003013; AAB70730.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18292 MW; 35012A9E01993C35 CRC64;

Query Match      100.0%; Score 45; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9
Db 82 SLYGTTLEQ 90

RESULT 13
Q89640 PRELIMINARY; PRT; 151 AA.
AC Q89640;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A.
RA Ponglikitmongkol M., Vaeteewoottacharn K.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34129; AAA91676.1; -.
DR EMBL; AF469198; AAO15693.1; -.
DR EMBL; U34115; AAA91662.1; -.
DR EMBL; U34120; AAA91667.1; -.
DR EMBL; U34124; AAA91671.1; -.

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DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18348 MW; FE3P2A2FCF0A6CB2 CRC64;

Query Match      100.0%; Score 45; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLYGTTLEQ 9
DB 82 SLYGTTLEQ 90

RESULT 14
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AC Q89708;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34126; AAA91673.1; -.
DR EMBL; U34111; AAA91658.1; -.
DR EMBL; U34121; AAA91668.1; -.
DR EMBL; U34123; AAA91670.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18334 MW; FF8F2A2FCFBA6C02 CRC64;

Query Match      100.0%; Score 45; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLYGTTLEQ 9
DB 82 SLYGTTLEQ 90

Search completed: June 28, 2005, 23:28:11
Job time : 55.1 secs

DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18348 MW; FE3P2A2FCF0A6CB2 CRC64;

Query Match      100.0%; Score 45; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLYGTTLEQ 9
DB 82 SLYGTTLEQ 90

RESULT 15
Q89755 PRELIMINARY; PRT; 151 AA.
AC Q89755;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34128; AAA91675.1; -.
DR EMBL; U34117; AAA91664.1; -.
DR EMBL; U34118; AAA91665.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18304 MW; 0F312A8BDBA6CF1F CRC64;

Query Match      100.0%; Score 45; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLYGTTLEQ 9
DB 82 SLYGTTLEQ 90

RESULT 15
Q89755 PRELIMINARY; PRT; 151 AA.
AC Q89755;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early transforming protein E6.
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96079021; PubMed=7494284;

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RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U34126; AAA91673.1; -.
DR EMBL; U34111; AAA91658.1; -.
DR EMBL; U34121; AAA91668.1; -.
DR EMBL; U34123; AAA91670.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18334 MW; FF8F2A2FCFBA6C02 CRC64;

Query Match      100.0%; Score 45; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLYGTTLEQ 9
DB 82 SLYGTTLEQ 90

Search completed: June 28, 2005, 23:28:11
Job time : 55.1 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:24:19 ; Search time 55.1 Seconds
(without alignments)
83.643 Million cell updates/sec

Title: US-08-170-344-52
Perfect score: 47
Sequence: 1 TTLEQQYNK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	81	2	Q80886 human papil
2	47	100.0	84	2	Q80882 human papil
3	47	100.0	90	2	Q80883 human papil
4	47	100.0	90	2	Q80884 human papil
5	47	100.0	90	2	Q80885 human papil
6	47	100.0	91	2	Q80887 human papil
7	47	100.0	99	2	Q80882 human papil
8	47	100.0	130	2	Q80882 human papil
9	47	100.0	130	2	Q80882 human papil
10	47	100.0	130	2	Q80882 human papil
11	47	100.0	130	2	Q80882 human papil
12	47	100.0	130	2	Q80882 human papil
13	47	100.0	130	2	Q80882 human papil
14	47	100.0	138	2	Q80882 human papil
15	47	100.0	143	2	Q80882 human papil
16	47	100.0	151	2	Q80882 human papil
17	47	100.0	151	2	Q80882 human papil
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22	47	100.0	151	2	Q80882 human papil
23	47	100.0	151	2	Q80882 human papil
24	47	100.0	151	2	Q80882 human papil
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28	47	100.0	151	2	Q80882 human papil
29	47	100.0	151	2	Q80882 human papil
30	47	100.0	151	2	Q80882 human papil
31	47	100.0	151	2	Q80882 human papil

32 47 100.0 151 2 Q8BB19 human papil
33 47 100.0 151 2 Q8BB20 human papil
34 47 100.0 151 2 Q8BB21 human papil
35 47 100.0 151 2 Q8W8C3 human papil
36 47 100.0 151 2 Q8W931 human papil
37 47 100.0 151 2 Q8WMP2 human papil
38 47 100.0 151 2 Q8WMP3 human papil
39 47 100.0 151 2 Q8WMP4 human papil
40 47 100.0 151 2 Q8WMP5 human papil
41 47 100.0 158 1 VE6 HPV16 human papil
42 47 100.0 158 2 Q8JMU8 human papil
43 47 100.0 158 2 Q8QHN0 human papil
44 47 100.0 158 2 Q8QHP5 human papil
45 47 100.0 158 2 Q8QHT0 human papil

ALIGNMENTS

RESULT 1
Q80886 PRELIMINARY; PRT; 81 AA.
AC Q80886;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OK NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBSJ databases.
DR EMBL; U14515; AAB60569.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
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DR Pfam; PF00518; E6; 1.
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Qy 1 TTLEQQYNK 9
Db 45 TTLEQQYNK 53
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DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OK NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBSJ databases.
DR EMBL; U14511; AAB60565.2; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.

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DR GO:0003677; F:DNA binding; IEA.
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DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 84
SQ SEQUENCE 84 AA; 10177 MW; 5AB6B896468E1CAA CRC64;
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Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 42 TTLEQQYNNK 50

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DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14512; AAB60566.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
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Query Match 100.0%; Score 47; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNNK 9
Db 45 TTLEQQYNNK 53

RESULT 4
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AC Q80884;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14513; AAB60567.2; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.

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FT NON_TER 1
FT NON_TER 90
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Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNNK 9
Db 45 TTLEQQYNNK 53

RESULT 5
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AC Q80885;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14514; AAB60568.2; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
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SQ SEQUENCE 90 AA; 10964 MW; BC2531643ACBA76C CRC64;
Query Match 100.0%; Score 47; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNNK 9
Db 45 TTLEQQYNNK 53

RESULT 6
Q80887 PRELIMINARY; PRT; 91 AA.
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DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10566;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16; TISSUE=Cervical tissue;
RA Haegert D.G., Galutira D.F., Younghusband B.H.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U14516; AAB60570.1; -.
DR GO:0042025; C:host cell nucleus; IEA.
DR GO:0003677; F:DNA binding; IEA.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
FT NON_TER 91
SQ SEQUENCE 91 AA; 11136 MW; 22PDF3EA185ACBA7 CRC64;

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NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jagtiani & Associates
STREET: 6126 Rocky Way Court
CITY: Centreville
STATE: VA
COUNTRY: USA
ZIP: 20120-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jagtiani, Ajay A.
REGISTRATION NUMBER: 35,205
REFERENCE/DOCKET NUMBER: UNME-0001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 817-9453
TELEFAX: (703) 803-9387
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 100.0%; Score 54; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.0079; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 QQYNKPLCD 9
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DB 97 QQYNKPLCD 105

RESULT 6
US-08-860-165-12
; Sequence 12, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12

Query Match 100.0%; Score 54; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.0084; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 QQYNKPLCD 9
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DB 35 QQYNKPLCD 43

RESULT 7
US-09-359-382-12
; Sequence 12, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-12

Query Match 100.0%; Score 54; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.0084; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

QY 1 QQYNKPLCD 9
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DB 35 QQYNKPLCD 43

RESULT 8
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 54; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.013; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 QQYNKPLCD 9
| | | | | | | |
Db 97 QQYNKPLCD 105

RESULT 9
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; FILE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; TITLE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 54; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
| | | | | | | |
Db 97 QQYNKPLCD 105

RESULT 10
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 54; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
| | | | | | | |
Db 97 QQYNKPLCD 105

RESULT 11
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match 100.0%; Score 54; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
| | | | | | | |
Db 203 QQYNKPLCD 211

RESULT 12
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10

Query Match 100.0%; Score 54; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
| | | | | | | |
Db 222 QQYNKPLCD 230

RESULT 13
US-09-485-885-6
; Sequence 6, Application US/09485885

```
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6

Query Match      100.0%; Score 54; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
Db 203 QQYNKPLCD 211

RESULT 14
US-09-485-885-14
; Sequence 14; Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-14

Query Match      100.0%; Score 54; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
Db 222 QQYNKPLCD 230

RESULT 15
US-08-934-915-164
; Sequence 164; Application US/08934915
; Patent No. 5932412
; GENERAL INFORMATION:
; APPLICANT: DILLNER, JOAKIM
; APPLICANT: DILLNER, LENA
; APPLICANT: CHENG, HWEE-MING
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
; NUMBER OF SEQUENCES: 193
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MASON & ASSOCIATES, P.A.
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Foutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-164

Query Match      90.7%; Score 49; DB 2; Length 20;
Best Local Similarity 88.9%; Pred. No. 0.0077;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQYNKPLCD 9
Db 6 QQYNKPLCN 14

Search completed: June 28, 2005, 23:37:51
Job time : 17.05 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:28:02 ; Search time 11.05 Seconds
(without alignments)
78.367 Million cell updates/sec

Title: US-08-170-344-52
Perfect score: 47
Sequence: 1 TTLEQQYNK 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	158	1 W6WLHS	protein E6 - human
2	36	76.6	546	2 A69484	hypothetical prote
3	36	76.6	739	2 T21769	hypothetical prote
4	36	76.6	863	2 A12077	ferrichrome iron r
5	36	76.6	2541	2 S11661	taln - mouse
6	34	72.3	276	2 E83900	2-hydroxyhepta-2,4
7	34	72.3	407	2 C45600	glutamate dehydrog
8	34	72.3	444	2 T10487	hypothetical prote
9	34	72.3	526	2 T27581	hypothetical prote
10	34	72.3	632	2 S69702	probable pona' pro
11	34	72.3	810	2 C70791	gp49 (Bacteriophag
12	33	70.2	310	2 AG1733	protein gp49 [Bact
13	33	70.2	324	2 AE1364	ketol-acid reducto
14	33	70.2	581	2 T06825	ketol-acid reducto
15	33	70.2	591	1 S30145	ketol-acid reducto
16	33	70.2	591	2 T45681	ketol-acid reducto
17	33	70.2	595	1 S17180	ketol-acid reducto
18	33	70.2	1173	2 T43527	sp8 protein - f
19	33	70.2	1301	1 A41622	protein-tyrosine-p
20	33	70.2	1390	2 T64237	DNA-directed RNA p
21	33	70.2	1607	2 T32550	hypothetical prote
22	33	70.2	1706	2 T39305	protein kinase - f
23	33	70.2	1727	2 T50073	myosin-like coiled
24	32	68.1	238	2 A12178	hypothetical prote
25	32	68.1	254	2 F84145	transposase (23) B
26	32	68.1	261	2 H84149	transposase (27) B
27	32	68.1	270	2 AB0345	probable phosphate
28	32	68.1	292	2 S15269	post-translocation
29	32	68.1	419	2 T23666	hypothetical prote

30 32 68.1 538 2 H96008 hypothetical prote
31 32 68.1 729 2 H86308 similar to disease
32 32 68.1 803 2 H87197 penicillin binding
33 32 68.1 880 2 AE0179 probable ATPase ch
34 32 68.1 882 2 AE0119 Clp ATPase [import
35 32 68.1 886 2 F3862 penicillin-binding
36 32 68.1 988 1 S35362 protein kinase C (h
37 31 66.0 194 2 T33345 hypothetical prote
38 31 66.0 201 2 F96833 hypothetical prote
39 31 66.0 208 2 H97211 S-adenosylmethioni
40 31 66.0 217 2 H85433 homeodomain protei
41 31 66.0 272 2 E96989 SAM-dependent meth
42 31 66.0 277 2 AF0083 probable aldo/keto
43 31 66.0 359 2 A48073 protein-tyrosine k
44 31 66.0 398 2 E71379 probable tpr prote
45 31 66.0 427 2 AC1425 hypothetical prote

protein E6 - human papillomavirus type 16
C:Species: human papillomavirus type 16
C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C:Accession: A03682; T10427
R:Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
Virology 145, 181-185, 1985
A:Title: Human papillomavirus type 16 DNA sequence.
A:Reference number: A22355; MUID:85246220; PMID:2990099
A:Accession: A03682
A:Molecule type: DNA
A:Residues: 1-158 <SEE>
A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
J.Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level
A:Reference number: 217014; MUID:91162763; PMID:1848319
A:Accession: T10427
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-158 <KSN>
A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
C:Genetics:
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:37-73/Region: zinc finger CCCC motif
F:110-146/Region: zinc finger CCCC motif

ALIGNMENTS

RESULT 1

W6WLHS

protein E6 - human papillomavirus type 16
C:Species: human papillomavirus type 16
C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C:Accession: A03682; T10427

R:Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
Virology 145, 181-185, 1985
A:Title: Human papillomavirus type 16 DNA sequence.
A:Reference number: A22355; MUID:85246220; PMID:2990099
A:Accession: A03682
A:Molecule type: DNA
A:Residues: 1-158 <SEE>
A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
J.Kennedy, I.M.; Haddow, J.K.; Clements, J.B.
J. Virol. 65, 2093-2097, 1991
A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level
A:Reference number: 217014; MUID:91162763; PMID:1848319
A:Accession: T10427
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-158 <KSN>
A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
C:Genetics:
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:37-73/Region: zinc finger CCCC motif
F:110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 47; DB 1; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNK 9
|||
Db 93 TTLEQQYNK 101

RESULT 2

A69484

hypothetical protein AF1874 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: A69484

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson,
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artisch, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: A69484
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-546 <KLE>
A;Cross-references: UNIPROT:Q28405; GB:AE000973; GB:AE000782; NID:g2689296; PIDN:AAB8938
C;Superfamily: Pyrococcus horikoshii probable helicase PH0917

Query Match 76.6%; Score 36; DB 2; Length 546;
Best Local Similarity 77.8%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTLEQQYNNK 9

Db 77 TLEDDQYNNK 85

RESULT 3

T21769

hypothetical protein F35E12.7 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T21769

R;Steward, C.

submitted to the EMBL Data Library, November 1996

A;Reference number: Z19470

A;Accession: T21769

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-739 <WIL>

A;Cross-references: UNIPROT:Q02360; EMBL:Z81527; PIDN:CAB04275.1; GSPDB:GN00023; CESP:F3

A;Experimental source: clone F35E12

C;Genetics:

A;Gene: CESP:F35E12.7

A;Map position: 5

A;Introns: 26/1; 61/3; 92/2; 131/1; 164/3; 240/1; 295/3; 319/2; 428/2; 482/3; 704/3

Query Match

Best Local Similarity 76.6%; Score 36; DB 2; Length 739;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNNK 9

Db 423 TTLDKYNNK 431

RESULT 4

AI2077

ferrichrome iron receptor [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C;Accession: AI2077

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takezawa, M.; Yamada, M.; Yasuda, M.; Tabata, S

DNA Res. 8, 205-213, 2001

A;Title: Complete genomic sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AI2077

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-863 <KUR>

A;Cross-references: UNIPROT:Q8YV06; GB:BA000019; PIDN:BAB73874.1; PID:g17131266; GSPDB:G

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: alr2175

C;Superfamily: ferrichrome-iron receptor 1; tonB-dependent receptor amino-terminal homol

Query Match

Best Local Similarity 76.6%; Score 36; DB 2; Length 863;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TLEQQYNNK 9

Db 408 TLDQYNNK 415

RESULT 5

S11661

talin - mouse

C;Species: Mus musculus (house mouse)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C;Accession: S11661

R;Rees, D.J.G.; Ades, S.E.; Singer, S.J.; Hynes, R.O.

Nature 347, 685-689, 1990

A;Title: Sequence and domain structure of talin.

A;Reference number: S11661; MUID:91015390; PMID:2120593

A;Accession: S11661

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-2541 <REE>

A;Cross-references: UNIPROT:P26039; EMBL:X56123; NID:g54257; PIDN:CAA39588.1; PID:g54258

C;Keywords: cytoskeleton

Query Match

Best Local Similarity 76.6%; Score 36; DB 2; Length 2541;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTLEQQYNNK 9

Db 430 TVLQQYNNR 438

RESULT 6

B83900

2-hydroxyhepta-2,4-diene-1,7-dioate isomerase BH2005 [imported] - Bacillus halodurans (st

C;Species: Bacillus halodurans

C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C;Accession: B83900

R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Saeaki, R.; Masui, N.; Fujii, F.; Hiran

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and s

A;Reference number: A83650; MUID:20512582; PMID:11058132

A;Accession: B83900

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-276 <STO>

A;Cross-references: UNIPROT:Q9KBC3; GB:AF001514; GB:BA000004; NID:g10174613; PIDN:BA8057;

A;Experimental source: strain C-125

C;Genetics:

A;Gene: BH2005

Query Match

Best Local Similarity 72.3%; Score 34; DB 2; Length 276;

Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNNK 9

Db 47 TTLEQYTHR 55

RESULT 7

C45600

asparagine-rich blood stage antigen (clone Pfa35-2) - Plasmodium falciparum (fragment)

C;Species: Plasmodium falciparum

C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: C45600; S27826

R;Nolte, D.; Knapp, B.

Mol. Biochem. Parasitol. 46, 319-321, 1991

A;Title: Partial sequences of three new asparagine-rich blood stage proteins of Plasmodi

A;Reference number: A45600; MUID:92018031; PMID:1922204

A;Accession: C45600

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-407 <NOL>

A;Cross-references: UNIPROT:Q03628; EMBL:M59474; NID:g160101; PID:g552184

A:Molecule type: DNA
A:Residues: 1-148 <TAK>
C:Superfamily: papillomavirus E6 protein

Query Match 80.0%; Score 36; DB 2; Length 148;
Best Local Similarity 77.8%; Pred. No. 4.5;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLYGTTLEQ 9
| | | | |
Db 82 SLYGKTL EE 90

RESULT 8
S36573
E6 protein - human papillomavirus type 52
C:Species: human papillomavirus type 52
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S36573
R:Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36573
A:Molecule type: DNA
A:Residues: 1-148
A:Cross-references: UNIPROT:P36814; EMBL:X74481; NID:G397038; PIDN:CAAS2585.1; PID:G3970
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 80.0%; Score 36; DB 2; Length 148;
Best Local Similarity 77.8%; Pred. No. 4.5;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLYGTTLEQ 9
| | | | |
Db 82 SLYGKTL EE 90

RESULT 9
WSMLR1
E6 protein - rhesus papillomavirus (type 1)
C:Species: rhesus papillomavirus
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: A38503
R:Ostrow, R.S.; LaBresh, K.V.; Faras, A.J.
Virology 181, 424-429, 1991
A:Title: Characterization of the complete RHPV 1 genomic sequence and an integration loc
A:Reference number: A38503; MUID:91135018; PMID:1847267
A:Accession: A38503
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-191 <OST>
A:Cross-references: UNIPROT:P22159; EMBL:M37717
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; transforming protein; zinc finger
F:60-96/Region: zinc finger CCCC motif
F:133-169/Region: zinc finger CCCC motif

Query Match 73.3%; Score 33; DB 1; Length 191;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLYGTTLEQ 9
| | | | |
Db 112 SLYGCTLER 120

RESULT 10
DB2181
GDEF family protein VC1593 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C:Accession: DB2181
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: DB2181
A:Molecule type: DNA
A>Status: preliminary
A:Residues: 1-429 <HEI>
A:Cross-references: UNIPROT:Q9KRP3; GB:AE004236; GB:AE003852; NID:G956095; PIDN:AAF9474;
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1593
A:Map position: 1

Query Match 73.3%; Score 33; DB 2; Length 429;
Best Local Similarity 85.7%; Pred. No. 60;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLYGTTLEQ 7
| | | | |
Db 372 SLYGTTI 378

RESULT 11
E72299
Glutamate synthase-related protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 16-Aug-2004
C:Accession: E72299
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: E72299
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-508 <ARN>
A:Cross-references: UNIPROT:Q9X0E8; GB:AE001766; GB:AE000512; NID:G4981600; PIDN:AAD3613;
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1058
C:Superfamily: Glutamate synthase, large subunit domain 2

Query Match 73.3%; Score 33; DB 2; Length 508;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SLYGTTLEQ 9
| | | | |
Db 412 SKYGTVEE 420

RESULT 12
G02165
human homolog of Drosophila lethal discs large 1 - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C:Accession: G02165
R:Albertsen, H.
submitted to the EMBL Data Library, October 1995
A:Reference number: G09264
A:Accession: G02165
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-585 <ALB>
A:Cross-references: UNIPROT:Q13368; EMBL:U37707; NID:G1022812; PIDN:AAB36964.1; PID:G102;
C:Genetics:
A:Gene: dlgs

F:142-214/Domain: GLGF domain homology <GLG>
 R:386-573/Domain: guanylate kinase homology <GKI>

Query Match 73.3%; Score 33; DB 2; Length 585;
 Best Local Similarity 75.0%; Pred. NO. 84;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLE 8
 Db :|||||: 460 NLYGTSLE 467

RESULT 13

S54489

phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) - yeast (Saccharo
 N/Alternate names: 5-aminimidazole-4-carboxamide ribotide transferase; protein YN856

C/Species: Saccharomyces cerevisiae

C/Date: 08-Jul-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004

C/Accession: S54489

R/Lye, G.; Church, C.M.

submitted to the EMBL Data Library, May 1995

A/Reference number: S54014

A/Accession: S54489

A/Molecule type: DNA

A/Residues: 1-592 <LYE>

A/Cross-references: UNIPROT:P38009; EMBL:Z49273; NID:g809577; PIDN:CAA89269.1; PID:g8095

C/Genetics:

A/Gene: SGD:ADB17; MIPS:YMR120C

A/Cross-references: SGD:S0004727; MIPS:YMR120C

A/Map position: 13R

C/Superfamily: purH bifunctional enzyme

C/Keywords: hydrolase; purine nucleotide biosynthesis; transferase

Query Match 73.3%; Score 33; DB 2; Length 592;
 Best Local Similarity 75.0%; Pred. NO. 85;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LYGTTLQ 9

Db :||| |||||

Db 380 VYGTLEQ 387

RESULT 14

T13952

membrane protein ptch2 - mouse

C/Species: Mus musculus (house mouse)

C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C/Accession: T13952

R/Motoyama, J.; Takabatake, T.; Takeshima, K.; Hui, C.

Nature Genet. 18, 104-106, 1998

A/Title: Ptch2, a second mouse patched gene is co-expressed with Sonic hedgehog.

A/Reference number: Z17830; MUID:98122566; PMID:9462734

A/Accession: T13952

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1182 <MOT>

A/Cross-references: UNIPROT:O35595; EMBL:AB010833; PIDN:BAR24691.1

A/Experimental source: strain BALB/cCrSlc

C/Genetics:

A/Gene: ptch2

C/Superfamily: Drosophila membrane protein patched

C/Keywords: transmembrane protein

Query Match 73.3%; Score 33; DB 2; Length 1182;
 Best Local Similarity 77.8%; Pred. NO. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9

Db :|||||: 700 SLYGATLVQ 708

RESULT 15

T18291

patched protein - zebra fish

C/Species: Brachydanio rerio (zebra fish)

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: T18291

R/Concordet, J.P.; Lewis, K.E.; Moore, J.W.; Goodrich, L.V.; Johnson, R.L.; Scott, M.P.;

Development 122, 2835-2846, 1996

A/Title: Spatial regulation of a zebrafish patched homologue reflects the roles of sonic

A/Reference number: Z18860; MUID:96379744; PMID:8787757

A/Accession: T18291

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-1220 <CON>

A/Cross-references: UNIPROT:Q98864; EMBL:X98883; PIDN:CAA67386.1

C/Genetics:

A/Gene: ptcl

C/Superfamily: Drosophila membrane protein patched

Query Match 73.3%; Score 33; DB 2; Length 1220;
 Best Local Similarity 85.7%; Pred. NO. 1.8e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTTL 7

Db :|||||: 753 SLYGTITM 759

Search completed: June 28, 2005, 23:32:07

Job time : 12.05 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 04:19:44 ; Search time 116.15 Seconds
(without alignments)
29.797 Million cell updates/sec

Title: US-08-170-344-52

Perfect score: 47

Sequence: 1 TTLEQQYNNK 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCT05_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	47	100.0	9	17 US-10-751-845-73	Sequence 73, Appl
2	47	100.0	10	17 US-10-751-845-77	Sequence 77, Appl
3	47	100.0	15	16 US-10-476-570-36	Sequence 36, Appl
4	47	100.0	15	16 US-10-476-570-37	Sequence 37, Appl
5	47	100.0	20	16 US-10-476-570-35	Sequence 35, Appl
6	47	100.0	23	17 US-10-751-845-66	Sequence 66, Appl
7	47	100.0	29	16 US-10-476-570-13	Sequence 13, Appl
8	47	100.0	29	16 US-10-476-570-55	Sequence 55, Appl
9	47	100.0	29	17 US-10-858-384-8	Sequence 8, Appl
10	47	100.0	117	17 US-10-751-845-126	Sequence 126, App
11	47	100.0	151	14 US-10-177-390-6	Sequence 6, Appl

12	47	100.0	151	17	US-10-484-063-20	Sequence 20, Appl
13	47	100.0	151	17	US-10-484-063-27	Sequence 27, Appl
14	47	100.0	158	17	US-10-858-384-2	Sequence 2, Appl
15	47	100.0	158	17	US-10-367-057-16	Sequence 16, Appl
16	47	100.0	171	16	US-10-472-724-2	Sequence 2, Appl
17	47	100.0	236	17	US-10-751-845-157	Sequence 157, App
18	47	100.0	237	17	US-10-751-845-158	Sequence 158, App
19	47	100.0	261	17	US-10-751-845-160	Sequence 160, App
20	47	100.0	266	9	US-09-367-309A-1	Sequence 1, Appl
21	47	100.0	273	13	US-10-000-903-4	Sequence 4, Appl
22	47	100.0	273	13	US-10-899-771-4	Sequence 4, Appl
23	47	100.0	292	13	US-10-000-903-10	Sequence 10, Appl
24	47	100.0	292	17	US-10-899-771-10	Sequence 10, Appl
25	47	100.0	371	13	US-10-000-903-6	Sequence 6, Appl
26	47	100.0	371	13	US-10-899-771-6	Sequence 6, Appl
27	47	100.0	390	13	US-10-000-903-14	Sequence 14, Appl
28	47	100.0	390	17	US-10-899-771-14	Sequence 14, Appl
29	36	76.6	10	17	US-10-751-845-90	Sequence 90, Appl
30	36	76.6	11	16	US-10-432-688A-14	Sequence 14, Appl
31	36	76.6	300	16	US-10-606-038-8	Sequence 8, Appl
32	36	76.6	336	9	US-09-848-294-6	Sequence 6, Appl
33	36	76.6	336	14	US-10-293-231-6	Sequence 6, Appl
34	36	76.6	450	16	US-10-606-038-7	Sequence 7, Appl
35	36	76.6	1024	14	US-10-211-362-41	Sequence 41, Appl
36	36	76.6	1024	14	US-10-211-362-49	Sequence 49, Appl
37	36	76.6	2540	16	US-10-606-038-6	Sequence 6, Appl
38	36	76.6	2541	14	US-10-177-293-470	Sequence 470, App
39	36	76.6	2541	16	US-10-719-993-535	Sequence 535, App
40	36	76.6	2541	16	US-10-719-993-536	Sequence 536, App
41	35	74.5	109	15	US-10-424-599-239661	Sequence 239661, Sequence 239858,
42	35	74.5	127	15	US-10-424-599-239858	Sequence 232289,
43	35	74.5	136	15	US-10-424-599-232289	Sequence 264895,
44	35	74.5	164	15	US-10-424-599-264895	Sequence 265261,
45	35	74.5	187	15	US-10-424-599-265261	

ALIGNMENTS

RESULT 1

US-10-751-845-73
; Sequence 73, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiccz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10751.845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-73

Query Match 100.0%; Score 47; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNNK 9

Db 1 TTLEQQYNNK 9

RESULT 2

US-10-751-845-77
 ; Sequence 77, Application US/10751845
 ; Publication No. US20050100928A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hedley, Mary Lynne
 ; APPLICANT: Urban, Robert G.
 ; APPLICANT: Chicz, Roman M.
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
 ; FILE REFERENCE: 08191-013001
 ; CURRENT APPLICATION NUMBER: US/10/751,845
 ; CURRENT FILING DATE: 2004-01-05
 ; PRIOR APPLICATION NUMBER: US/09/664,225
 ; PRIOR FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: US 60/169,846
 ; PRIOR FILING DATE: 1999-12-09
 ; PRIOR APPLICATION NUMBER: US 60/154,665
 ; PRIOR FILING DATE: 1999-09-16
 ; NUMBER OF SEQ ID NOS: 163
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 77
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Human Papilloma virus
 US-10-751-845-77

Query Match 100.0%; Score 47; DB 17; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNK 9

|||||

Db 2 TTLEQQYNK 10

RESULT 3

US-10-476-570-36
 ; Sequence 36, Application US/10476570
 ; Publication No. US20040170644A1
 ; GENERAL INFORMATION:
 ; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
 ; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
 ; APPLICANT: MAILLIERE, Bernard
 ; APPLICANT: BOURGAULT-VILLADA, Isabelle
 ; APPLICANT: POUVELLE-MORATILLE, Sandra
 ; APPLICANT: GUILLET, Jean-Gerard
 ; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
 ; FILE REFERENCE: 45636-5071-US
 ; CURRENT APPLICATION NUMBER: US/10/476,570
 ; CURRENT FILING DATE: 2003-11-04
 ; PRIOR APPLICATION NUMBER: PCT/FR02/01533
 ; PRIOR FILING DATE: 2002-05-03
 ; PRIOR APPLICATION NUMBER: FR 01 05980
 ; PRIOR FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 36
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of the artificial sequence: peptide E6 89-103
 US-10-476-570-36

Query Match 100.0%; Score 47; DB 16; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNK 9

|||||

Db 5 TTLEQQYNK 13

RESULT 4

US-10-476-570-37
 ; Sequence 37, Application US/10476570
 ; Publication No. US20040170644A1
 ; GENERAL INFORMATION:
 ; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
 ; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
 ; APPLICANT: MAILLIERE, Bernard
 ; APPLICANT: BOURGAULT-VILLADA, Isabelle
 ; APPLICANT: POUVELLE-MORATILLE, Sandra
 ; APPLICANT: GUILLET, Jean-Gerard
 ; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
 ; FILE REFERENCE: 45636-5071-US
 ; CURRENT APPLICATION NUMBER: US/10/476,570
 ; CURRENT FILING DATE: 2003-11-04
 ; PRIOR APPLICATION NUMBER: PCT/FR02/01533
 ; PRIOR FILING DATE: 2002-05-03
 ; PRIOR APPLICATION NUMBER: FR 01 05980
 ; PRIOR FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 37
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of the artificial sequence: peptide E6 93-107
 US-10-476-570-37

Query Match 100.0%; Score 47; DB 16; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNK 9

|||||

Db 1 TTLEQQYNK 9

RESULT 5

US-10-476-570-35
 ; Sequence 35, Application US/10476570
 ; Publication No. US20040170644A1
 ; GENERAL INFORMATION:
 ; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
 ; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
 ; APPLICANT: MAILLIERE, Bernard
 ; APPLICANT: BOURGAULT-VILLADA, Isabelle
 ; APPLICANT: POUVELLE-MORATILLE, Sandra
 ; APPLICANT: GUILLET, Jean-Gerard
 ; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
 ; FILE REFERENCE: 45636-5071-US
 ; CURRENT APPLICATION NUMBER: US/10/476,570
 ; CURRENT FILING DATE: 2003-11-04
 ; PRIOR APPLICATION NUMBER: PCT/FR02/01533
 ; PRIOR FILING DATE: 2002-05-03
 ; PRIOR APPLICATION NUMBER: FR 01 05980
 ; PRIOR FILING DATE: 2001-05-04
 ; NUMBER OF SEQ ID NOS: 63
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 35
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of the artificial sequence: peptide E6 91-110
 US-10-476-570-35

Query Match

Best Local Similarity 100.0%; Score 47; DB 16; Length 20;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTLEQQYNK 9
Db 3 TTLEQQYNK 11

RESULT 6
US-10-751-845-66
; Sequence 66, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-66

Query Match 100.0%; Score 47; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTLEQQYNK 9
Db 15 TTLEQQYNK 23

RESULT 7
US-10-476-570-13
; Sequence 13, Application US/10476570
; Publication No. US2004017064A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 29
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 91-119
US-10-476-570-13

Query Match 100.0%; Score 47; DB 16; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTLEQQYNK 9
Db 15 TTLEQQYNK 23

RESULT 8
US-10-476-570-55
; Sequence 55, Application US/10476570
; Publication No. US2004017064A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 29
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 80-108
US-10-476-570-55

Query Match 100.0%; Score 47; DB 16; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTLEQQYNK 9
Db 3 TTLEQQYNK 11

RESULT 9
US-10-858-384-8
; Sequence 8, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
```

; OTHER INFORMATION: for E6 of HPV
US-10-858-384-8

Query Match 100.0%; Score 47; DB 17; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNK 9
|||
Db 14 TTLEQQYNK 22

RESULT 10

US-10-751-845-126
; Sequence 126, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-126

Query Match 100.0%; Score 47; DB 17; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNK 9
|||
Db 59 TTLEQQYNK 67

RESULT 11

US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerp Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; FILE REFERENCE: Polynucleotides by Electroporation
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6

Query Match 100.0%; Score 47; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNK 9
|||
Db 86 TTLEQQYNK 94

RESULT 12

US-10-484-063-20
; Sequence 20, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-20

Query Match 100.0%; Score 47; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNK 9
|||
Db 86 TTLEQQYNK 94

RESULT 13

US-10-484-063-27
; Sequence 27, Application US/10484063
; Publication No. US20050048467A1
; GENERAL INFORMATION:
; APPLICANT: SASTRY, K. JAGANNADHA
; APPLICANT: TORTOLERO-LUNA, GUILLERMO
; APPLICANT: FOLLEN, MICHELE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
; FILE REFERENCE: UTSC:560US
; CURRENT APPLICATION NUMBER: US/10/484,063
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23198
; PRIOR FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 60/306,809
; PRIOR FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-484-063-27

Query Match 100.0%; Score 47; DB 17; Length 151;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNK 9
|||
Db 86 TTLEQQYNK 94

RESULT 14
US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication NO. US20050033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match 100.0%; Score 47; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTLEQQYNK 9
DB 93 TTLEQQYNK 101

RESULT 15
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication NO. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match 100.0%; Score 47; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTLEQQYNK 9
DB 93 TTLEQQYNK 101

Search completed: June 29, 2005, 05:18:14
Job time : 116.15 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:28:02 ; Search time 11.05 Seconds
(without alignments)
78.367 Million cell updates/sec

Title: US-08-170-344-51
Perfect score: 45
Sequence: 1 SLYGTTLEQ 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	100.0	158	1	protein E6 - human
2	39	86.7	149	1	E6 protein - human
3	38	84.4	149	1	E6 protein - human
4	37	82.2	149	1	E6 protein - human
5	37	82.2	151	1	E6 protein - human
6	37	82.2	774	2	neprilysin (BC 3.4
7	36	80.0	148	2	E6 protein - human
8	36	80.0	148	2	E6 protein - human
9	33	73.3	191	1	E6 protein - rhesu
10	33	73.3	429	2	GGDEF family prote
11	33	73.3	508	2	glutamate synthase
12	33	73.3	585	2	human homolog of D
13	33	73.3	592	2	phosphoribosylamin
14	33	73.3	1182	2	membrane protein p
15	33	73.3	1220	2	patched protein -
16	32	71.1	86	2	hypothetical prote
17	32	71.1	149	1	E6 protein - human
18	32	71.1	150	2	E6 protein - human
19	32	71.1	155	1	E6 protein - human
20	32	71.1	155	2	E6 protein - human
21	32	71.1	158	1	E6 protein - human
22	32	71.1	158	2	E6 protein - human
23	32	71.1	255	2	cytochrome-c oxida
24	32	71.1	279	2	S28662
25	32	71.1	345	2	type II site-speci
26	32	71.1	419	2	hypothetical prote
27	32	71.1	419	2	probable outer mem
28	32	71.1	421	2	19S proteasome sub
29	32	71.1	530	2	hypothetical prote

30	32	71.1	533	2	AE2984
31	32	71.1	537	2	B98299
32	32	71.1	624	2	T21072
33	32	71.1	965	2	T21073
34	32	71.1	1237	2	T14633
35	31	68.9	148	2	S36515
36	31	68.9	158	1	W6WL39
37	31	68.9	158	1	W6WLPR
38	31	68.9	184	2	T12457
39	31	68.9	187	2	T09390
40	31	68.9	235	2	H82262
41	31	68.9	240	2	AG2085
42	31	68.9	248	2	E75162
43	31	68.9	251	2	T43928
44	31	68.9	255	2	T42936
45	31	68.9	260	2	C70675

ALIGNMENTS

RESULT 1

W6WLHS

protein E6 - human papillomavirus type 16

C;Species: human papillomavirus type 16

C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004

C;Accession: A03682; T10427

R;Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.

Virology 145, 181-185, 1985

A;Title: Human papillomavirus type 16 DNA sequence.

A;Reference number: A22355; MUID:85246220; PMID:2990099

A;Accession: A03682

A;Molecule type: DNA

A;Residues: 1-158 <SEE>

A;Cross-references: UNIPROT:P03126; GB:K02718; NID:g333031; PIDN:AAA46939.1; PID:g333032

R;Kennedy, I.M.; Haddock, J.K.; Clements, J.B.

J. Virol. 65, 2093-2097, 1991

A;Title: A negative element in the human poapillomavirus type 16 genome acts at the level

A;Reference number: 217014; MUID:91162763; PMID:1848319

A;Accession: T10427

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-158 <KEN>

A;Cross-references: EMBL:K02718; NID:g333031; PIDN:AAA46939.1; PID:g333032

C;Genetics:

C;Gene: E6

C;Superfamily: papillomavirus E6 protein

C;Keywords: DNA binding; early protein; zinc finger

F;37-73/Region: zinc finger CCCC motif

F;110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 45; DB 1; Length 158;

Best Local Similarity 100.0%; Pred. No. 0.063; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0;

Oy 1 SLYGTTLEQ 9

|||||||

Db 89 SLYGTTLEQ 97

RESULT 2

W6WL58

E6 protein - human papillomavirus type 58

C;Species: human papillomavirus type 58

A;Note: host Homo sapiens (man)

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004

C;Accession: E36779

R;Kirii, Y.; Iwamoto, S.; Matsukura, T.

Virology 185, 424-427, 1991

A;Title: Human papillomavirus type 58 DNA sequence.

A;Reference number: A36779; MUID:92024102; PMID:1656594

A;Accession: E36779

A;Status: translation not shown

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A:Molecule type: DNA
A:Residues: 1-149 <K1E>
A:Cross-references: UNIPROT:P26555; GB:D90400; NID:g222386; PIDN:BA31845.1; PID:g333709
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match      86.7%; Score 39; DB 1; Length 149;
Best Local Similarity 88.9%; Pred. No. 1.1;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 SLYGTTLEQ 9
      |||||
Db      82 SLYGTTLEQ 90

RESULT 3
W6WL31
E6 protein - human papillomavirus type 31
C:Species: human papillomavirus type 31
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: A32444
R:Goldeborough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.
Virology 171, 306-311, 1989
A:Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associated
A:Reference number: A94398; MUID:89299478; PMID:2545036
A:Accession: A32444
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-149 <GOL>
A:Cross-references: UNIPROT:P17386; GB:J04353; NID:g333048; PIDN:AAA46950.1; PID:g459916
C:Comment: This protein may be involved in the oncogenic potential of this virus.
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match      84.4%; Score 38; DB 1; Length 149;
Best Local Similarity 77.8%; Pred. No. 1.7;
Matches      7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SLYGTTLEQ 9
      |||||
Db      82 SVYGTLEK 90

RESULT 4
W6WL33
E6 protein - human papillomavirus type 33
C:Species: human papillomavirus type 33
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: A03683
R:Cole, S.T.; Streack, R.E.
J. Virol. 58, 991-995, 1986
A:Title: Genome organization and nucleotide sequence of human papillomavirus type 33, which
A:Reference number: A93020; MUID:86200464; PMID:3009902
A:Accession: A03683
A:Molecule type: DNA
A:Residues: 1-149 <COL>
A:Cross-references: UNIPROT:P06427; GB:M12732; NID:g333049; PIDN:AAA46958.1; PID:g463177
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match      82.2%; Score 37; DB 1; Length 149;
Best Local Similarity 77.8%; Pred. No. 2.8;
Matches      7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 SLYGTTLEQ 9
      |||||

```

```

Db      82 SVYGTLEQ 90

RESULT 5
W6WL51
E6 protein - human papillomavirus type 51
C:Species: human papillomavirus type 51
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: E40415
R:Lungu, O.; Crum, C.P.; Silverstein, S.J.
J. Virol. 65, 4216-4225, 1991
A:Title: Biologic properties and nucleotide sequence analysis of human papillomavirus type
A:Reference number: A40415; MUID:91303675; PMID:1649326
A:Accession: E40415
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-151 <LUN>
A:Cross-references: UNIPROT:P26554; GB:M62877
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match      82.2%; Score 37; DB 1; Length 151;
Best Local Similarity 87.5%; Pred. No. 2.9;
Matches      7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SLYGTTLE 8
      |||||
Db      82 SVYGTLE 89

RESULT 6
JC7265
neprilysin (EC 3.4.24.11) II - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C:Accession: JC7265
R:Tanja, O.; Facchinetti, P.; Rose, C.; Bonhomme, M.C.; Gros, C.; Schwartz, J.C.
Biochem. Biophys. Res. Commun. 271, 565-570, 2000
A:Title: Neprilysin II: A putative novel metalloprotease and its isoforms in CNS and testis
A:Reference number: JC7265
A:Contents: Brain and testis
A:Accession: JC7265
A:Molecule type: mRNA
A:Residues: 1-774 <TAN>
C:Genetics:
A:Gene: nepII
C:Superfamily: neprilysin
C:Keywords: brain; glycoprotein; hydrolase; metalloproteinase; neuropeptide; testis; trypsin

Query Match      82.2%; Score 37; DB 2; Length 774;
Best Local Similarity 66.7%; Pred. No. 16;
Matches      6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SLYGTLEQ 9
      :|||||:
Db      420 ALYGTWEE 428

RESULT 7
A61237
E6 protein - human papillomavirus type 52
C:Species: human papillomavirus type 52
C:Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 03-May-1996
C:Accession: A61237
R:Takami, Y.; Kondoh, G.; Saito, J.; Noda, K.; Sudiro, T.M.; Sjahrurachman, A.; Warsa, U.
Int. J. Cancer 48, 516-522, 1991
A:Title: Cloning and characterization of human papillomavirus type 52 from cervical carcinoma
A:Reference number: A61237; MUID:91258022; PMID:1646174
A:Accession: A61237
A:Status: preliminary

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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:33:36 ; Search time 17.05 Seconds
(without alignments)
39.404 Million cell updates/sec

Title: US-08-170-344-52

Perfect score: 47

Sequence: 1 TTLEQQYNNK 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/ECTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	9	US-08-159-339A-78	Sequence 78, Appl
2	47	100.0	10	US-08-159-339A-77	Sequence 77, Appl
3	47	100.0	20	US-08-934-915-45	Sequence 45, Appl
4	47	100.0	20	US-08-934-915-164	Sequence 164, App
5	47	100.0	29	US-09-980-523A-8	Sequence 8, Appli
6	47	100.0	158	US-09-980-523A-2	Sequence 2, Appli
7	47	100.0	162	US-08-316-239B-3	Sequence 3, Appli
8	47	100.0	162	US-08-316-239B-4	Sequence 4, Appli
9	47	100.0	172	US-08-860-165-12	Sequence 12, Appl
10	47	100.0	172	US-09-359-382-12	Sequence 12, Appl
11	47	100.0	266	US-08-860-165-10	Sequence 10, Appl
12	47	100.0	266	US-09-359-382-10	Sequence 10, Appl
13	47	100.0	266	US-09-367-309A-1	Sequence 1, Appli
14	47	100.0	273	US-09-485-885-4	Sequence 4, Appli
15	47	100.0	292	US-09-485-885-10	Sequence 10, Appl
16	47	100.0	371	US-09-485-885-6	Sequence 6, Appli
17	47	100.0	390	US-09-485-885-14	Sequence 14, Appl
18	37	78.7	182	US-08-117-083-10	Sequence 10, Appl
19	36	76.6	336	US-09-848-294-6	Sequence 6, Appli
20	36	76.6	1024	US-09-562-737-41	Sequence 41, Appl
21	36	76.6	1024	US-09-562-737-49	Sequence 49, Appl
22	35	74.5	677	US-09-328-352-7826	Sequence 7826, Ap
23	34	72.3	199	US-09-540-236-1962	Sequence 1962, Ap
24	34	72.3	1024	US-09-562-737-42	Sequence 42, Appl
25	34	72.3	1024	US-09-562-737-43	Sequence 43, Appl
26	34	72.3	1024	US-09-562-737-48	Sequence 48, Appl
27	32	68.1	185	US-09-248-796A-16048	Sequence 16048, A

28	68.1	821	4	US-08-311-731A-33	Sequence 33, Appl
29	31	66.0	134	US-09-248-796A-27186	Sequence 27186, A
30	31	66.0	137	US-09-270-767-32262	Sequence 32262, A
31	31	66.0	137	US-09-270-767-47479	Sequence 47479, A
32	31	66.0	661	US-09-575-081B-23	Sequence 23, Appl
33	31	66.0	670	US-09-575-081B-24	Sequence 24, Appl
34	31	66.0	670	US-09-575-081B-26	Sequence 26, Appl
35	31	66.0	684	US-09-248-796A-19794	Sequence 19794, A
36	31	66.0	865	US-09-328-352-7498	Sequence 7498, Ap
37	31	66.0	913	US-09-949-016-7294	Sequence 7294, Ap
38	31	66.0	919	US-09-248-796A-15156	Sequence 15156, A
39	31	66.0	1024	US-09-562-737-44	Sequence 44, Appl
40	31	66.0	1024	US-09-562-737-50	Sequence 50, Appl
41	31	66.0	1031	US-09-914-259-24	Sequence 24, Appl
42	31	66.0	1052	US-08-863-118-1	Sequence 1, Appli
43	31	66.0	1052	US-08-863-118-2	Sequence 2, Appli
44	31	66.0	1052	US-09-377-310-2	Sequence 2, Appli
45	31	66.0	1053	US-08-863-118-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-159-339A-78
; Sequence 78, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-78

Query Match 100.0%; Score 47; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNK 9
| | | | | | | | | |
Db 1 TTLEQQYNK 9

RESULT 2

US-08-159-339A-77

; Sequence 77, Application US/08159339A

; Patent No. 6037135

; GENERAL INFORMATION:

; APPLICANT: Kubo, Ralph T.

; APPLICANT: Grey, Howard M.

; APPLICANT: Sette, Alessandro

; APPLICANT: Celis, Esteban

; TITLE OF INVENTION: HLA Binding peptides and Their

; TITLE OF INVENTION: Uses

; NUMBER OF SEQUENCES: 1254

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/159,339A

; FILING DATE: 29-NOV-1993

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/926,666

; FILING DATE: 07-AUG-1992

; APPLICATION NUMBER: US 08/027,746

; FILING DATE: 05-MAR-1993

; APPLICATION NUMBER: US 08/103,396

; FILING DATE: 06-AUG-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Weber, Ellen Lauver

; REGISTRATION NUMBER: 32,762

; REFERENCE/DOCKET NUMBER: 018623-005030US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; TELEX:

; INFORMATION FOR SEQ ID NO: 77:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-159-339A-77

Query Match 100.0%; Score 47; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0059;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNK 9
| | | | | | | | | |
Db 2 TTLEQQYNK 10

RESULT 3

US-08-934-915-45

; Sequence 45, Application US/08934915

; Patent No. 5932412

; GENERAL INFORMATION:

; APPLICANT: DILLNER, JOAKIM

; APPLICANT: DILLNER, LENA

; APPLICANT: CHENG, HWEE-MING

; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN

; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,

; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,

; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR

; TITLE OF INVENTION: DIAGNOSTIC PURPOSES

; NUMBER OF SEQUENCES: 193

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MASON & ASSOCIATES, P.A.

; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500

; CITY: CLEARWATER

; STATE: FLORIDA

; COUNTRY: U.S.A.

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows 3.0

; SOFTWARE: Microsoft Word 6.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/934,915

; FILING DATE: 22-SEP-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/949,836

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: LOUISE A. Foutch

; REGISTRATION NUMBER: 37,133

; REFERENCE/DOCKET NUMBER: 1946.6

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 813-538-3800

; TELEFAX: 813-538-3820

; TELEX:

; INFORMATION FOR SEQ ID NO: 45:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 20 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-934-915-45

Query Match 100.0%; Score 47; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNK 9
| | | | | | | | | |
Db 2 TTLEQQYNK 10

RESULT 4

US-08-934-915-164

; Sequence 164, Application US/08934915

; Patent No. 5932412

; GENERAL INFORMATION:

; APPLICANT: DILLNER, JOAKIM

; APPLICANT: DILLNER, LENA

; APPLICANT: CHENG, HWEE-MING

; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN

; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,

; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,

; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR

; TITLE OF INVENTION: DIAGNOSTIC PURPOSES

; NUMBER OF SEQUENCES: 193

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MASON & ASSOCIATES, P.A.

; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500

; CITY: CLEARWATER
; STATE: FLORIDA
; COUNTRY: U.S.A.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 3.0
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,915
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/949,836
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: LOUISE A. Poutch
; REGISTRATION NUMBER: 37,133
; REFERENCE/DOCKET NUMBER: 1946.6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 813-538-3800
; TELEFAX: 813-538-3820
; TELEX:
; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-934-915-164

Query Match 100.0%; Score 47; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNK 9
Db 2 TTLEQQYNK 10

RESULT 5
US-09-980-523A-8
; Sequence 8, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGALT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO81 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Human Papillomavirus
; US-09-980-523A-8

Query Match 100.0%; Score 47; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNK 9

Db 14 TTLEQQYNK 22

RESULT 6
US-09-980-523A-2
; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGALT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO81 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
; US-09-980-523A-2

Query Match 100.0%; Score 47; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNK 9
Db 93 TTLEQQYNK 101

RESULT 7
US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 817-9453
TELEFAX: (703) 803-9387
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 100.0%; Score 47; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.11; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 TTLEQQYNK 9
| | | | | | | | | |
Db 93 TTLEQQYNK 101

RESULT 8
US-08-316-239B-4
Sequence 4, Application US/08316239B
Patent No. 5679509
GENERAL INFORMATION:
APPLICANT: Wheeler, Cosette M.
APPLICANT: Farmerter, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
TITLE OF INVENTION: Cervical Cancer
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jagtiani & Associates
STREET: 6126 Rocky Way Court
CITY: Centreville
STATE: VA
COUNTRY: USA
ZIP: 20120-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jagtiani, Ajay A.
REGISTRATION NUMBER: 35,205
REFERENCE/DOCKET NUMBER: UNNE-0001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 817-9453
TELEFAX: (703) 803-9387
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 162 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-316-239B-4

Query Match 100.0%; Score 47; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.11; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 TTLEQQYNK 9
| | | | | | | | | |
Db 93 TTLEQQYNK 101

Db 93 TTLEQQYNK 101

RESULT 9
US-08-860-165-12
Sequence 12, Application US/08860165A
Patent No. 6004557
GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PN0157
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 172
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12

Query Match 100.0%; Score 47; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 TTLEQQYNK 9
| | | | | | | | | |
Db 31 TTLEQQYNK 39

RESULT 10
US-09-359-382-12
Sequence 12, Application US/09359382
Patent No. 6306397
GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 017227/0148
CURRENT APPLICATION NUMBER: US/09/359,382
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: US 08/860,165
EARLIER FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PN0157/94
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 172
TYPE: PRT
ORGANISM: Human papillomavirus type 16
US-09-359-382-12

Query Match 100.0%; Score 47; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Qy 1 TTLEQQYNK 9
| | | | | | | | | |
Db 31 TTLEQQYNK 39

RESULT 11
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; PRIOR FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 47; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNNK 9
Db 93 TTLEQQYNNK 101

RESULT 12
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; PRIOR FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 47; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNNK 9
Db 93 TTLEQQYNNK 101

RESULT 13
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 47; DB 4; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNNK 9
Db 93 TTLEQQYNNK 101

RESULT 14
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match 100.0%; Score 47; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTLEQQYNNK 9
Db 199 TTLEQQYNNK 207

RESULT 15
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:

```
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10

Query Match      100.0%; Score 47; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTLEQQYNK 9
Db      218 TTLEQQYNK 226
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Search completed: June 28, 2005, 23:37:51
Job time : 18.05 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 29, 2005, 04:19:44 ; Search time 116.15 Seconds
(without alignments)
29.797 Million cell updates/sec

Title: US-08-170-344-51

Perfect score: 45

Sequence: 1 SLXTTLEQ 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	45	100.0	15	16	US-10-476-570-34
2	45	100.0	15	16	US-10-476-570-36
3	45	100.0	23	17	US-10-751-845-66
4	45	100.0	29	16	US-10-476-570-55
5	45	100.0	29	17	US-10-858-384-8
6	45	100.0	117	17	US-10-751-845-126
7	45	100.0	158	17	US-10-858-384-2
8	45	100.0	158	17	US-10-367-057-16
9	45	100.0	171	16	US-10-472-724-2
10	45	100.0	236	17	US-10-751-845-157
11	45	100.0	237	17	US-10-751-845-158

12	45	100.0	261	17	US-10-751-845-160	Sequence 160, Appl
13	45	100.0	266	9	US-09-367-309A-1	Sequence 1, Appli
14	45	100.0	273	13	US-10-000-903-4	Sequence 4, Appli
15	45	100.0	273	17	US-10-899-771-4	Sequence 4, Appli
16	45	100.0	292	13	US-10-000-903-10	Sequence 10, Appl
17	45	100.0	292	17	US-10-899-771-10	Sequence 10, Appl
18	45	100.0	371	13	US-10-000-903-6	Sequence 6, Appli
19	45	100.0	371	17	US-10-899-771-6	Sequence 6, Appli
20	45	100.0	390	13	US-10-000-903-14	Sequence 14, Appl
21	45	100.0	390	17	US-10-899-771-14	Sequence 14, Appl
22	42	93.3	151	14	US-10-177-390-6	Sequence 6, Appli
23	42	93.3	151	17	US-10-484-063-20	Sequence 20, Appl
24	42	93.3	151	17	US-10-484-063-27	Sequence 27, Appl
25	41	91.1	10	17	US-10-751-845-90	Sequence 90, Appl
26	37	82.2	20	16	US-10-476-570-35	Sequence 35, Appl
27	37	82.2	29	16	US-10-476-570-13	Sequence 13, Appl
28	37	82.2	95	15	US-10-424-599-201912	Sequence 201912, A
29	37	82.2	212	15	US-10-425-114-68027	Sequence 68027, A
30	37	82.2	320	15	US-10-424-599-201908	Sequence 201908, A
31	37	82.2	389	14	US-10-156-761-11356	Sequence 11356, A
32	36	80.0	426	16	US-10-408-765A-2901	Sequence 2901, Ap
33	36	80.0	501	14	US-10-124-498-2	Sequence 2, Appli
34	36	80.0	501	14	US-10-066-521-2	Sequence 2, Appli
35	36	80.0	765	15	US-10-267-502-257	Sequence 257, App
36	36	80.0	991	16	US-10-794-342-14	Sequence 14, Appl
37	35	77.8	9	17	US-10-751-845-85	Sequence 85, Appl
38	35	77.8	20	16	US-10-476-570-33	Sequence 33, Appl
39	35	77.8	20	16	US-10-476-570-12	Sequence 12, Appl
40	35	77.8	71	16	US-10-425-115-349387	Sequence 349387, A
41	35	77.8	82	16	US-10-425-115-219864	Sequence 219864, A
42	35	77.8	96	16	US-10-425-115-195893	Sequence 195893, A
43	34	75.6	242	17	US-10-732-923-2076	Sequence 2076, Ap
44	34	75.6	242	17	US-10-732-923-2089	Sequence 2089, Ap
45	34	75.6	245	17	US-10-732-923-2126	Sequence 2126, Ap

ALIGNMENTS

RESULT 1

US-10-476-570-34
; Sequence 34, Application US/10476570
; Publication No. US20040170644A1

; GENERAL INFORMATION:

; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE

; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE

; APPLICANT: MAILLERE, Bernard

; APPLICANT: BOURGAULT-VILLADA, Isabelle

; APPLICANT: POUVELLE-MORATILLE, Sandra

; APPLICANT: GUILLET, Jean-Gerard

; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7

; TITLE OF INVENTION: papillomavirus proteins and uses thereof

; FILE REFERENCE: 45636-5071-US

; CURRENT APPLICATION NUMBER: US/10/476,570

; CURRENT FILING DATE: 2003-11-04

; PRIOR APPLICATION NUMBER: PCT/FR02/01533

; PRIOR FILING DATE: 2002-05-03

; PRIOR APPLICATION NUMBER: FR 01 05980

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 34

; LENGTH: 15

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: Description of the artificial sequence: peptide E6 84-98

US-10-476-570-34

Query Match 100.0%; Score 45; DB 16; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.025;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9
|||||||
Db 6 SLYGTTLEQ 14

RESULT 2
US-10-476-570-36
; Sequence 36, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 89-103
US-10-476-570-36

Query Match 100.0%; Score 45; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9
|||||||
Db 1 SLYGTTLEQ 9

RESULT 3
US-10-751-845-66
; Sequence 66, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Human Papilloma virus
US-10-751-845-66

Query Match 100.0%; Score 45; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9
|||||||
Db 11 SLYGTTLEQ 19

RESULT 4
US-10-476-570-55
; Sequence 55, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUVELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 29
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 80-108
US-10-476-570-55

Query Match 100.0%; Score 45; DB 16; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9
|||||||
Db 10 SLYGTTLEQ 18

RESULT 5
US-10-858-384-8
; Sequence 8, Application US/10858384
; Publication No. US2005003025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment
; OTHER INFORMATION: for E6 of HPV
US-10-858-384-8

Query Match 100.0%; Score 45; DB 17; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9
| | | | | | | | |
Db 10 SLYGTTLEQ 18

RESULT 6
US-10-751-845-126
; Sequence 126, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-126

Query Match 100.0%; Score 45; DB 17; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9
| | | | | | | | |
Db 55 SLYGTTLEQ 63

RESULT 7
US-10-858-384-2
; Sequence 2, Application US/10858384
; Publication No. US2005033025A1
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
; TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
; FILE REFERENCE: 0508-1037-1
; CURRENT APPLICATION NUMBER: US/10/858,384
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: FR 9907012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 3.2.
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-10-858-384-2

Query Match 100.0%; Score 45; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9
| | | | | | | | |
Db 89 SLYGTTLEQ 97

RESULT 8
US-10-367-057-16
; Sequence 16, Application US/10367057
; Publication No. US20050100554A1
; GENERAL INFORMATION:
; APPLICANT: Cuthill, Scott;
; APPLICANT: Jackson, Amanda;
; APPLICANT: Lewin, David A.;
; APPLICANT: Ooi, Chean Eng
; TITLE OF INVENTION: Complexes and Methods of Using Same
; FILE REFERENCE: 21402-559
; CURRENT APPLICATION NUMBER: US/10/367,057
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: 60/256,911
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 198
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 16
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-367-057-16

Query Match 100.0%; Score 45; DB 17; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.35;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9
| | | | | | | | |
Db 89 SLYGTTLEQ 97

RESULT 9
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match 100.0%; Score 45; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9
| | | | | | | | |
Db 94 SLYGTTLEQ 102

```
RESULT 10
US-10-751-845-157
; Sequence 157, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-157

Query Match      100.0%; Score 45; DB 17; Length 236;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLYGTTLEQ 9
      |||||
Db      55 SLYGTTLEQ 63

RESULT 11
US-10-751-845-158
; Sequence 158, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-158

Query Match      100.0%; Score 45; DB 17; Length 237;
Best Local Similarity 100.0%; Pred. No. 0.55;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLYGTTLEQ 9
      |||||
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```
Db      56 SLYGTTLEQ 64

RESULT 12
US-10-751-845-160
; Sequence 160, Application US/10751845
; Publication No. US20050100928A1
; GENERAL INFORMATION:
; APPLICANT: Hedley, Mary Lynne
; APPLICANT: Urban, Robert G.
; APPLICANT: Chiciz, Roman M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDE POLYPEPTIDES
; FILE REFERENCE: 08191-013001
; CURRENT APPLICATION NUMBER: US/10/751,845
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US/09/664,225
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: US 60/169,846
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: US 60/154,665
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 163
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 261
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-160

Query Match      100.0%; Score 45; DB 17; Length 261;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLYGTTLEQ 9
      |||||
Db      80 SLYGTTLEQ 88

RESULT 13
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match      100.0%; Score 45; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SLYGTTLEQ 9
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Db      89 SLYGTTLEQ 97

RESULT 14
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Search completed: June 29, 2005, 05:18:14
Job time : 117.15 secs

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US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4

Query Match      100.0%; Score 45; DB 13; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLYGTTLEQ 9
DB 195 SLYGTTLEQ 203

RESULT 15
US-10-899-771-4
; Sequence 4, Application US/10899771
; Publication No. US20050031638A1
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
; TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/10/899,771
; CURRENT FILING DATE: 2004-07-27
; PRIOR APPLICATION NUMBER: US/09/581,976
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilus
; OTHER INFORMATION: influenzae B and B6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-10-899-771-4

Query Match      100.0%; Score 45; DB 17; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SLYGTTLEQ 9
DB 195 SLYGTTLEQ 203
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 28, 2005, 21:33:36 ; Search time 17.05 Seconds
(without alignments)
39.404 Million cell updates/sec

Title: US-08-170-344-51
Perfect score: 45
Sequence: 1 SLXGTLBQ 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA*
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5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	100.0	9	3	US-08-159-339A-230
2	45	100.0	29	4	US-09-980-523A-8
3	45	100.0	158	4	US-09-980-523A-2
4	45	100.0	162	1	US-08-316-239B-3
5	45	100.0	172	3	US-08-860-165-12
6	45	100.0	172	3	US-09-359-382-12
7	45	100.0	182	1	US-08-117-083-10
8	45	100.0	266	3	US-08-860-165-10
9	45	100.0	266	3	US-09-359-382-10
10	45	100.0	266	4	US-09-367-309A-1
11	45	100.0	273	3	US-09-485-885-4
12	45	100.0	292	3	US-09-485-885-10
13	45	100.0	371	3	US-09-485-885-6
14	45	100.0	390	3	US-09-485-885-14
15	42	93.3	162	1	US-08-316-239B-4
16	40	88.9	20	2	US-08-934-915-44
17	40	88.9	20	2	US-08-934-915-163
18	36	80.0	742	4	US-09-704-611-2
19	36	80.0	765	4	US-09-704-611-1
20	35	77.8	9	3	US-08-159-339A-244
21	35	77.8	9	3	US-08-159-339A-563
22	35	77.8	11	3	US-08-159-339A-1171
23	35	77.8	172	3	US-08-860-165-14
24	35	77.8	172	3	US-09-359-382-14
25	34	75.6	403	4	US-09-270-767-46690
26	33	73.3	190	4	US-09-270-767-43726
27	33	73.3	345	4	US-09-107-532A-7021

28	33	73.3	529	3	US-09-500-063-2	Sequence 2, Appli
29	33	73.3	613	4	US-09-949-016-9601	Sequence 9601, Ap
30	33	73.3	619	4	US-09-902-540-14059	Sequence 14059, A
31	33	73.3	1182	3	US-09-293-505-7	Sequence 7, Appli
32	33	73.3	1182	4	US-09-060-939A-7	Sequence 7, Appli
33	33	73.3	1203	3	US-09-207-857-2	Sequence 2, Appli
34	33	73.3	1203	3	US-09-293-505-2	Sequence 2, Appli
35	33	73.3	1203	4	US-09-909-280A-2	Sequence 2, Appli
36	33	73.3	1203	4	US-09-060-939A-2	Sequence 2, Appli
37	32	71.1	9	3	US-08-159-339A-89	Sequence 89, Appli
38	32	71.1	32	1	US-08-466-285-4	Sequence 4, Appli
39	32	71.1	32	3	US-08-164-788-4	Sequence 4, Appli
40	32	71.1	94	4	US-09-270-767-36202	Sequence 36202, A
41	32	71.1	94	4	US-09-270-767-51419	Sequence 51419, A
42	32	71.1	103	4	US-09-902-540-12613	Sequence 12613, A
43	32	71.1	147	4	US-09-270-767-61789	Sequence 61789, A
44	32	71.1	149	4	US-09-540-236-2255	Sequence 2255, Ap
45	32	71.1	158	2	US-08-247-904B-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-08-159-339A-230
; Sequence 230, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; TITLE OF INVENTION: Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 230:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-159-339A-230

Query Match 100.0%; Score 45; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9
| | | | | | | | |
Db 1 SLYGTTLEQ 9

RESULT 2

US-09-980-523A-8

; Sequence 8, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO81 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-8

Query Match 100.0%; Score 45; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9
| | | | | | | | |
Db 10 SLYGTTLEQ 18

RESULT 3

US-09-980-523A-2

; Sequence 2, Application US/09980523A
; Patent No. 6783763
; GENERAL INFORMATION:
; APPLICANT: CHOPPIN, JEANNINE
; APPLICANT: BOURGAULT VILLADA, ISABELLE
; APPLICANT: GUILLET, JEAN-GERARD
; APPLICANT: CONNAN, FRANCINE
; APPLICANT: FERRIES, ESTELLE
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION
; FILE REFERENCE: WO81 AO INS
; CURRENT APPLICATION NUMBER: US/09/980,523A
; CURRENT FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: PCT/FR00/01513
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: FR 99/07012
; PRIOR FILING DATE: 1999-06-03
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 158
; TYPE: PRT

; ORGANISM: Human Papillomavirus
US-09-980-523A-2

Query Match 100.0%; Score 45; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9
| | | | | | | | |
Db 89 SLYGTTLEQ 97

RESULT 4

US-08-316-239B-3
; Sequence 3, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNME-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-3

Query Match 100.0%; Score 45; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9
| | | | | | | | |
Db 89 SLYGTTLEQ 97

RESULT 5

US-08-860-165-12
; Sequence 12, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper

```
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12

Query Match      100.0%; Score 45; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SLYGTTLQ 9
Db      27 SLYGTTLQ 35

RESULT 6
US-09-359-382-12
; Sequence 12, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-12

Query Match      100.0%; Score 45; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SLYGTTLQ 9
Db      27 SLYGTTLQ 35

RESULT 7
US-08-117-083-10
; Sequence 10, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Boursnell, Michael E.
; APPLICANT: Inglis, Stephen C.
; APPLICANT: Munro, Alan J.
```

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; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
; OTHER INFORMATION: /note= "Xaa refers to stop codon in
; OTHER INFORMATION: the open reading frame."
US-08-117-083-10

Query Match      100.0%; Score 45; DB 1; Length 182;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SLYGTTLQ 9
Db      70 SLYGTTLQ 78

RESULT 8
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

Query Match 100.0%; Score 45; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9
| | | | | | | |
Db 89 SLYGTTLEQ 97

RESULT 9

US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

Query Match 100.0%; Score 45; DB 3; Length 266;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9
| | | | | | | |
Db 89 SLYGTTLEQ 97

RESULT 10

US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 45; DB 4; Length 266;

Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9
| | | | | | | |
Db 89 SLYGTTLEQ 97

RESULT 11

US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match 100.0%; Score 45; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9
| | | | | | | |
Db 195 SLYGTTLEQ 203

RESULT 12

US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10

Query Match 100.0%; Score 45; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9
|:|||||
Db 214 SLYGTTLEQ 222

RESULT 13
US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6

Query Match 100.0%; Score 45; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9
|:|||||
Db 195 SLYGTTLEQ 203

RESULT 14
US-09-485-885-14
; Sequence 14, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-14

Query Match 100.0%; Score 45; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SLYGTTLEQ 9
|:|||||
Db 214 SLYGTTLEQ 222

RESULT 15
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Cosette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNWE-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-316-239B-4
Query Match 93.3%; Score 42; DB 1; Length 162;
Best Local Similarity 88.9%; Pred. No. 0.64;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SLYGTTLEQ 9
|:|||||
Db 89 SLYGTTLEQ 97
Search completed: June 28, 2005, 23:37:50
Job time : 17.05 secs

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OM protein - protein search, using sw model

Run on: June 29, 2005, 05:18:25 ; Search time 53.8517 Seconds
(without alignments)
64.268 Million cell updates/sec

Title: US-08-170-344-62

Perfect score: 51

Sequence: 1 KCDSTRLC 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1717557 seqs, 384547976 residues

Total number of hits satisfying chosen parameters: 1717557

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
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- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Match	Length	ID	Description
1	51	100.0	15	16	US-10-476-570-16
2	51	100.0	15	16	US-10-306-541-67
3	51	100.0	15	16	US-10-306-541-93
4	51	100.0	15	16	US-10-306-541-96
5	51	100.0	19	9	US-09-888-721-7
6	51	100.0	19	15	US-10-668-400-9
7	51	100.0	20	15	US-10-432-465-49
8	51	100.0	20	16	US-10-890-526-74
9	51	100.0	98	9	US-09-728-466-1
10	51	100.0	98	9	US-09-820-765-4
11	51	100.0	98	9	US-09-824-017-4
					Sequence 16, Appl
					Sequence 67, Appl
					Sequence 93, Appl
					Sequence 96, Appl
					Sequence 9, Appl
					Sequence 7, Appl
					Sequence 49, Appl
					Sequence 74, Appl
					Sequence 1, Appl
					Sequence 4, Appl

Query Match 100.0%; Score 51; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

12	51	100.0	98	10	US-09-986-118A-4	Sequence 4, Appl
13	51	100.0	98	14	US-10-267-311-8	Sequence 8, Appl
14	51	100.0	98	14	US-10-177-390-8	Sequence 8, Appl
15	51	100.0	98	14	US-10-201-764-19	Sequence 19, Appl
16	51	100.0	98	15	US-10-392-113-29	Sequence 29, Appl
17	51	100.0	98	15	US-10-654-129-4	Sequence 4, Appl
18	51	100.0	98	15	US-10-681-410-19	Sequence 19, Appl
19	51	100.0	98	16	US-10-772-988-3	Sequence 3, Appl
20	51	100.0	98	16	US-10-479-541-5	Sequence 5, Appl
21	51	100.0	98	17	US-10-042-526A-4	Sequence 4, Appl
22	51	100.0	98	17	US-10-657-399-1	Sequence 1, Appl
23	51	100.0	98	17	US-10-858-384-12	Sequence 12, Appl
24	51	100.0	98	17	US-10-484-063-26	Sequence 26, Appl
25	51	100.0	98	17	US-10-343-448-5	Sequence 5, Appl
26	51	100.0	98	17	US-10-679-956-8	Sequence 8, Appl
27	51	100.0	98	17	US-10-367-057-17	Sequence 17, Appl
28	51	100.0	99	15	US-10-115-440-7	Sequence 7, Appl
29	51	100.0	111	16	US-10-472-724-4	Sequence 4, Appl
30	51	100.0	121	14	US-10-267-311-12	Sequence 12, Appl
31	51	100.0	121	17	US-10-679-956-12	Sequence 12, Appl
32	51	100.0	198	14	US-10-267-311-35	Sequence 35, Appl
33	51	100.0	198	17	US-10-679-956-35	Sequence 35, Appl
34	51	100.0	220	13	US-10-000-903-1	Sequence 1, Appl
35	51	100.0	220	13	US-10-000-903-8	Sequence 8, Appl
36	51	100.0	220	17	US-10-899-771-1	Sequence 1, Appl
37	51	100.0	220	17	US-10-899-771-8	Sequence 8, Appl
38	51	100.0	239	13	US-10-000-903-12	Sequence 12, Appl
39	51	100.0	239	17	US-10-899-771-12	Sequence 12, Appl
40	51	100.0	266	9	US-09-367-309A-1	Sequence 1, Appl
41	51	100.0	289	15	US-10-115-440-5	Sequence 5, Appl
42	51	100.0	295	14	US-10-267-311-33	Sequence 33, Appl
43	51	100.0	295	17	US-10-679-956-33	Sequence 33, Appl
44	51	100.0	324	14	US-10-267-311-25	Sequence 25, Appl
45	51	100.0	324	17	US-10-679-956-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1

US-10-476-570-16
; Sequence 16, Application US/10476570
; Publication No. US20040170644A1
; GENERAL INFORMATION:
; APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
; APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
; APPLICANT: MAILLIERE, Bernard
; APPLICANT: BOURGAULT-VILLADA, Isabelle
; APPLICANT: POUELLE-MORATILLE, Sandra
; APPLICANT: GUILLET, Jean-Gerard
; TITLE OF INVENTION: Mixture of peptides derived from B6 and/or E7
; TITLE OF INVENTION: papillomavirus proteins and uses thereof
; FILE REFERENCE: 45636-5071-US
; CURRENT APPLICATION NUMBER: US/10/476,570
; CURRENT FILING DATE: 2003-11-04
; PRIOR APPLICATION NUMBER: PCT/FR02/01533
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: FR 01 05980
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 15
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E7 60-74

US-10-476-570-16

Qy 1 KCDSTLRLC 9
 Db 1 KCDSTLRLC 9

RESULT 2

US-10-306-541-67
 ; Sequence 67, Application US/10306541
 ; Publication No. US20040171081A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mittelman, Abraham
 ; APPLICANT: Kanduc, Darja
 ; TITLE OF INVENTION: Improved Antigens
 ; FILE REFERENCE: 12354/4
 ; CURRENT APPLICATION NUMBER: US/10/306,541
 ; CURRENT FILING DATE: 2003-11-25
 ; PRIOR APPLICATION NUMBER: 60/333,249
 ; PRIOR FILING DATE: 2001-11-23
 ; NUMBER OF SEQ ID NOS: 108
 ; SOFTWARE: WordPerfect 8.0 for Windows
 ; SEQ ID NO 67
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: human papillomavirus
 US-10-306-541-67

Query Match 100.0%; Score 51; DB 16; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.036;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
 Db 2 KCDSTLRLC 10

RESULT 3

US-10-306-541-93
 ; Sequence 93, Application US/10306541
 ; Publication No. US20040171081A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mittelman, Abraham
 ; APPLICANT: Kanduc, Darja
 ; TITLE OF INVENTION: Improved Antigens
 ; FILE REFERENCE: 12354/4
 ; CURRENT APPLICATION NUMBER: US/10/306,541
 ; CURRENT FILING DATE: 2003-11-25
 ; PRIOR APPLICATION NUMBER: 60/333,249
 ; PRIOR FILING DATE: 2001-11-23
 ; NUMBER OF SEQ ID NOS: 108
 ; SOFTWARE: WordPerfect 8.0 for Windows
 ; SEQ ID NO 93
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: human papillomavirus
 US-10-306-541-93

Query Match 100.0%; Score 51; DB 16; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.036;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
 Db 1 KCDSTLRLC 9

RESULT 4

US-10-306-541-96
 ; Sequence 96, Application US/10306541
 ; Publication No. US20040171081A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mittelman, Abraham
 ; APPLICANT: Kanduc, Darja
 ; TITLE OF INVENTION: Improved Antigens

; FILE REFERENCE: 12354/4
 ; CURRENT APPLICATION NUMBER: US/10/306,541
 ; CURRENT FILING DATE: 2003-11-25
 ; PRIOR APPLICATION NUMBER: 60/333,249
 ; PRIOR FILING DATE: 2001-11-23
 ; NUMBER OF SEQ ID NOS: 108
 ; SOFTWARE: WordPerfect 8.0 for Windows
 ; SEQ ID NO 96
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: human papillomavirus
 US-10-306-541-96

Query Match 100.0%; Score 51; DB 16; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.036;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
 Db 7 KCDSTLRLC 15

RESULT 5

US-09-888-721-7
 ; Sequence 7, Application US/09888721
 ; Patent No. US20020132990A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Huston, James S.
 ; APPLICANT: Wils, Pierre
 ; APPLICANT: Zhu, Quan
 ; APPLICANT: Laurent, Olivier
 ; APPLICANT: Marasco, Wayne A.
 ; APPLICANT: Scherman, Daniel
 ; TITLE OF INVENTION: BIOENGINEERED VEHICLES FOR TARGETED NUCLEIC ACID
 ; FILE REFERENCE: 23611-A USA
 ; CURRENT APPLICATION NUMBER: US/09/888,721
 ; CURRENT FILING DATE: 2001-06-25
 ; PRIOR APPLICATION NUMBER: 60/213,653
 ; PRIOR FILING DATE: 2000-06-23
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 7
 ; LENGTH: 19
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus
 US-09-888-721-7

Query Match 100.0%; Score 51; DB 9; Length 19;
 Best Local Similarity 100.0%; Pred. No. 0.045;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KCDSTLRLC 9
 Db 1 KCDSTLRLC 9

RESULT 6

US-10-668-400-9
 ; Sequence 9, Application US/10668400
 ; Publication No. US20040058859A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bay, Sylvie
 ; APPLICANT: Cantacuzene, Daniele
 ; APPLICANT: Leclerc, Claude
 ; APPLICANT: Lo-Man, Richard
 ; TITLE OF INVENTION: MULTIPLE ANTIGEN GLYCOPOLYMER CARBOHYDRATE,
 ; FILE REFERENCE: 102.166A-1
 ; CURRENT APPLICATION NUMBER: US/10/668,400
 ; CURRENT FILING DATE: 2003-09-23
 ; PRIOR APPLICATION NUMBER: US 09/049,847
 ; PRIOR FILING DATE: 1998-03-27